

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 22:59:08; Search time 19949 Seconds  
(without alignments)  
11711.609 Million cell updates/sec

Title: US-09-923-327a-263  
Perfect score: 5711  
Sequence: 1 agctcgtgagacttctgg.....tccccacagccactactga 5711

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0  
Searched: 2889711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:

- 1: gb.ba.\*
- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.on.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
- 12: gb.sy.\*
- 13: gb.un.\*
- 14: gb.vi.\*
- 15: em.ba.\*
- 16: em.fun.\*
- 17: em.hum.\*
- 18: em.in.\*
- 19: em.mu.\*
- 20: em.om.\*
- 21: em.or.\*
- 22: em.ov.\*
- 23: em.pat.\*
- 24: em.ph.\*
- 25: em.pl.\*
- 26: em.ro.\*
- 27: em.sts.\*
- 28: em.un.\*
- 29: em.vi.\*
- 30: em.htg.hum.\*
- 31: em.htg.inv.\*
- 32: em.htg.other.\*
- 33: em.htg.mus.\*
- 34: em.htg.pln.\*
- 35: em.htg.rod.\*
- 36: em.htg.mam.\*
- 37: em.htg.vrt.\*
- 38: em.sv.\*
- 39: em.htgo.hum.\*
- 40: em.htgo.mus.\*
- 41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	5711	100.0	5711	6	AR007333	AR007333 Sequence
2	5711	100.0	5711	6	AR112808	AR112808 Sequence
3	5711	100.0	5711	6	I59546	I59546 Sequence 1
4	5709.4	100.0	5711	6	AR007335	AR007335 Sequence
5	5709.4	100.0	5711	6	AR112809	AR112809 Sequence
6	5701.4	99.8	5711	6	AR007334	AR007334 Sequence
7	5701.4	99.8	5711	6	AR112810	AR112810 Sequence
8	5699.8	99.8	5711	6	AR033056	AR033056 Sequence
9	5699.8	99.8	5711	6	AX659576	AX659576 Sequence
10	5699.8	99.8	5711	9	HSU14680	U14680 Homo sapien
11	5699.8	99.8	5712	6	AR070223	AR070223 Sequence
12	5699.8	99.8	5712	6	AR118507	AR118507 Sequence
13	5699.8	99.8	5712	6	AR125601	AR125601 Sequence
14	5699.8	99.8	5712	6	AR184044	AR184044 Sequence
15	5699.8	99.8	5914	6	AR004673	AR004673 Sequence
16	5699.8	99.8	5914	6	AR008159	AR008159 Sequence
17	5699.8	99.8	5914	6	AR136942	AR136942 Sequence
18	5699.8	99.8	5914	6	BD105583	BD105583 Genes sen
19	5699.8	99.8	5914	6	I76943	I76943 Sequence 1
20	5699.8	99.8	5914	6	I80938	I80938 Sequence 1
21	5699.8	99.8	5914	6	I81034	I81034 Sequence 1
22	5698.2	99.8	5711	6	AR048660	AR048660 Sequence
23	5698.2	99.8	5711	6	AR048666	AR048666 Sequence
24	5698.2	99.8	5711	6	AR278112	AR278112 Sequence
25	5698.2	99.8	5711	6	AR278118	AR278118 Sequence
26	5698.2	99.8	5711	6	I40795	I40795 Sequence 4
27	5698.2	99.8	5711	6	I40801	I40801 Sequence 10
28	5688.8	99.6	5712	6	AR048668	AR048668 Sequence
29	5688.8	99.6	5712	6	AR278120	AR278120 Sequence
30	5688.8	99.6	5712	6	I40803	I40803 Sequence 12
31	5687.8	99.6	5710	6	AR048662	AR048662 Sequence
32	5687.8	99.6	5710	6	AR278114	AR278114 Sequence
33	5687.8	99.6	5710	6	I40797	I40797 Sequence 6
34	5685.8	99.6	5709	6	AR048658	AR048658 Sequence
35	5685.8	99.6	5709	6	AR048663	AR048663 Sequence
36	5685.8	99.6	5709	6	AR048664	AR048664 Sequence
37	5685.8	99.6	5709	6	AR048665	AR048665 Sequence
38	5685.8	99.6	5709	6	AR278110	AR278110 Sequence
39	5685.8	99.6	5709	6	AR278115	AR278115 Sequence
40	5685.8	99.6	5709	6	AR278116	AR278116 Sequence
41	5685.8	99.6	5709	6	AR278117	AR278117 Sequence
42	5685.8	99.6	5709	6	I40793	I40793 Sequence 2
43	5685.8	99.6	5709	6	I40798	I40798 Sequence 7
44	5685.8	99.6	5709	6	I40799	I40799 Sequence 8
45	5685.8	99.6	5709	6	I40800	I40800 Sequence 9

ALIGNMENTS

RESULT 1  
AR007333  
LOCUS AR007333 5711 bp DNA linear PAT 04-DEC-1998  
DEFINITION Sequence 1 from patent US 5750400.  
ACCESSION AR007333  
VERSION AR007333.1 GI:3966817  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 5711)  
AUTHORS Murphy,P.D., Allen,A.C., Alvares,C.P., Critz,B.S., Olson,S.J.,  
Schelter,D.B. and Zeng,B.  
TITLE Coding sequences of the human BRCA1 gene  
JOURNAL Patent: US 5750400-A 1 12-MAY-1998;

FEATURES		Location/Qualifiers	
source		1..5711	
BASE COUNT		1953 a 1099 c 1277 g 1382 t	
ORIGIN		/organism="unknown"	
Query Match		100.0%; Score 5711; DB 6; Length 5711;	
Best Local Similarity		100.0%; Pred. No. 0;	
Matches 5711; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	AGCTCGCTGAGACTTCCTGGACCCCGACACAGGCTGTGGGTTCTCAGATAACTGGGCC	60
Db	1	AGCTCGCTGAGACTTCCTGGACCCCGACACAGGCTGTGGGTTCTCAGATAACTGGGCC	60
Qy	61	CCTGGCTCAGGAGGCTTCACCTCTCTCTGGGTAAAGTTCAATTGGAACAGAAAGAA	120
Db	61	CCTGGCTCAGGAGGCTTCACCTCTCTCTGGGTAAAGTTCAATTGGAACAGAAAGAA	120
Qy	121	TGGATTTATCTGCTTCCGCTTGAAGAAAGTACAAATGTCAATTAATGCTATGCAGAA	180
Db	121	TGGATTTATCTGCTTCCGCTTGAAGAAAGTACAAATGTCAATTAATGCTATGCAGAA	180
Qy	181	TCCTAGAGTCCCATCTGTCTGAGTTGATCAAGAAACCTGTCTCCAAAGTGTGACC	240
Db	181	TCCTAGAGTCCCATCTGTCTGAGTTGATCAAGAAACCTGTCTCCAAAGTGTGACC	240
Qy	241	ACATATTTTGCAATTTTGATGCTGAAACTTCTCAACCAAGAAAGGGCTTCACAGT	300
Db	241	ACATATTTTGCAATTTTGATGCTGAAACTTCTCAACCAAGAAAGGGCTTCACAGT	300
Qy	301	GTCCTTTATGTAAGATGATATAACCAAGAGGAGCTACAGAAAGTACGAGATTTAGTC	360
Db	301	GTCCTTTATGTAAGATGATATAACCAAGAGGAGCTACAGAAAGTACGAGATTTAGTC	360
Qy	361	AACCTGTTGAGAGCTATTGAAATCAATTTGTGCTTTTACGCTTGACAGAGTTGGAGT	420
Db	361	AACCTGTTGAGAGCTATTGAAATCAATTTGTGCTTTTACGCTTGACAGAGTTGGAGT	420
Qy	421	ATGCAACAGCTATAATTTTCAAAAAGGAAATAACTCTCCGTAACATCTAAAGATG	480
Db	421	ATGCAACAGCTATAATTTTCAAAAAGGAAATAACTCTCCGTAACATCTAAAGATG	480
Qy	481	AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCAAAGACTTCTACAGAGTG	540
Db	481	AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCAAAGACTTCTACAGAGTG	540
Qy	541	AACCCGAATCTCTCTGAGAAACCACTCTCAGTGTCCAACTCTCTAACCTTGAA	600
Db	541	AACCCGAATCTCTCTGAGAAACCACTCTCAGTGTCCAACTCTCTAACCTTGAA	600
Qy	601	CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCTCAAGACGCTGTCTACATTG	660
Db	601	CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCTCAAGACGCTGTCTACATTG	660
Qy	661	AATTGGATCTGATCTTCTGAAGATACCGTTTAAAGGCAACTTATTGCAAGTGTGGAG	720
Db	661	AATTGGATCTGATCTTCTGAAGATACCGTTTAAAGGCAACTTATTGCAAGTGTGGAG	720
Qy	721	ATCAGAAATTTTACAATCACCCCTCAAGAAACCGGATGAATCAGTTGGATCTG	780
Db	721	ATCAGAAATTTTACAATCACCCCTCAAGAAACCGGATGAATCAGTTGGATCTG	780
Qy	781	CAAAAAGGCTGTGTGAAATTTTCTGAGACGGATGTAACAAATCTGAACTCATCAAC	840
Db	781	CAAAAAGGCTGTGTGAAATTTTCTGAGACGGATGTAACAAATCTGAACTCATCAAC	840
Qy	841	CCAGTAATATGATTTGAAACCACTGAGAGCGTGCAGCTGAGAGGCATCCAGAAAGT	900
Db	841	CCAGTAATATGATTTGAAACCACTGAGAGCGTGCAGCTGAGAGGCATCCAGAAAGT	900
Qy	901	ATCAGGCTGCTCTGTTTCAACTTGTGATGTGAGCCATGTGGCAAAATCTCATGCCA	960
Db	901	ATCAGGCTGCTCTGTTTCAACTTGTGATGTGAGCCATGTGGCAAAATCTCATGCCA	960

Qy	961	GCTCATTACAGCATGAGAACAGCAGTATTATTACTCTCTAAAGACAGAAATGAATGTAGAAA	1020
Db	961	GCTCATTACAGCATGAGAACAGCAGTATTATTACTCTCTAAAGACAGAAATGAATGTAGAAA	1020
Qy	1021	AGGCTGAATTCGTGTAATAAAGCAACAGCCTGGCTTAGCAAGGAGCAACATACAGAT	1080
Db	1021	AGGCTGAATTCGTGTAATAAAGCAACAGCCTGGCTTAGCAAGGAGCAACATACAGAT	1080
Qy	1081	GGGCTGGAAGTAAGAAACATGTAAATGATAGGGGACTCCAGCAGACAGAAAAAGGTAG	1140
Db	1081	GGGCTGGAAGTAAGAAACATGTAAATGATAGGGGACTCCAGCAGACAGAAAAAGGTAG	1140
Qy	1141	ATCTGAATGCTGATCCCTCTGTGTGAGAAAGAAAGTAAAGCAGAAAACTGCATGCT	1200
Db	1141	ATCTGAATGCTGATCCCTCTGTGTGAGAAAGAAAGTAAAGCAGAAAACTGCATGCT	1200
Qy	1201	CAGAGAAATCCTAGAGATATCTGAAGATGTTCTTGGATAACACATAAGTAGCAGCATTCAGA	1260
Db	1201	CAGAGAAATCCTAGAGATATCTGAAGATGTTCTTGGATAACACATAAGTAGCAGCATTCAGA	1260
Qy	1261	AAGTTAATGATGGTGTTCAGAAAGTGAATGAATGAACTGTTAGTCTCTGATGACTCATGATG	1320
Db	1261	AAGTTAATGATGGTGTTCAGAAAGTGAATGAATGAACTGTTAGTCTCTGATGACTCATGATG	1320
Qy	1321	GGGAGTCTGAATCAAAATGCCAAGTAGCTGATGATTTGGAGCTTAAATGAGGTAGATG	1380
Db	1321	GGGAGTCTGAATCAAAATGCCAAGTAGCTGATGATTTGGAGCTTAAATGAGGTAGATG	1380
Qy	1381	AATATTCCTGTTCTTCAGAGAAATAGACTTACTTGGCCAGTGTCTCTCATGAGGCTTTAA	1440
Db	1381	AATATTCCTGTTCTTCAGAGAAATAGACTTACTTGGCCAGTGTCTCTCATGAGGCTTTAA	1440
Qy	1441	TATGTAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGAGTAATATTGAAGACAAAATAT	1500
Db	1441	TATGTAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGAGTAATATTGAAGACAAAATAT	1500
Qy	1501	TTGGGAAACCTATCCGAGAGAGGAGCCCTCCCAACTTAAAGCCATGTAACCTGAAATC	1560
Db	1501	TTGGGAAACCTATCCGAGAGAGGAGCCCTCCCAACTTAAAGCCATGTAACCTGAAATC	1560
Qy	1561	TAATATTAGGAGCATTTGTTTACTGAGCCACAGATAATACAAAGAGCGTCCCTCACAAATA	1620
Db	1561	TAATATTAGGAGCATTTGTTTACTGAGCCACAGATAATACAAAGAGCGTCCCTCACAAATA	1620
Qy	1621	AATTAAGCGTAAAGAGAGACCTACATCAGGCTTCTCATCTGAGGATTTTATCAAGAAAG	1680
Db	1621	AATTAAGCGTAAAGAGAGACCTACATCAGGCTTCTCATCTGAGGATTTTATCAAGAAAG	1680
Qy	1681	CAGATTTGGCAGTTCAAAAGACTCCTGAAATGATAATCAGGAACTTAACCAACCGGAGC	1740
Db	1681	CAGATTTGGCAGTTCAAAAGACTCCTGAAATGATAATCAGGAACTTAACCAACCGGAGC	1740
Qy	1741	AGAATGGTCAAGTGATCAATATTACTTAATAGTGGTCTCATGAGATAAAACAAAAGGTGATT	1800
Db	1741	AGAATGGTCAAGTGATCAATATTACTTAATAGTGGTCTCATGAGATAAAACAAAAGGTGATT	1800
Qy	1801	CTATTGAGAAATGAGAAAAATCTTAAACCAATAGAACTCATCGAAAAAGAAATCTGCTTTCA	1860
Db	1801	CTATTGAGAAATGAGAAAAATCTTAAACCAATAGAACTCATCGAAAAAGAAATCTGCTTTCA	1860
Qy	1861	AAACGAAAGCTGAACCTATAAGCAGCAGTATAGCAATATGGAACTCGAAATTAATATCC	1920
Db	1861	AAACGAAAGCTGAACCTATAAGCAGCAGTATAGCAATATGGAACTCGAAATTAATATCC	1920
Qy	1921	ACAAATCAAAAGCACCTTAAAGAAATAGGCTGAGGAGGAGTCTTCTACAGGCATATTC	1980
Db	1921	ACAAATCAAAAGCACCTTAAAGAAATAGGCTGAGGAGGAGTCTTCTACAGGCATATTC	1980
Qy	1981	ATGCGCTTGAACTAGTAGTACGTAGAAATCTTAAGCCCACTAATTTGCTACTGAATTCGAA	2040
Db	1981	ATGCGCTTGAACTAGTAGTACGTAGAAATCTTAAGCCCACTAATTTGCTACTGAATTCGAA	2040

Qy	2041	TTGATAGTTGTTCTAGCAGTGAAGAGATAAAGAAAAAAGTACAAACAAATGCCAGTCA	2100
Db	2041	TTGATAGTTGTTCTAGCAGTGAAGAGATAAAGAAAAAAGTACAAACAAATGCCAGTCA	2100
Qy	2101	GGCAGCAGAGAAACCTCAACCTCATGAAGGTAAAGAACCTGCAACCTGGAGCCCAAGAGA	2160
Db	2101	GGCAGCAGAGAAACCTCAACCTCATGAAGGTAAAGAACCTGCAACCTGGAGCCCAAGAGA	2160
Qy	2161	GTAAACAAGCCAAATGAACAGACAAGTAAGAACATGACAGTGATCTTTCCAGAGCTGA	2220
Db	2161	GTAAACAAGCCAAATGAACAGACAAGTAAGAACATGACAGTGATCTTTCCAGAGCTGA	2220
Qy	2221	AGTTAAACAATGACACCTGGTCTTTTACTAGTGTCTAAATACCAAGTGAACCTTAAAGAA	2280
Db	2221	AGTTAAACAATGACACCTGGTCTTTTACTAGTGTCTAAATACCAAGTGAACCTTAAAGAA	2280
Qy	2281	TTGTCAATCTCTAGGCTTCCAGAGAGAGAAAAAGAGAGAACTAGAACACAGTCTAAAGTGT	2340
Db	2281	TTGTCAATCTCTAGGCTTCCAGAGAGAGAAAAAGAGAGAACTAGAACACAGTCTAAAGTGT	2340
Qy	2341	CTAATAATGCTGAAGACCCCAAGATCTCATGTTTAAAGTGGAGAAAGGGTTTTGCCAAACTG	2400
Db	2341	CTAATAATGCTGAAGACCCCAAGATCTCATGTTTAAAGTGGAGAAAGGGTTTTGCCAAACTG	2400
Qy	2401	AAAGATCTGTAGAGTAGCAGTATTTTCACTGGTACCTGGTACTGATATGGCACTCAGG	2460
Db	2401	AAAGATCTGTAGAGTAGCAGTATTTTCACTGGTACCTGGTACTGATATGGCACTCAGG	2460
Qy	2461	AAAGTATCTGTTACTGGAGTTAGCACTCTAGGGAAGGCAAAACAGAACCAATAAAT	2520
Db	2461	AAAGTATCTGTTACTGGAGTTAGCACTCTAGGGAAGGCAAAACAGAACCAATAAAT	2520
Qy	2521	GTGTGAGTCAGTGTGCAGCATTTGAAACCCCAAGGCACTAATTCATGGTTGTTCCAAAG	2580
Db	2521	GTGTGAGTCAGTGTGCAGCATTTGAAACCCCAAGGCACTAATTCATGGTTGTTCCAAAG	2580
Qy	2581	ATAATAGAAATGACACAGAGGCTTTTAAAGTATCCATTGGGACATGAAGTTAACACAGTC	2640
Db	2581	ATAATAGAAATGACACAGAGGCTTTTAAAGTATCCATTGGGACATGAAGTTAACACAGTC	2640
Qy	2641	GGGAAACAAGCATAGAAATGGAAGAGTGAACCTTGATGCTCAGTATTTGAGAGATACAT	2700
Db	2641	GGGAAACAAGCATAGAAATGGAAGAGTGAACCTTGATGCTCAGTATTTGAGAGATACAT	2700
Qy	2701	TCAAGGTTTCAAAGGCCAGTCATTTGCTCTGTTTTCAAATCCAGGAAATGCAGAGAGG	2760
Db	2701	TCAAGGTTTCAAAGGCCAGTCATTTGCTCTGTTTTCAAATCCAGGAAATGCAGAGAGG	2760
Qy	2761	AATGTGCAACATTTCTGCCCCACTCTGGGTCCTTAAAGAAACAAAGTCCAAAAGTCACTT	2820
Db	2761	AATGTGCAACATTTCTGCCCCACTCTGGGTCCTTAAAGAAACAAAGTCCAAAAGTCACTT	2820
Qy	2821	TTGAATGTGAACAAAGGAAGAAATCAAGAAAGATGAGTCTTAATATCAAGCTGTAC	2880
Db	2821	TTGAATGTGAACAAAGGAAGAAATCAAGAAAGATGAGTCTTAATATCAAGCTGTAC	2880
Qy	2881	AGACAGTTTAATATCACTGCAGGCTTCTGCTGGTTGGTCAGAAAGATGAAGCCAGTTGATA	2940
Db	2881	AGACAGTTTAATATCACTGCAGGCTTCTGCTGGTTGGTCAGAAAGATGAAGCCAGTTGATA	2940
Qy	2941	ATGCCAAATGPAGTATCAAGAGGCTCTAGGTTTTGTCTATCATCTCAGTTCCAGAGGCA	3000
Db	2941	ATGCCAAATGPAGTATCAAGAGGCTCTAGGTTTTGTCTATCATCTCAGTTCCAGAGGCA	3000
Qy	3001	ACGAAACTGGACTCATTTACTCCAAATAAACATGACATTTTACAAACCCATATCGTATAC	3060
Db	3001	ACGAAACTGGACTCATTTACTCCAAATAAACATGACATTTTACAAACCCATATCGTATAC	3060
Qy	3061	CACCACCTTTTCCCATCAAGTCATTTGTTAAACTTAAATGTAAGAAAAATCTGCTAGAGG	3120
Db	3061	CACCACCTTTTCCCATCAAGTCATTTGTTAAACTTAAATGTAAGAAAAATCTGCTAGAGG	3120
Qy	3121	AAAACTTTGAGGAACATTTCAATGTCACTGAAAGAGAAATGGGAAATGAGAACATTTCCAA	3180

Db	3121	AAAACTTTGAGGAACATTTCAATGTCACTGAAAGAGAAATGGGAAATGAGAACATTTCCAA	3180
Qy	3181	GTACAGTGAGCACAAATTAGCCGTAAATACATTAGAGAAAAATGTTTTTAAAGGAGCCAGCT	3240
Db	3181	GTACAGTGAGCACAAATTAGCCGTAAATACATTAGAGAAAAATGTTTTTAAAGGAGCCAGCT	3240
Qy	3241	CAAGCAATATAATGAAGTAGGTTTGCACCTAGTACTAATGAAGTGGCTCCAGTATTAATGAAA	3300
Db	3241	CAAGCAATATAATGAAGTAGGTTTGCACCTAGTACTAATGAAGTGGCTCCAGTATTAATGAAA	3300
Qy	3301	TAGGTTCCAGTGATGAAAAATTTCAACAGCAGAACCTAGCTAGBAAACAGAGGGCCAAAATTGA	3360
Db	3301	TAGGTTCCAGTGATGAAAAATTTCAACAGCAGAACCTAGCTAGBAAACAGAGGGCCAAAATTGA	3360
Qy	3361	ATGCTATGCTTAGATTAGGGTTTTGCACCTAGGCTCTATAAAACAAAGTCTTCTCTGAAA	3420
Db	3361	ATGCTATGCTTAGATTAGGGTTTTGCACCTAGGCTCTATAAAACAAAGTCTTCTCTGAAA	3420
Qy	3421	GTAAATGTAAAGCATCTCGAAATAAAAAAGCAAGAAATATGAAGAGTAGTTCAGACTGTGA	3480
Db	3421	GTAAATGTAAAGCATCTCGAAATAAAAAAGCAAGAAATATGAAGAGTAGTTCAGACTGTGA	3480
Qy	3481	ATACAGATTTTCTCTCCATATCTGATTTTCAAGTAACTTAGAACAGCCTATGCGAAGTAGTC	3540
Db	3481	ATACAGATTTTCTCTCCATATCTGATTTTCAAGTAACTTAGAACAGCCTATGCGAAGTAGTC	3540
Qy	3541	ATGCATCTCAGGTTTGTCTTGAGACACCTGATGACCTGTTAGATGATGGTCAAAATAAAGG	3600
Db	3541	ATGCATCTCAGGTTTGTCTTGAGACACCTGATGACCTGTTAGATGATGGTCAAAATAAAGG	3600
Qy	3601	AAGTACTAGTTTTGCTGAAAAATGACATTAAGGAAAGTTCTGCTTTTTAGCAAAAAGCG	3660
Db	3601	AAGTACTAGTTTTGCTGAAAAATGACATTAAGGAAAGTTCTGCTTTTTAGCAAAAAGCG	3660
Qy	3661	TCCAGACAGAGAGCTTTAGCAGGAGTCTAGGCCCTTTTCAACCATACACATTTGGCTCAGG	3720
Db	3661	TCCAGACAGAGAGCTTTAGCAGGAGTCTAGGCCCTTTTCAACCATACACATTTGGCTCAGG	3720
Qy	3721	GTACCCAGAGAGGGCCCAAGAAATTTAGAGTCTCAGAGAGAACTTATCTAGTGAGGATG	3780
Db	3721	GTACCCAGAGAGGGCCCAAGAAATTTAGAGTCTCAGAGAGAACTTATCTAGTGAGGATG	3780
Qy	3781	AAGAGCTTCCCTGCTTCCAAACATCTGTTATTTGGTAAAGTAAACAATACTTCTCAGT	3840
Db	3781	AAGAGCTTCCCTGCTTCCAAACATCTGTTATTTGGTAAAGTAAACAATACTTCTCAGT	3840
Qy	3841	CTACTAGGCATAGCACCCGTTGCTACCGAGTGTCTGTCTAAGAACACAGAGAGAAATTTAT	3900
Db	3841	CTACTAGGCATAGCACCCGTTGCTACCGAGTGTCTGTCTAAGAACACAGAGAGAAATTTAT	3900
Qy	3901	TATCATTTGAAGAAATAGCTTAAATGACCTGCACTAACCCAGGTAATATTGSCAAAGGCATCTC	3960
Db	3901	TATCATTTGAAGAAATAGCTTAAATGACCTGCACTAACCCAGGTAATATTGSCAAAGGCATCTC	3960
Qy	3961	AGGAACATCACTTTAGTGAGGAAACAAAATGTTCTGCTAGCTTGTTTTTTCTTACAGTGCA	4020
Db	3961	AGGAACATCACTTTAGTGAGGAAACAAAATGTTCTGCTAGCTTGTTTTTTCTTACAGTGCA	4020
Qy	4021	GTGAATTTGGAAGACTTGACTGCAAAATACAAACACCCAGGATCCTTTCTTGAATGGTCTT	4080
Db	4021	GTGAATTTGGAAGACTTGACTGCAAAATACAAACACCCAGGATCCTTTCTTGAATGGTCTT	4080
Qy	4081	CCAAACAATAGGCACTCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGACAAAGAAATGG	4140
Db	4081	CCAAACAATAGGCACTCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGACAAAGAAATGG	4140
Qy	4141	TTTCAGATGATGAAGAAAGAGGAGCGGCTTTGGAGAAAAATAAATCAAGAGAGCAAGCA	4200
Db	4141	TTTCAGATGATGAAGAAAGAGGAGCGGCTTTGGAGAAAAATAAATCAAGAGAGCAAGCA	4200
Qy	4201	TGGATTCAAACTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAAACAAAGCTCTCTGAAG	4260
Db	4201	TGGATTCAAACTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAAACAAAGCTCTCTGAAG	4260

Db 4201 TGGATTCAAACTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAACAACAGCGTCTCTGAAG 4260  
Qy 4261 ACTGCTCAGGGCTATCCCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGATACCAATGC 4320  
Db 4261 ACTGCTCAGGGCTATCCCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGATACCAATGC 4320  
Qy 4321 AACATAAAGCTGATTAAGCTCCAGCAGGAAATGGCTGAACTAGAAAGCTGTGTAGAACAGC 4380  
Db 4321 AACATAAAGCTGATTAAGCTCCAGCAGGAAATGGCTGAACTAGAAAGCTGTGTAGAACAGC 4380  
Qy 4381 ATGGAGGACGCTTCTAAACAGTACCTTCCATCATATAAGTGAATCTCTCTGCCCTTGAGG 4440  
Db 4381 ATGGAGGACGCTTCTAAACAGTACCTTCCATCATATAAGTGAATCTCTCTGCCCTTGAGG 4440  
Qy 4441 ACCTGCGAAATCCAGAACAGACATCAGAAAAGCAGTATTAACTTTCAGAAAAGTA 4500  
Db 4441 ACCTGCGAAATCCAGAACAGACATCAGAAAAGCAGTATTAACTTTCAGAAAAGTA 4500  
Qy 4501 GTGAATACCTTATAAGCCAGAAATCCAGAAAGCCCTTCTGCTGACAAAGTTTGAGGTGCTG 4560  
Db 4501 GTGAATACCTTATAAGCCAGAAATCCAGAAAGCCCTTCTGCTGACAAAGTTTGAGGTGCTG 4560  
Qy 4561 CAGATAGTTTACAGATTAATAAAGAAACAGAGGTGAAAGTCAATCCCTTCTAAAT 4620  
Db 4561 CAGATAGTTTACAGATTAATAAAGAAACAGAGGTGAAAGTCAATCCCTTCTAAAT 4620  
Qy 4621 GCCCATCATATAGATGATAGTGTGATGACATGACAGTCTGCTGGAGTCTTCAGAAATAGAA 4680  
Db 4621 GCCCATCATATAGATGATAGTGTGATGACATGACAGTCTGCTGGAGTCTTCAGAAATAGAA 4680  
Qy 4681 ACTACCATCTCAAGAGGAGCTCATTAAGTGTGTGATGAGGAGCAACAGCTGGAAG 4740  
Db 4681 ACTACCATCTCAAGAGGAGCTCATTAAGTGTGTGATGAGGAGCAACAGCTGGAAG 4740  
Qy 4741 AGTCTGGGCCACAGATTTGACGAAACATCTTACTTGCACAAATACATCTCAACCTCTGCANTGA 4800  
Db 4741 AGTCTGGGCCACAGATTTGACGAAACATCTTACTTGCACAAATACATCTCAACCTCTGCANTGA 4800  
Qy 4801 CCCCTTACCTGGAATCTGGAATCAGCTCTTCTCTGATGACCTGATCTGATCTGCTCTG 4860  
Db 4801 CCCCTTACCTGGAATCTGGAATCAGCTCTTCTCTGATGACCTGATCTGATCTGCTCTG 4860  
Qy 4861 AAGCAGAGGCCAGAGTCACTGCTGTGTGCAACATACATCTTCAACCTCTGCANTGA 4920  
Db 4861 AAGCAGAGGCCAGAGTCACTGCTGTGTGCAACATACATCTTCAACCTCTGCANTGA 4920  
Qy 4921 AAGTTCCTCCAAATGAAAGTTGCAAGATCTGCCAGGGTCCAGCTGTCTCATACTACTG 4980  
Db 4921 AAGTTCCTCCAAATGAAAGTTGCAAGATCTGCCAGGGTCCAGCTGTCTCATACTACTG 4980  
Qy 4981 ATACTGCTGGGTATAATGCAATGAAGAAAGTGTGAGCAGGAGAACCCAGAAATGACAG 5040  
Db 4981 ATACTGCTGGGTATAATGCAATGAAGAAAGTGTGAGCAGGAGAACCCAGAAATGACAG 5040  
Qy 5041 CTTCAACAGAAAGGTTCAACAAAGAAATGTCATGTTGCTGCTGCTGCTGCTGCTGCTGCTG 5100  
Db 5041 CTTCAACAGAAAGGTTCAACAAAGAAATGTCATGTTGCTGCTGCTGCTGCTGCTGCTGCTG 5100  
Qy 5101 AATTATGCTGCTGTACAGTTTCCAGAAACACCAATCACTTAACTAACTAACTAACTAACTA 5160  
Db 5101 AATTATGCTGCTGTACAGTTTCCAGAAACACCAATCACTTAACTAACTAACTAACTAACTA 5160  
Qy 5161 CTGAAGAGACTACTCATGTTTGTATGAAGAAACAGATGCTGAGTTTGTGTGTGTAACGGACAC 5220  
Db 5161 CTGAAGAGACTACTCATGTTTGTATGAAGAAACAGATGCTGAGTTTGTGTGTGTAACGGACAC 5220  
Qy 5221 TGAATAATTTTCTAGGAATTCGGGAGGAAATGGGTAGTATGCTTCTGCGGTGACCC 5280  
Db 5221 TGAATAATTTTCTAGGAATTCGGGAGGAAATGGGTAGTATGCTTCTGCGGTGACCC 5280  
Qy 5281 AGTCTATTAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAGAGGAGATGTGG 5340  
Db 5281 AGTCTATTAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAGAGGAGATGTGG 5340

Qy 5341 TCAATGGAAGAAACCAACCAAGTCCAAAGCGAGCAAGAGATCCAGACAGAAAGATCT 5400  
Db 5341 TCAATGGAAGAAACCAACCAAGTCCAAAGCGAGCAAGAGATCCAGACAGAAAGATCT 5400  
Qy 5401 TCAGGGGCTAGAAATCTGTTGCTATGGGCCCTTCAACCAATGCCACAGATCAACTGG 5460  
Db 5401 TCAGGGGCTAGAAATCTGTTGCTATGGGCCCTTCAACCAATGCCACAGATCAACTGG 5460  
Qy 5461 AATGATGATACAGCTGTGTGGTCTTCTGTGTGAAAGAGCTTTCATTCACCTTTG 5520  
Db 5461 AATGATGATACAGCTGTGTGGTCTTCTGTGTGAAAGAGCTTTCATTCACCTTTG 5520  
Qy 5521 GCACAGGTGTCACCCCAATTTGTGGTGTGACGACAGATGCTGACAGAGCAATGGCT 5580  
Db 5521 GCACAGGTGTCACCCCAATTTGTGGTGTGACGACAGATGCTGACAGAGCAATGGCT 5580  
Qy 5581 TCCATGCAATTTGGGCAGATGTGTGGGACCTGTGGTGACCCGAGAGTGGGTGTGGACA 5640  
Db 5581 TCCATGCAATTTGGGCAGATGTGTGGGACCTGTGGTGACCCGAGAGTGGGTGTGGACA 5640  
Qy 5641 GTGTAGCACTTACCACTGAGTGCAGAGCTGACACCTACCTGATACCCAGATCCCCACA 5700  
Db 5641 GTGTAGCACTTACCACTGAGTGCAGAGCTGACACCTACCTGATACCCAGATCCCCACA 5700  
Qy 5701 GCCACTACTGA 5711  
Db 5701 GCCACTACTGA 5711

RESULT 2  
ARL12808  
LOCUS ARL12808 5711 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 1 from patent US 6130322.  
ACCESSION ARL12808  
VERSION ARL12808.1 GI:14092708  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 5711)  
AUTHORS Murphy, P.D., Allen, A.C.P., Alvares, C.P., Critz, B.S., Olson, S.J.,  
Thurber, D. and Zeng, B.  
TITLE Coding sequences of the human BRCAL gene  
JOURNAL Patent: US 6130322-A 1 10-OCT-2000;  
FEATURES Location/Qualifiers  
source 1. 5711  
BASE COUNT 1953 a 1099 c 1277 g 1382 t  
ORIGIN

Query Match 100.0%; Score 5711; DB 6; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTCTCGTGAAGCTTCTGAGACCCGCCACAGAGCTGGGGTTCTCAGATAACTGGCC 60  
Db 1 AGTCTCGTGAAGCTTCTGAGACCCGCCACAGAGCTGGGGTTCTCAGATAACTGGCC 60  
Qy 61 CTTGCGCTCAGAGGCGCTTCAACCTCTGCTCTGGTAAAGTTCAATTTGGAAACAGAAAGAA 120  
Db 61 CTTGCGCTCAGAGGCGCTTCAACCTCTGCTCTGGTAAAGTTCAATTTGGAAACAGAAAGAA 120  
Qy 121 TGAATTTATCTGCTCTTCGGGTGAAAGAGTACAAATGTCATTAATGCTATGTCAGAAAA 180  
Db 121 TGAATTTATCTGCTCTTCGGGTGAAAGAGTACAAATGTCATTAATGCTATGTCAGAAAA 180  
Qy 181 TCTTAGAGTCTCCATCTGTCTGAGTGTATCAAGGAACCTGCTCCACAAAGTGTGACC 240  
Db 181 TCTTAGAGTCTCCATCTGTCTGAGTGTATCAAGGAACCTGCTCCACAAAGTGTGACC 240  
Qy 241 ACATATTTTCAAAATTTTGCATGCTGAAACTTCTCAACCAAGAAAGGCGCTTTCACAGT 300  
Db 241 ACATATTTTCAAAATTTTGCATGCTGAAACTTCTCAACCAAGAAAGGCGCTTTCACAGT 300



Db 241 ACATAATTTTGCATGCTGAAACTTCTCAACGAGAAAGGGCCTTCACAGT 300  
Qy 301 GTCTTTATGTAAGATGATATAACCAAAAGGAGCCTACAAGAAAGTACGAGATTTAGTC 360  
Db 301 GTCTTTATGTAAGATGATATAACCAAAAGGAGCCTACAAGAAAGTACGAGATTTAGTC 360  
Qy 361 AACTTGTGTAAGAGCTATTGAAATCATTTTGTGCTTTTTCAGCTTGACACAGGTTTGGAGT 420  
Db 361 AACTTGTGTAAGAGCTATTGAAATCATTTTGTGCTTTTTCAGCTTGACACAGGTTTGGAGT 420  
Qy 421 ATGCAAAACAGCTATAATTTTCAAAAAAGGAAATAACTCTCTGAAACATCTAAAAAGATG 480  
Db 421 ATGCAAAACAGCTATAATTTTCAAAAAAGGAAATAACTCTCTGAAACATCTAAAAAGATG 480  
Qy 481 AAGTTTCTATCATCCAAAGTAGTGGCTACAGAAACCGTGCCAAAGAGCTTCTACAGAGTG 540  
Db 481 AAGTTTCTATCATCCAAAGTAGTGGCTACAGAAACCGTGCCAAAGAGCTTCTACAGAGTG 540  
Qy 541 AACCAGAAATCCTTCTGTGAGGAAACAGCTCTCAGTGTCCAACCTCTCTAACCTTGGAA 600  
Db 541 AACCAGAAATCCTTCTGTGAGGAAACAGCTCTCAGTGTCCAACCTCTCTAACCTTGGAA 600  
Qy 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCTCAAAAGAGCTCTCTACATTG 660  
Db 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCTCAAAAGAGCTCTCTACATTG 660  
Qy 661 AATTTGGATCTGATTTCTTCTGAAGATACCGTTAATAAGGCAACTTATTGCAAGTGTGGAG 720  
Db 661 AATTTGGATCTGATTTCTTCTGAAGATACCGTTAATAAGGCAACTTATTGCAAGTGTGGAG 720  
Qy 721 ATCAAGAAATGTTTACAAATCAACCTCAAGGAAACGAGGATGAAATCAGTTTGGATTTCTG 780  
Db 721 ATCAAGAAATGTTTACAAATCAACCTCAAGGAAACGAGGATGAAATCAGTTTGGATTTCTG 780  
Qy 781 CAAAAAGGCTGTTGTAATTTCTGAGACGAGTGTAACTAACTGAAATCATCATCAAC 840  
Db 781 CAAAAAGGCTGTTGTAATTTCTGAGACGAGTGTAACTAACTGAAATCATCATCAAC 840  
Qy 841 CCAGTAATAATGATTTGAACCACTGAGAAAGCGTGCACTGAGAGGATCCAGAAAGT 900  
Db 841 CCAGTAATAATGATTTGAACCACTGAGAAAGCGTGCACTGAGAGGATCCAGAAAGT 900  
Qy 901 ATCAGGAGTGTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCAAAATCTCATGCCA 960  
Db 901 ATCAGGAGTGTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCAAAATCTCATGCCA 960  
Qy 961 GCTCATTAACGATGAGAACGACAGTATTACTCACTAAAGACAGATGATGTAGAAA 1020  
Db 961 GCTCATTAACGATGAGAACGACAGTATTACTCACTAAAGACAGATGATGTAGAAA 1020  
Qy 1021 AGGCTGAATCTGTATAAAGCAACAGCCTGGCTTAGCAAGGAGCCAACTAACAGAT 1080  
Db 1021 AGGCTGAATCTGTATAAAGCAACAGCCTGGCTTAGCAAGGAGCCAACTAACAGAT 1080  
Qy 1081 GGGCTGGAAGTAAGGAAACATGTATATAGTGGCGACTCCAGCAAGAAAAAGGTAAG 1140  
Db 1081 GGGCTGGAAGTAAGGAAACATGTATATAGTGGCGACTCCAGCAAGAAAAAGGTAAG 1140  
Qy 1141 ATCTGAATGCTGATCCCTGTGTAGAGAAAGAAATGGAATGGAATGGAATGGAATGGAATG 1200  
Db 1141 ATCTGAATGCTGATCCCTGTGTAGAGAAAGAAATGGAATGGAATGGAATGGAATGGAATG 1200  
Qy 1201 CAGAGAACTCTAGAGATGTAAGATGTTCTTGGATAACACTAAATAGCAGCATTCAGA 1260  
Db 1201 CAGAGAACTCTAGAGATGTAAGATGTTCTTGGATAACACTAAATAGCAGCATTCAGA 1260  
Qy 1261 AAGTTAATGAGTGGTTTTCCAGAAAGTATGAACTGTATTAGTTTCTGATGACTCACATGATG 1320  
Db 1261 AAGTTAATGAGTGGTTTTCCAGAAAGTATGAACTGTATTAGTTTCTGATGACTCACATGATG 1320  
Qy 1321 GGGAGTCTGAATCAAAATCCAAAGTAGCTGATGTTTGGAGCTTCTAAATGAGGTAGATG 1380  
Db 1321 GGGAGTCTGAATCAAAATCCAAAGTAGCTGATGTTTGGAGCTTCTAAATGAGGTAGATG 1380

Qy 1381 AATATTTCTGGTTTCTTACAGAGAAAAATAGACTTTACTTGGCCAGTGATCCTCATGAGGCTTTAA 1440  
Db 1381 AATATTTCTGGTTTCTTACAGAGAAAAATAGACTTTACTTGGCCAGTGATCCTCATGAGGCTTTAA 1440  
Qy 1441 TATGTAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGAGTAATATTGAAGACAAAAATAT 1500  
Db 1441 TATGTAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGAGTAATATTGAAGACAAAAATAT 1500  
Qy 1501 TTGGGAAAACTTATCGGAAGAAAGGCAAGCCTCCCAACTTAAGCCATGTAATCAAAATC 1560  
Db 1501 TTGGGAAAACTTATCGGAAGAAAGGCAAGCCTCCCAACTTAAGCCATGTAATCAAAATC 1560  
Qy 1561 TAAATATAGGAGCAATTTTACTGAGCCACAGATAATAACAAGAGGTCCTCCCTCAAAATA 1620  
Db 1561 TAAATATAGGAGCAATTTTACTGAGCCACAGATAATAACAAGAGGTCCTCCCTCAAAATA 1620  
Qy 1621 AATTAAGAGCGTAAAGAGAGCTACATCAGCCCTTCACTCAGGAGTTTATCAAGAAAG 1680  
Db 1621 AATTAAGAGCGTAAAGAGAGCTACATCAGGAGCTTCACTCAGGAGTTTATCAAGAAAG 1680  
Qy 1681 CAGATTTGGCAGTTCAAAAGAGCTCTGAAATGATAAATCAGGAACTAACCAACGGAGC 1740  
Db 1681 CAGATTTGGCAGTTCAAAAGAGCTCTGAAATGATAAATCAGGAACTAACCAACGGAGC 1740  
Qy 1741 AGAATGTCAGTGAATTAATTAATAGTGTCTAGAGAAATAAACAAGAGTGATTT 1800  
Db 1741 AGAATGTCAGTGAATTAATTAATAGTGTCTAGAGAAATAAACAAGAGTGATTT 1800  
Qy 1801 CTATTTCAAGATGAGAAATCTTAAACCCAAATAGAACTCACTCGAAAGAAATCTGCTTCA 1860  
Db 1801 CTATTTCAAGATGAGAAATCTTAAACCCAAATAGAACTCACTCGAAAGAAATCTGCTTCA 1860  
Qy 1861 AAACGAAAGCTGAACTTATTAAGCAGCAGTATAAGCAATATGCAACTCGAAATTAATATCC 1920  
Db 1861 AAACGAAAGCTGAACTTATTAAGCAGCAGTATAAGCAATATGCAACTCGAAATTAATATCC 1920  
Qy 1921 ACAATTTCAAAAGCCTTAAAGAAATAGGCTGAGGAGGAAGTCTTCTACAGGCAATTC 1980  
Db 1921 ACAATTTCAAAAGCCTTAAAGAAATAGGCTGAGGAGGAAGTCTTCTACAGGCAATTC 1980  
Qy 1981 ATGCGCTTGAATAGTAGTAGTAATACTTAAGCCCACTTAATGTACTGATTTGCAAA 2040  
Db 1981 ATGCGCTTGAATAGTAGTAGTAATACTTAAGCCCACTTAATGTACTGATTTGCAAA 2040  
Qy 2041 TTGATAGTTGTTCTAGCAGTGAAGATAAAGAAAAAAGTACAACTGAGGCTGCAAGTCA 2100  
Db 2041 TTGATAGTTGTTCTAGCAGTGAAGATAAAGAAAAAAGTACAACTGAGGCTGCAAGTCA 2100  
Qy 2101 GGCACAGCAGAAACCTTACAACTCATGGAAGTAAAGAACTGCAACTGGAGCCAAAGAA 2160  
Db 2101 GGCACAGCAGAAACCTTACAACTCATGGAAGTAAAGAACTGCAACTGGAGCCAAAGAA 2160  
Qy 2161 GTAAACAAGCCAAATGAAACAGACATGACAGTATGATGATGATGATGATGATGATGATG 2220  
Db 2161 GTAAACAAGCCAAATGAAACAGACATGACAGTATGATGATGATGATGATGATGATGATG 2220  
Qy 2221 AGTTAAACAATGACCTGCTTCTTAACTAAGTGTCTAAATACCACTGCAACTTAAAGAA 2280  
Db 2221 AGTTAAACAATGACCTGCTTCTTAACTAAGTGTCTAAATACCACTGCAACTTAAAGAA 2280  
Qy 2281 TTGTCAATCTCTAGCCTTCCAAAGAGAGAAAGAAAGAGAGAACTAGAAACAGTTAAAGTGT 2340  
Db 2281 TTGTCAATCTCTAGCCTTCCAAAGAGAGAAAGAAAGAGAGAACTAGAAACAGTTAAAGTGT 2340  
Qy 2341 CTAATAATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGGTTTGGAACTG 2400  
Db 2341 CTAATAATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGGTTTGGAACTG 2400  
Qy 2401 AAAGATCTGTAGAGTAGCAGTATTTTCACTGGTACCTGGTACTGATTTATGCACTCAGG 2460  
Db 2401 AAAGATCTGTAGAGTAGCAGTATTTTCACTGGTACCTGGTACTGATTTATGCACTCAGG 2460

Qy	2461	AAAGTATCTCGTTACTGGAAGTTAGCACTCTGAGGAAGGCCAAAACAGAAACCAATAAAT	2520
Db	2461	AAAGTATCTCGTTACTGGAAGTTAGCACTCTGAGGAAGGCCAAAACAGAAACCAATAAAT	2520
Qy	2521	GTGTGAGTTCAGTGTGCAGCATTTTCGAAACCCCAAGGCACCTAAATTCATGTTGTTGCCAAG	2580
Db	2521	GTGTGAGTTCAGTGTGCAGCATTTTCGAAACCCCAAGGCACCTAAATTCATGTTGTTGCCAAG	2580
Qy	2581	ATAATAGAAATGACACAGAAAGGCTTTTAAGTATCCATTTGGGACATGAAGTTAAACACAGTC	2640
Db	2581	ATAATAGAAATGACACAGAAAGGCTTTTAAGTATCCATTTGGGACATGAAGTTAAACACAGTC	2640
Qy	2641	GGGAAACAGCATAGAAATGGAAGAAAGTGAACTTTGATGCTCAGTATTTGCAGAAATACAT	2700
Db	2641	GGGAAACAGCATAGAAATGGAAGAAAGTGAACTTTGATGCTCAGTATTTGCAGAAATACAT	2700
Qy	2701	TCAGGTTTCAAAGCGCCAGTCATTTGCTCTGTGTTTCAAATCCAGGAAATGCAGAGAGG	2760
Db	2701	TCAGGTTTCAAAGCGCCAGTCATTTGCTCTGTGTTTCAAATCCAGGAAATGCAGAGAGG	2760
Qy	2761	AATGTGCAACATTTCTGTGCCACCTCTGGGTCCCTTAAAGAAACAAAGTCCAAAAGTCACTT	2820
Db	2761	AATGTGCAACATTTCTGTGCCACCTCTGGGTCCCTTAAAGAAACAAAGTCCAAAAGTCACTT	2820
Qy	2821	TTGAATGTGAACAAAGAAAGAAATCAAGGAAGAAATGAGTCTTAATATCAAGCCCTGTAC	2880
Db	2821	TTGAATGTGAACAAAGAAAGAAATCAAGGAAGAAATGAGTCTTAATATCAAGCCCTGTAC	2880
Qy	2881	AGACAGTTAATATCACTGCAGGCTTTCTCTGTGTTGGTCAAGAAAGTAAGCCAGTTGATA	2940
Db	2881	AGACAGTTAATATCACTGCAGGCTTTCTCTGTGTTGGTCAAGAAAGTAAGCCAGTTGATA	2940
Qy	2941	ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTTGTCATCATCTCAGTTCAGAGGCA	3000
Db	2941	ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTTGTCATCATCTCAGTTCAGAGGCA	3000
Qy	3001	ACGAACTGGACTCATTTACTCCAAATAAACAATGGAGCTTTTACAAAACCCATATCGTATAC	3060
Db	3001	ACGAACTGGACTCATTTACTCCAAATAAACAATGGAGCTTTTACAAAACCCATATCGTATAC	3060
Qy	3061	CACCACHTTTCCCATCAAGTCATTTGTTTAAACTTAAATGTAGAAAAATCTCCTAGAGG	3120
Db	3061	CACCACHTTTCCCATCAAGTCATTTGTTTAAACTTAAATGTAGAAAAATCTCCTAGAGG	3120
Qy	3121	AAAACTTGAGGAACATTTCAATGTCACTCGAAAGAGAAATGGGAAATGAGAAACATTTCCAA	3180
Db	3121	AAAACTTGAGGAACATTTCAATGTCACTCGAAAGAGAAATGGGAAATGAGAAACATTTCCAA	3180
Qy	3181	GTACAGTGAGCACAATTTAGCCGTAATAACATTAGAGAAATGTTTTTAAAGGAGCCAGCT	3240
Db	3181	GTACAGTGAGCACAATTTAGCCGTAATAACATTAGAGAAATGTTTTTAAAGGAGCCAGCT	3240
Qy	3241	CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA	3300
Db	3241	CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA	3300
Qy	3301	TAGTTCCAGTGTAGAAAACATTTCAAGCAAACTAGTAGAAAACAGAGGCGCCAAAATTGA	3360
Db	3301	TAGTTCCAGTGTAGAAAACATTTCAAGCAAACTAGTAGAAAACAGAGGCGCCAAAATTGA	3360
Qy	3361	ATGCTATGCTTAGATTAGGGGTTTTGCAACCTCAGGCTCTATAACAAAGTCTTCTCTGGAA	3420
Db	3361	ATGCTATGCTTAGATTAGGGGTTTTGCAACCTCAGGCTCTATAACAAAGTCTTCTCTGGAA	3420
Qy	3421	GTAATTTGAAGCATCTTGAAATTAAGCAAGATATGAAGAAGTAGTTCAGACTGTGTA	3480
Db	3421	GTAATTTGAAGCATCTTGAAATTAAGCAAGATATGAAGAAGTAGTTCAGACTGTGTA	3480
Qy	3481	ATACAGATTTCTCTCCATATCTGATTTTCAGATAACTTAGAACAGCCCTATGGGAGTAGTC	3540
Db	3481	ATACAGATTTCTCTCCATATCTGATTTTCAGATAACTTAGAACAGCCCTATGGGAGTAGTC	3540
Qy	3541	ATGCATCTCAGGTTTTGTTTCTGAGACACCTGATGACCTGTTAGATGATGTTGMAATAAAG	3600

[illegible]

Db 4621 GCCCATATTAGATGATAGGTGGTACATGACAGTTGCTCTGGGAGTCTTTCAGAAATAGAA 4680  
Qy 4681 ACTACCCATCTCAAGAGGAGCTCATTTAAGGTGTTGATGTGGAGGACAAACAGCTGGAAG 4740  
Db 4681 ACTACCCATCTCAAGAGGAGCTCATTTAAGGTGTTGATGTGGAGGACAAACAGCTGGAAG 4740  
Qy 4741 AGTCTGGGCCACACAGATTTGACGGAACATCTTACTTGGCCAAAGGCAAGATCTAGAGGAA 4800  
Db 4741 AGTCTGGGCCACACAGATTTGACGGAACATCTTACTTGGCCAAAGGCAAGATCTAGAGGAA 4800  
Qy 4801 CCCCTTACTCTGAATCTGGAATCAGCCTCTCTCTGATGACCTGAATCTCATCTCTCTG 4860  
Db 4801 CCCCTTACTCTGAATCTGGAATCAGCCTCTCTCTGATGACCTGAATCTCATCTCTCTG 4860  
Qy 4861 AAGACAGAGCCCCCAGAGTCAGCTCGTGTGGCAACATACCATCTTCAACCTCTGCATTTGA 4920  
Db 4861 AAGACAGAGCCCCCAGAGTCAGCTCGTGTGGCAACATACCATCTTCAACCTCTGCATTTGA 4920  
Qy 4921 AAGTTCCTCCCAATTGAAAGTTGCAGATCTGCCAGGGTCCAGCTGCTCATCTACTG 4980  
Db 4921 AAGTTCCTCCCAATTGAAAGTTGCAGATCTGCCAGGGTCCAGCTGCTCATCTACTG 4980  
Qy 4981 ATACTGCTGGGTATATCAATGGAAGAAAGTGTGAGCAGGAGGAGCCAGAAATTTGACAG 5040  
Db 4981 ATACTGCTGGGTATATCAATGGAAGAAAGTGTGAGCAGGAGGAGCCAGAAATTTGACAG 5040  
Qy 5041 CTTCAACAGAAAGGGTCAACAAAAGATGTCCATGGTGTGTCTGGCCCTGACCCAGAG 5100  
Db 5041 CTTCAACAGAAAGGGTCAACAAAAGATGTCCATGGTGTGTCTGGCCCTGACCCAGAG 5100  
Qy 5101 AATTATATCTCGTGTACAAAGTTTGCAGAAACACCAATCACTTTTAACTAATCTAATTA 5160  
Db 5101 AATTATATCTCGTGTACAAAGTTTGCAGAAACACCAATCACTTTTAACTAATCTAATTA 5160  
Qy 5161 CTGAGAGACTACTCATCTGTTATGAAAACAGATGCTGAGTTGTGTGTAACGGACAC 5220  
Db 5161 CTGAGAGACTACTCATCTGTTATGAAAACAGATGCTGAGTTGTGTGTAACGGACAC 5220  
Qy 5221 TGAATATTTTCTAGGAATTCGGGAGGAAATGGGTAGTTAGCTATTTCCTGGGTGACCC 5280  
Db 5221 TGAATATTTTCTAGGAATTCGGGAGGAAATGGGTAGTTAGCTATTTCCTGGGTGACCC 5280  
Qy 5281 AGTCTATTAAAGAAAGAAAATGCTGAATGAGCATGATTTTGAAGTCAGAGGAGATGTGG 5340  
Db 5281 AGTCTATTAAAGAAAGAAAATGCTGAATGAGCATGATTTTGAAGTCAGAGGAGATGTGG 5340  
Qy 5341 TCAATGGAAGAAACACCAAGGTCCAAAGCGAGCAAGAAATCCAGGACAGAAAGATCT 5400  
Db 5341 TCAATGGAAGAAACACCAAGGTCCAAAGCGAGCAAGAAATCCAGGACAGAAAGATCT 5400  
Qy 5401 TCAGGGGCTAGAAATCTGTTGCTATGGCCCTTCAACCAATGCCCACAGATCAACTGG 5460  
Db 5401 TCAGGGGCTAGAAATCTGTTGCTATGGCCCTTCAACCAATGCCCACAGATCAACTGG 5460  
Qy 5461 AATGGATGGTACAGCTGTGTGTGCTCTGTGGTGAAGAGCTTTTCATTCACCCCTTG 5520  
Db 5461 AATGGATGGTACAGCTGTGTGTGCTCTGTGGTGAAGAGCTTTTCATTCACCCCTTG 5520  
Qy 5521 GCACAGGTGTCCACCAATTTGGTGTGTGACCCAGATGCCTGGACAGAGCAATGGCT 5580  
Db 5521 GCACAGGTGTCCACCAATTTGGTGTGTGACCCAGATGCCTGGACAGAGCAATGGCT 5580  
Qy 5581 TCCATGCAATTTGGGAGATGTGTGAGGACCTGTGTCACCGAGAGTGGGTGTTGGACA 5640  
Db 5581 TCCATGCAATTTGGGAGATGTGTGAGGACCTGTGTCACCGAGAGTGGGTGTTGGACA 5640  
Qy 5641 GTGTAGCACTTACACAGTCCAGGAGCTGGACACCTACTGATACCCAGATCCCCACCA 5700  
Db 5641 GTGTAGCACTTACACAGTCCAGGAGCTGGACACCTACTGATACCCAGATCCCCACCA 5700  
Qy 5701 GCCACTACTGA 5711  
Db 5701 GCCACTACTGA 5711

RESULT 3  
159546  
LOCUS  
DEFINITION Sequence 1 from patent US 5654155.  
ACCESSION 159546  
VERSION 159546.1 GI:2478178  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 5711)  
AUTHORS Murphy, P.D., Allen, A.C., Alvares, C.P., Critz, B.S., Olson, S.J.,  
Schelter, D.B., and Zeng, B.  
TITLE Consensus sequence of the human BRCA1 gene  
JOURNAL Patent: US 5654155-A 1 05-AUG-1997;  
FEATURES Location/Qualifiers  
source 1..5711  
BASE COUNT 1953 a 1099 c 1277 g 1382 t  
ORIGIN  
Query Match 100.0%; Score 5711; DB 6; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AGCTCGCTGAGACTTCTGGACCCCGCACAGGCTGTGGGCTTTCTCAGATAAAGTGGGCC 60  
Db 1 AGCTCGCTGAGACTTCTGGACCCCGCACAGGCTGTGGGCTTTCTCAGATAAAGTGGGCC 60  
Qy 61 CCTCGCTCAGGAGGCTTCACTCTGCTGTGGTAAAGTTCAATTGGAACAGAAAGAAA 120  
Db 61 CCTCGCTCAGGAGGCTTCACTCTGCTGTGGTAAAGTTCAATTGGAACAGAAAGAAA 120  
Qy 121 TGGATTTATCTGCTTCTCGCGTTGAGNAGTACAAATGTCAATTAATCTATGCAAGAAA 180  
Db 121 TGGATTTATCTGCTTCTCGCGTTGAGNAGTACAAATGTCAATTAATCTATGCAAGAAA 180  
Qy 181 TCTTAGAGTGTCCCATCTGTCTGGAGTTGATCAAGGAACCTGTCTCCAAAGTGTGACC 240  
Db 181 TCTTAGAGTGTCCCATCTGTCTGGAGTTGATCAAGGAACCTGTCTCCAAAGTGTGACC 240  
Qy 241 ACATATTTTGCAAAATTTTGCAATGCTGAACTTCTCAACAGAAAGAGGCTTCCAGT 300  
Db 241 ACATATTTTGCAAAATTTTGCAATGCTGAACTTCTCAACAGAAAGAGGCTTCCAGT 300  
Qy 301 GTCTTTTATGTAAGATGATATAACCAAGAGGCTTACAAAGAGTACGAGATTTAGTC 360  
Db 301 GTCTTTTATGTAAGATGATATAACCAAGAGGCTTACAAAGAGTACGAGATTTAGTC 360  
Qy 361 AACTTTTGAAGAGCTATTGAAAATCATTTGCTGCTTTTTCAGCTTGCACAGGTTTGGAGT 420  
Db 361 AACTTTTGAAGAGCTATTGAAAATCATTTGCTGCTTTTTCAGCTTGCACAGGTTTGGAGT 420  
Qy 421 ATGCAAAACAGCTATAAATTTTGCAAAAAGGAAAATAAATCTCTCTGAAACATCTTAAAGATG 480  
Db 421 ATGCAAAACAGCTATAAATTTTGCAAAAAGGAAAATAAATCTCTCTGAAACATCTTAAAGATG 480  
Qy 481 AAGTTTCTATCATTCAAAAGTATGGCTACAGAAACCGTGCCAAAAGACTTCTACAGAGTG 540  
Db 481 AAGTTTCTATCATTCAAAAGTATGGCTACAGAAACCGTGCCAAAAGACTTCTACAGAGTG 540  
Qy 541 AACCCGAAATCTCTTCTTGCAGGAAACAGTCTCAGTGTCCAACTCTCTAACCTTTGAA 600  
Db 541 AACCCGAAATCTCTTCTTGCAGGAAACAGTCTCAGTGTCCAACTCTCTAACCTTTGAA 600  
Qy 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCAAAAGACGCTGTGTACATTG 660  
Db 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCAAAAGACGCTGTGTACATTG 660  
Qy 661 AATTGGGATCTGATTTCTTGAAGATACCGTTTAAAGGCAACTTATTGCAAGTGTGGAG 720  
Db 661 AATTGGGATCTGATTTCTTGAAGATACCGTTTAAAGGCAACTTATTGCAAGTGTGGAG 720

661	Db	AATTGGGATCTGATCTTCTTGAAGATACCGGTAAATAAGGCAACTTATTGTCAGTGTGGAG	720
721	Qy	ATCAAGAATTTGTTACAAATCACCCCTCAAGGAACAGGGAATGAATCAGTTTGGATTTCTG	780
721	Db	ATCAAGAATTTGTTACAAATCACCCCTCAAGGAACAGGGAATGAATCAGTTTGGATTTCTG	780
781	Qy	CAAAAAAGGCTGCTTGTGAATTTTCTTGAGACGGATGTAACAAACTCTGAACATCATCAAC	840
781	Db	CAAAAAAGGCTGCTTGTGAATTTTCTTGAGACGGATGTAACAAACTCTGAACATCATCAAC	840
841	Qy	CCAGTAAATGATTTGTAACACCACTGAGAGCGTGCAGCTGAGAGGATCCAGAAAAAGT	900
841	Db	CCAGTAAATGATTTGTAACACCACTGAGAGCGTGCAGCTGAGAGGATCCAGAAAAAGT	900
901	Qy	ATCAGGCTAGTCTTGTGTTTCAAACTTGATGTGGAGCCATGTGGCACAAAATACTCATGCCA	960
901	Db	ATCAGGCTAGTCTTGTGTTTCAAACTTGATGTGGAGCCATGTGGCACAAAATACTCATGCCA	960
961	Qy	GCTCATTTACAGCATGAGAACACAGCTGTTATTACTCACTAAAGACAGAAATGAATGTAGAA	1020
961	Db	GCTCATTTACAGCATGAGAACACAGCTGTTATTACTCACTAAAGACAGAAATGAATGTAGAA	1020
1021	Qy	AGGCTGAATTTCTGTAATAAAGCAAAACAGCCTGCTTAGCAGAGGCAACATCAACAGAT	1080
1021	Db	AGGCTGAATTTCTGTAATAAAGCAAAACAGCCTGCTTAGCAGAGGCAACATCAACAGAT	1080
1081	Qy	GGGCTGGAAGTAAGGAAACATGTAATGATAGCGGAGTCCACAGCACAGAAAAAAGGTAG	1140
1081	Db	GGGCTGGAAGTAAGGAAACATGTAATGATAGCGGAGTCCACAGCACAGAAAAAAGGTAG	1140
1141	Qy	ATCTGAATGCTGATPCCCTGTGTGAGAGAAAAGAAATGGAATTAAGCAGAAAACCTGCGATGCT	1200
1141	Db	ATCTGAATGCTGATPCCCTGTGTGAGAGAAAAGAAATGGAATTAAGCAGAAAACCTGCGATGCT	1200
1201	Qy	CAGAGAACTCTAGAGATCTGAAGATGTTCTTGGATTAACATAATAGCAGCAATTCAGA	1260
1201	Db	CAGAGAACTCTAGAGATCTGAAGATGTTCTTGGATTAACATAATAGCAGCAATTCAGA	1260
1261	Qy	AAGTTAATGAGTGGTTTTCCAGAAAGTCATGAACCTGTTAGGTTCTGATGACTCACTGATG	1320
1261	Db	AAGTTAATGAGTGGTTTTCCAGAAAGTCATGAACCTGTTAGGTTCTGATGACTCACTGATG	1320
1321	Qy	GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGTATTGGACGTTCTAAATGAGGTAGATG	1380
1321	Db	GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGTATTGGACGTTCTAAATGAGGTAGATG	1380
1381	Qy	AATATTTCTGTTCTTCAGAGAAAATAGACTTACCTGGCCAGTGAATCTCTATGAGGCTTTAA	1440
1381	Db	AATATTTCTGTTCTTCAGAGAAAATAGACTTACCTGGCCAGTGAATCTCTATGAGGCTTTAA	1440
1441	Qy	TATGTAAGTGAAGAGGTTTCACTCCAAAATCAGTAGAGAGTGAATATTGAGAGACAAATAT	1500
1441	Db	TATGTAAGTGAAGAGGTTTCACTCCAAAATCAGTAGAGAGTGAATATTGAGAGACAAATAT	1500
1501	Qy	TTGGAAAACTATPCGGAAGAGCAAGCCTCCCAACTTTAAGCCATGTAACTGAAAAATC	1560
1501	Db	TTGGAAAACTATPCGGAAGAGCAAGCCTCCCAACTTTAAGCCATGTAACTGAAAAATC	1560
1561	Qy	TAATATTAGGAGCATTTGTTTACTGAGCCAAGATAATAAGAGCGGTCCCTCACAAATA	1620
1561	Db	TAATATTAGGAGCATTTGTTTACTGAGCCAAGATAATAAGAGCGGTCCCTCACAAATA	1620
1621	Qy	AATTAAGCGTAAAGAGACCTTACATCAGGCTTCACTCTGAGGATTTTATCAAGNAAG	1680
1621	Db	AATTAAGCGTAAAGAGACCTTACATCAGGCTTCACTCTGAGGATTTTATCAAGNAAG	1680
1681	Qy	CAGATTTGGCAGTTTCAAAAGACTCCTGAAAATGATAAATCAGGCACTTAACCAACGGAGC	1740
1681	Db	CAGATTTGGCAGTTTCAAAAGACTCCTGAAAATGATAAATCAGGCACTTAACCAACGGAGC	1740
1741	Qy	AGAAATGGTCAAGTGAATGAATTAATTAATAGTGGTCAATGAGATAAACAAGGTGATT	1800
1741	Db	AGAAATGGTCAAGTGAATGAATTAATTAATAGTGGTCAATGAGATAAACAAGGTGATT	1800

Qy	1801	CTATTTCAGAAATGAGAAAAATCTTAACCCAAATAGAATCACTCGAAAAAGAAATCTGCTTTCA	1860
Db	1801	CTATTTCAGAAATGAGAAAAATCTTAACCCAAATAGAATCACTCGAAAAAGAAATCTGCTTTCA	1860
Qy	1861	AAACGGAAGCTGAACTTATAAGCAGCAGTATAGCAATATGGNACTCGAATTTAAATATCC	1920
Db	1861	AAACGGAAGCTGAACTTATAAGCAGCAGTATAGCAATATGGNACTCGAATTTAAATATCC	1920
Qy	1921	ACAATTCAAAGACACCTTAAAAAGAAATAGGCTGAGGAGGAAGTCTTCTTACCGAGCATATTC	1980
Db	1921	ACAATTCAAAGACACCTTAAAAAGAAATAGGCTGAGGAGGAAGTCTTCTTACCGAGCATATTC	1980
Qy	1981	ATGCGCTTGAACCTAGTAGTCAGTAGAGAAATCTAAGCCCACTAATTTGCTACTGAAATTCGAAA	2040
Db	1981	ATGCGCTTGAACCTAGTAGTCAGTAGAGAAATCTAAGCCCACTAATTTGCTACTGAAATTCGAAA	2040
Qy	2041	TTGATAGTTGTTCTTAGCAGTGAAGAGATTAAGAAAAAAGATACAAACCAAAATGCCAGTCA	2100
Db	2041	TTGATAGTTGTTCTTAGCAGTGAAGAGATTAAGAAAAAAGATACAAACCAAAATGCCAGTCA	2100
Qy	2101	GGCACACGAAACCTTACAACTCATCGAAGGTAAAGAACTCGCACTGGAGCGCAAGAACA	2160
Db	2101	GGCACACGAAACCTTACAACTCATCGAAGGTAAAGAACTCGCACTGGAGCGCAAGAACA	2160
Qy	2161	GTAACAAAGCCAAATGAACAGACAAAGTAAAGACATGACAGTGTATCTTTCCAGAGCTGA	2220
Db	2161	GTAACAAAGCCAAATGAACAGACAAAGTAAAGACATGACAGTGTATCTTTCCAGAGCTGA	2220
Qy	2221	AGTTAAACAAATGACACCTGGTCTTTTCTAAGTGTTCAAATACCAGTGAACCTTAAAGAAAT	2280
Db	2221	AGTTAAACAAATGACACCTGGTCTTTTCTAAGTGTTCAAATACCAGTGAACCTTAAAGAAAT	2280
Qy	2281	TTGTCAATCTGAGCTTCCAGAGAGAGAAAGAGAGAGAACTAGNAACAGTTAAAGTGT	2340
Db	2281	TTGTCAATCTGAGCTTCCAGAGAGAGAAAGAGAGAGAACTAGNAACAGTTAAAGTGT	2340
Qy	2341	CTAATAATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGGTTTTGCAAACTG	2400
Db	2341	CTAATAATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGGTTTTGCAAACTG	2400
Qy	2401	AAAGATCTGTAGAGAGTAGCAGTAATTTCACTGGTACCTGGTACTGANTATGSCACTCAGG	2460
Db	2401	AAAGATCTGTAGAGAGTAGCAGTAATTTCACTGGTACCTGGTACTGANTATGSCACTCAGG	2460
Qy	2461	AAAGTATCTGTTACTGGAGTTAGCACCTCTAGGGNAGGCAAAAACAGAACCAATTAAT	2520
Db	2461	AAAGTATCTGTTACTGGAGTTAGCACCTCTAGGGNAGGCAAAAACAGAACCAATTAAT	2520
Qy	2521	GTGTGAGTCACTGTGACAGATTTGAAAACCCCAAGGGACTAATTCATGGTGTGTCCAAAG	2580
Db	2521	GTGTGAGTCACTGTGACAGATTTGAAAACCCCAAGGGACTAATTCATGGTGTGTCCAAAG	2580
Qy	2581	ATAATAGAAATGACACAGAAGGCTTTTAAGTATCCATTGGGACATGAAGTTAACCCAGTTC	2640
Db	2581	ATAATAGAAATGACACAGAAGGCTTTTAAGTATCCATTGGGACATGAAGTTAACCCAGTTC	2640
Qy	2641	GGGAAACAAGCATAGAAAATGGAAGAAAGTGAACCTTGATGCTCAGTATTTTGCAAGATACAT	2700
Db	2641	GGGAAACAAGCATAGAAAATGGAAGAAAGTGAACCTTGATGCTCAGTATTTTGCAAGATACAT	2700
Qy	2701	TCAAGGTTTTCAAAGCCCACTGATTTGCTGCTGTTTTCAAATCCAGGAATGCAGAAAGG	2760
Db	2701	TCAAGGTTTTCAAAGCCCACTGATTTGCTGCTGTTTTCAAATCCAGGAATGCAGAAAGG	2760
Qy	2761	AATGTGCAACATTTCTCTGCCCCACTCTGGGTCTCTTAAAGAAAACAAAGTCCAAAAGTCACTT	2820
Db	2761	AATGTGCAACATTTCTCTGCCCCACTCTGGGTCTCTTAAAGAAAACAAAGTCCAAAAGTCACTT	2820
Qy	2821	TTGAATGTGAACAAAAGGAGAAATCAAGGAAAGAAATGAAGTCTTAATATCAAGCCTGTAC	2880
Db	2821	TTGAATGTGAACAAAAGGAGAAATCAAGGAAAGAAATGAAGTCTTAATATCAAGCCTGTAC	2880

Qy	2881	AGACAGTTAATATCACTGCGAGGCTTTCTGTGGTGGTTCAGAAAAGATAAGCCAGTTGATA	2940
Ds	2881		
Ds	2881	AGACAGTTAATATCACTGCGAGGCTTTCTGTGGTGGTTCAGAAAAGATAAGCCAGTTGATA	2940
Qy	2941	ATGCAAAATGAGTATCAAAAGGAGCTCTAGTTTCTGTATCATCTCAGTTTCAGAGGCA	3000
Ds	2941		
Ds	2941	ATGCAAAATGAGTATCAAAAGGAGCTCTAGTTTCTGTATCATCTCAGTTTCAGAGGCA	3000
Qy	3001	ACGAAATCGGACTCATTTACTCCAAATAAACAATGGAATTTTACAAAACCCATATCGTATAC	3060
Ds	3001		
Ds	3001	ACGAAATCGGACTCATTTACTCCAAATAAACAATGGAATTTTACAAAACCCATATCGTATAC	3060
Qy	3061	CACACATTTTCCCACTCAAGTCATTTGTTTAAACTTAAATGTAAGAAAATCTGCTAGAGG	3120
Ds	3061		
Ds	3061	CACACATTTTCCCACTCAAGTCATTTGTTTAAACTTAAATGTAAGAAAATCTGCTAGAGG	3120
Qy	3121	AAAACTTTGAGGAACATTTCAATGTCACCTGAAAGAGAAATGGGAAATGAGAAACATTTCAA	3180
Ds	3121		
Ds	3121	AAAACTTTGAGGAACATTTCAATGTCACCTGAAAGAGAAATGGGAAATGAGAAACATTTCAA	3180
Qy	3181	GTACAGTGAGCACAAATAGCCGTAAATAACATTAGAGAAAATGTTTTAAAGAGGCCAGCT	3240
Ds	3181		
Ds	3181	GTACAGTGAGCACAAATAGCCGTAAATAACATTAGAGAAAATGTTTTAAAGAGGCCAGCT	3240
Qy	3241	CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA	3300
Ds	3241		
Ds	3241	CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA	3300
Qy	3301	TAGGTTCCAGTGATGAACAACTTCAAGCAGAACTAGGTAGAAAACAGAGGGCCAAATTTGA	3360
Ds	3301		
Ds	3301	TAGGTTCCAGTGATGAACAACTTCAAGCAGAACTAGGTAGAAAACAGAGGGCCAAATTTGA	3360
Qy	3361	ATGCTATGCTTAGATTTAGGGGTTTTGCAACTGAGGCTATAAAACAAAGTCTTCTCTGAA	3420
Ds	3361		
Ds	3361	ATGCTATGCTTAGATTTAGGGGTTTTGCAACTGAGGCTATAAAACAAAGTCTTCTCTGAA	3420
Qy	3421	GTAATTTGAAGTATCTCGAATAAATAAGCAAGAAATATGAAGAGTAGTTTCAGACTGTTA	3480
Ds	3421		
Ds	3421	GTAATTTGAAGTATCTCGAATAAATAAGCAAGAAATATGAAGAGTAGTTTCAGACTGTTA	3480
Qy	3481	ATACAGATTTCTCCATATCTGATTTTCAGATTAATTTAGACAGCCTATGGGAGTAGTC	3540
Ds	3481		
Ds	3481	ATACAGATTTCTCCATATCTGATTTTCAGATTAATTTAGACAGCCTATGGGAGTAGTC	3540
Qy	3541	ATGCAATCTCAGGTTGTTCTGAGACACCTGATGACCTGTTAGATGATGGTCAAAATAAAGG	3600
Ds	3541		
Ds	3541	ATGCAATCTCAGGTTGTTCTGAGACACCTGATGACCTGTTAGATGATGGTCAAAATAAAGG	3600
Qy	3601	AAGATACATGTTTTGCTGAAAATGACATTAAGGAAAGTTCTGCTGTTTTTACCAAAAGCG	3660
Ds	3601		
Ds	3601	AAGATACATGTTTTGCTGAAAATGACATTAAGGAAAGTTCTGCTGTTTTTACCAAAAGCG	3660
Qy	3661	TCCAGAGGAGAGCTTAGCAGGAGTCTAGCCCTTTCCACCATACACATTTGGCTCAGG	3720
Ds	3661		
Ds	3661	TCCAGAGGAGAGCTTAGCAGGAGTCTAGCCCTTTCCACCATACACATTTGGCTCAGG	3720
Qy	3721	GTTACCGAAGAGGGGCCAAGAAATTTAGAGTCTCTCAGAAAGAACTTATCTAGTCAGGATG	3780
Ds	3721		
Ds	3721	GTTACCGAAGAGGGGCCAAGAAATTTAGAGTCTCTCAGAAAGAACTTATCTAGTCAGGATG	3780
Qy	3781	AAGAGCTTCCCTGCTCCAACTGTTTATTTGGTAAAGTAAACAAATATACCTTCTCAGT	3840
Ds	3781		
Ds	3781	AAGAGCTTCCCTGCTCCAACTGTTTATTTGGTAAAGTAAACAAATATACCTTCTCAGT	3840
Qy	3841	CTACTAGGCATAGCACCGTTCCTACCGAGTGTCTGTCTAAGAAACACAGAGGAGATTTAT	3900
Ds	3841		
Ds	3841	CTACTAGGCATAGCACCGTTCCTACCGAGTGTCTGTCTAAGAAACACAGAGGAGATTTAT	3900
Qy	3901	TATCATTTGAAGATAGCTTTAAATGACTGCTAGTAAACAGGTAATTTGGCAAGGATCTC	3960
Ds	3901		
Ds	3901	TATCATTTGAAGATAGCTTTAAATGACTGCTAGTAAACAGGTAATTTGGCAAGGATCTC	3960
Qy	3961	AGGAACATCACCTTAGTGAGGAAACAAAATGTTCTGTAGTGTGTTTTTCTTTCACAGTGCA	4020
Ds	3961		

Ds	3961	AGGAACATCACCTTAGTGAGGAAACAAAATGTTCTGTAGCTGTTTTTCTTTCACAGTGCA	4020
Qy	4021	GTGAATTTGGAAGACTTCTGACTGCAAAATACAAACACCCAGGATCCCTTTCTTGATTTGGTCTT	4080
Ds	4021		
Ds	4021	GTGAATTTGGAAGACTTCTGACTGCAAAATACAAACACCCAGGATCCCTTTCTTGATTTGGTCTT	4080
Qy	4081	CCAAACAAATAGAGCATCAGTCTGAAAAGCCAGGAGTTGGTCTGAGTGACAAGAAATGG	4140
Ds	4081		
Ds	4081	CCAAACAAATAGAGCATCAGTCTGAAAAGCCAGGAGTTGGTCTGAGTGACAAGAAATGG	4140
Qy	4141	TTTCAGATGATGAAGAAGAGGACGGCTTTGGAGAAATAAATCAAGAGAGCAAGCA	4200
Ds	4141		
Ds	4141	TTTCAGATGATGAAGAAGAGGACGGCTTTGGAGAAATAAATCAAGAGAGCAAGCA	4200
Qy	4201	TGGATTCAAAATCTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAAAACAAAGCTCTCTGAAG	4260
Ds	4201		
Ds	4201	TGGATTCAAAATCTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAAAACAAAGCTCTCTGAAG	4260
Qy	4261	ACTGCTCAGGGCTATCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGATACCATGC	4320
Ds	4261		
Ds	4261	ACTGCTCAGGGCTATCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGATACCATGC	4320
Qy	4321	AACATAACCTGATTAAGCTCCAGCAGGAAATGGCTGAACTAGAAAGCTGTGTAGAACAGC	4380
Ds	4321		
Ds	4321	AACATAACCTGATTAAGCTCCAGCAGGAAATGGCTGAACTAGAAAGCTGTGTAGAACAGC	4380
Qy	4381	ATGGAGCCAGGCTTTCTAACAGCTTACCTTCCATCATTAAGTGACTCTCTGCCCTTTGAGG	4440
Ds	4381		
Ds	4381	ATGGAGCCAGGCTTTCTAACAGCTTACCTTCCATCATTAAGTGACTCTCTGCCCTTTGAGG	4440
Qy	4441	ACCTGCGAAATCCAGAACAAAGCAATCAGAAAAAGCAGTATTAACCTTCACAGAAAAAGTA	4500
Ds	4441		
Ds	4441	ACCTGCGAAATCCAGAACAAAGCAATCAGAAAAAGCAGTATTAACCTTCACAGAAAAAGTA	4500
Qy	4501	GTGAATACCTTATTAAGCCAGAAATCCAGAAAGGCTTTCTGCTGACAAGTTTCAGGTTGCTG	4560
Ds	4501		
Ds	4501	GTGAATACCTTATTAAGCCAGAAATCCAGAAAGGCTTTCTGCTGACAAGTTTCAGGTTGCTG	4560
Qy	4561	CAGATAGTTCTTACCAGTAAATAAAGAAACAGAGGTGGAAGGTCATCCCTTCTTAAT	4620
Ds	4561		
Ds	4561	CAGATAGTTCTTACCAGTAAATAAAGAAACAGAGGTGGAAGGTCATCCCTTCTTAAT	4620
Qy	4621	GCCCATCATTAGATGATAGTGTGTAATGCAAGTGTCTCTGGAGTCTTCAGAAATAGAA	4680
Ds	4621		
Ds	4621	GCCCATCATTAGATGATAGTGTGTAATGCAAGTGTCTCTGGAGTCTTCAGAAATAGAA	4680
Qy	4681	ACTACCATCTCAAGAGAGCTCAATTAAGTTGTTGATGTGGAGGACCAAGCTGGAG	4740
Ds	4681		
Ds	4681	ACTACCATCTCAAGAGAGCTCAATTAAGTTGTTGATGTGGAGGACCAAGCTGGAG	4740
Qy	4741	AGTCTGGGCCACACGATTTGACCGAAACATCTTACTTGCACCAAGCAAGATCTAGAGGAA	4800
Ds	4741		
Ds	4741	AGTCTGGGCCACACGATTTGACCGAAACATCTTACTTGCACCAAGCAAGATCTAGAGGAA	4800
Qy	4801	CCCCCTTACCTGGAATCTGGAATCAGCCTCTTCTCTGATGACCCCTGATCTGATCTCTG	4860
Ds	4801		
Ds	4801	CCCCCTTACCTGGAATCTGGAATCAGCCTCTTCTCTGATGACCCCTGATCTGATCTCTG	4860
Qy	4861	AAGCAGAGCCCCAGAGTCTGCTGTGTGGCAACATACCATCTTCAACCTCTGCATTTGA	4920
Ds	4861		
Ds	4861	AAGCAGAGCCCCAGAGTCTGCTGTGTGGCAACATACCATCTTCAACCTCTGCATTTGA	4920
Qy	4921	AAGTTCCCAATTCAAAAGTTGCAGAAATCTGCCAGGGTCCAGCTGCTCTCATCTACTCTG	4980
Ds	4921		
Ds	4921	AAGTTCCCAATTCAAAAGTTGCAGAAATCTGCCAGGGTCCAGCTGCTCTCATCTACTCTG	4980
Qy	4981	ATACTGCTGGGTATAATGCAATGGAAGAGTGTGAGCAGGGAGAAAGCCAGAAATTTGACAG	5040
Ds	4981		
Ds	4981	ATACTGCTGGGTATAATGCAATGGAAGAGTGTGAGCAGGGAGAAAGCCAGAAATTTGACAG	5040
Qy	5041	CTTCAACAGAAAGGCTCAACAAAAGATGTCATGGTGGTCTCTGGCTGAGCCCCCAGAAAG	5100
Ds	5041		





Db 1081 GGGCTGGAAGTAAGGAAACATGTAATGATAGGCGGACTCCAGACACAGAAAAAGGTAG 1140  
Qy 1141 ATCTGAATGCTGATCCCTCTGTGAGAGAAAGAAATGGAATTAAGCAGAAATCGCATGCT 1200  
Db 1141 ATCTGAATGCTGATCCCTCTGTGAGAGAAAGAAATGGAATTAAGCAGAAATCGCATGCT 1200  
Qy 1201 CAGAGAAATCTTAGAGATACATGAAGATGTTCTTGGAATAACAATTAAGCAGCAATTCAGA 1260  
Db 1201 CAGAGAAATCTTAGAGATACATGAAGATGTTCTTGGAATAACAATTAAGCAGCAATTCAGA 1260  
Qy 1261 AAGTTAATGATGTTGTTTTCAGAGATGATGAACCTGTTAGGTTCTGATGACTCCATCATG 1320  
Db 1261 AAGTTAATGATGTTGTTTTCAGAGATGATGAACCTGTTAGGTTCTGATGACTCCATCATG 1320  
Qy 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGATTAATGGAGCTTCTAAATGAGGTAGATG 1380  
Db 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGATTAATGGAGCTTCTAAATGAGGTAGATG 1380  
Qy 1381 AATATTCTGGTTCTTCAGAGAAATAGACTTTACTGGCCAGTGATCCTCATGAGGCTTTAA 1440  
Db 1381 AATATTCTGGTTCTTCAGAGAAATAGACTTTACTGGCCAGTGATCCTCATGAGGCTTTAA 1440  
Qy 1441 TATGTAAAGTGAAGAGTTCACTCCAAATCAGTAGAGAGTAATTAATGAAGACAAAATAT 1500  
Db 1441 TATGTAAAGTGAAGAGTTCACTCCAAATCAGTAGAGAGTAATTAATGAAGACAAAATAT 1500  
Qy 1501 TTGGGAAAACTATCGGAAGAGGCAAGCCCTCCCAACTTAAGCCATGTAACCTGAAATC 1560  
Db 1501 TTGGGAAAACTATCGGAAGAGGCAAGCCCTCCCAACTTAAGCCATGTAACCTGAAATC 1560  
Qy 1561 TAATTATAGGAGCAATTTGTTACTGAGCCACAGATAATAAGAGCGTCCCTCACAATA 1620  
Db 1561 TAATTATAGGAGCAATTTGTTACTGAGCCACAGATAATAAGAGCGTCCCTCACAATA 1620  
Qy 1621 AATTAAAGCTGAAAGAGACCTACATCAGGCTTCACTCGAGGATTTTATCAAGAAAG 1680  
Db 1621 AATTAAAGCTGAAAGAGACCTACATCAGGCTTCACTCGAGGATTTTATCAAGAAAG 1680  
Qy 1681 CAGATTTGGCAGTTCAAAAGACTCCTGAAATGATAAATCAGGGAACCTAACCAAGCGAGC 1740  
Db 1681 CAGATTTGGCAGTTCAAAAGACTCCTGAAATGATAAATCAGGGAACCTAACCAAGCGAGC 1740  
Qy 1741 AGAATGCTCAAGTGATCAATTAATTAATAGTGGTCATGAGAATAAAACAAAAGGTGATT 1800  
Db 1741 AGAATGCTCAAGTGATCAATTAATTAATAGTGGTCATGAGAATAAAACAAAAGGTGATT 1800  
Qy 1801 CTATTCAAGATGAGAAAAATCCTAACCCCAATAGAAATCACTCGAAAAAGAAATCTGCTTTCA 1860  
Db 1801 CTATTCAAGATGAGAAAAATCCTAACCCCAATAGAAATCACTCGAAAAAGAAATCTGCTTTCA 1860  
Qy 1861 AAACGAAAGCTGAAACCTTATAGCAGCAGTATAAGCAATATGGAATCGAAATTAATATCC 1920  
Db 1861 AAACGAAAGCTGAAACCTTATAGCAGCAGTATAAGCAATATGGAATCGAAATTAATATCC 1920  
Qy 1921 ACAATTCAAAAGCACCCTTAAAGAAATAGGCTGAGGAGGAAGTCTTACACAGGCATATTC 1980  
Db 1921 ACAATTCAAAAGCACCCTTAAAGAAATAGGCTGAGGAGGAAGTCTTACACAGGCATATTC 1980  
Qy 1981 ATGCGCTTGAATAGTAGTCAAGTAAATCTAAGCCCACTTAATTTGTAATGTAATGCAAA 2040  
Db 1981 ATGCGCTTGAATAGTAGTCAAGTAAATCTAAGCCCACTTAATTTGTAATGTAATGCAAA 2040  
Qy 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATAAGAAAAAAGTATACCAAAATGCCAGTCA 2100  
Db 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATAAGAAAAAAGTATACCAAAATGCCAGTCA 2100  
Qy 2101 GGCCAGCAGAAAACTCAACTCTGGAAGGTAAAGAACTGGAAGCCCAAGAGA 2160  
Db 2101 GGCCAGCAGAAAACTCAACTCTGGAAGGTAAAGAACTGGAAGCCCAAGAGA 2160  
Qy 2161 GTAAACAGCCAAATGAACAGAGTAAAGACATGACAGTGATATCTTTCCAGAGCTGA 2220  
Db 2161 GTAAACAGCCAAATGAACAGAGTAAAGACATGACAGTGATATCTTTCCAGAGCTGA 2220

Qy 2221 AGTTAACAAAATGCACCTGGTCTTTTACTAAGTGTTCAAAATACCAAGTGAACTTAAAGAA 2280  
Db 2221 AGTTAACAAAATGCACCTGGTCTTTTACTAAGTGTTCAAAATACCAAGTGAACTTAAAGAA 2280  
Qy 2281 TTGTCAATCTAGCCTTCCAAAGAGAGAAAAAGAGAACTAGAGAACAGTAAAGTGT 2340  
Db 2281 TTGTCAATCTAGCCTTCCAAAGAGAGAAAAAGAGAACTAGAGAACAGTAAAGTGT 2340  
Qy 2341 CTAAATATGCTGAAGACCCCAAGATCTCATGTTAACTGAGAGAAAGGTTTTCAAAACCTG 2400  
Db 2341 CTAAATATGCTGAAGACCCCAAGATCTCATGTTAACTGAGAGAAAGGTTTTCAAAACCTG 2400  
Qy 2401 AAAGATCTGTAGAGAGTAGCAGTATTTCACTGGTACCTGGTACTGATTATGGCACTCAGG 2460  
Db 2401 AAAGATCTGTAGAGAGTAGCAGTATTTCACTGGTACCTGGTACTGATTATGGCACTCAGG 2460  
Qy 2461 AAAGTATCTCGTTACTGGNAAGTTAGCACTCTAGGGAAGGCCAAAACAGAACCAATTAAT 2520  
Db 2461 AAAGTATCTCGTTACTGGNAAGTTAGCACTCTAGGGAAGGCCAAAACAGAACCAATTAAT 2520  
Qy 2521 GTGTGAGTCAAGTGTGACAGCAATTTGAAAAACCCCAAGGACCTAATTCATGGTTGTTCCAAAG 2580  
Db 2521 GTGTGAGTCAAGTGTGACAGCAATTTGAAAAACCCCAAGGACCTAATTCATGGTTGTTCCAAAG 2580  
Qy 2581 ATATAGAAAAATGCACAGAAAGGCTTTAAGTATCCATTTGGGACATGAAGTTAAACCAAGTC 2640  
Db 2581 ATATAGAAAAATGCACAGAAAGGCTTTAAGTATCCATTTGGGACATGAAGTTAAACCAAGTC 2640  
Qy 2641 GGGAAAAACAGATAGAAATGGAGAAAGTGAACCTTGATGCTCAGTATTTGAGAGATACAT 2700  
Db 2641 GGGAAAAACAGATAGAAATGGAGAAAGTGAACCTTGATGCTCAGTATTTGAGAGATACAT 2700  
Qy 2701 TCAAGGTTTCAAAAGCGCCAGTCATTGCTCTGTTTCAAAATCCAGGAAATCCAGAAAGG 2760  
Db 2701 TCAAGGTTTCAAAAGCGCCAGTCATTGCTCTGTTTCAAAATCCAGGAAATCCAGAAAGG 2760  
Qy 2761 AATGTGCAACATTTCTGCCCCACTCTGGGCTCTTTAAAGAAAAAAAAGTCCAAAAGTCAC 2820  
Db 2761 AATGTGCAACATTTCTGCCCCACTCTGGGCTCTTTAAAGAAAAAAAAGTCCAAAAGTCAC 2820  
Qy 2821 TTGAATGTGAACAAAAGGAGAAAAATCAAGGAAAGATGAGTCTAATATCAAGCCTGTAC 2880  
Db 2821 TTGAATGTGAACAAAAGGAGAAAAATCAAGGAAAGATGAGTCTAATATCAAGCCTGTAC 2880  
Qy 2881 AGACAGTTAATATACATGCGAGGCTTCTGCTGGTGTGTCAGAAAGATAAGCCAGTTGATA 2940  
Db 2881 AGACAGTTAATATACATGCGAGGCTTCTGCTGGTGTGTCAGAAAGATAAGCCAGTTGATA 2940  
Qy 2941 ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTCCAGAGGCA 3000  
Db 2941 ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTCCAGAGGCA 3000  
Qy 3001 ACGAAACTGGACTCATTTACTCCAAATAAACAATGAGCTTTTACAAAACCCATATCGTATAC 3060  
Db 3001 ACGAAACTGGACTCATTTACTCCAAATAAACAATGAGCTTTTACAAAACCCATATCGTATAC 3060  
Qy 3061 CACCACCTTTTCCCATCAAGTCATTTGTTAAATCTAATGTAAAGAAATCTGCTAGAGG 3120  
Db 3061 CACCACCTTTTCCCATCAAGTCATTTGTTAAATCTAATGTAAAGAAATCTGCTAGAGG 3120  
Qy 3121 AAAACTTTTGAGAAACATTTCAATGTCACTGAAAGAAATGGGAAATGAGAAATCTCCAA 3180  
Db 3121 AAAACTTTTGAGAAACATTTCAATGTCACTGAAAGAAATGGGAAATGAGAAATCTCCAA 3180  
Qy 3181 GTACAGTGAGCAAAATTAGCCGTAAATAACATTAGAGAAATTTGTTTTAAAGGAGCAGCT 3240  
Db 3181 GTACAGTGAGCAAAATTAGCCGTAAATAACATTAGAGAAATTTGTTTTAAAGGAGCAGCT 3240  
Qy 3241 CAAGCAATTAATTAAGTAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTATGAAA 3300  
Db 3241 CAAGCAATTAATTAAGTAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTATGAAA 3300





Db 5461 AATGATGGTACAGCTGTGTGGTCTCTGTGGTGAAGAGCTTTTCATCATTCACCCCTTG 5520  
Qy 5521 GCACAGGTGTCCACCCAAATTTGGTGTGTGACGCGAGATGCTTGGACAGAGCAATGGCT 5580  
Db 5521 GCACAGGTGTCCACCCAAATTTGGTGTGTGACGCGAGATGCTTGGACAGAGCAATGGCT 5580  
Qy 5581 TCCATGCAATTTGGGAGATGTGTGAGGACCTGTGTGGTACCCGAGAGTGGTGTGGACA 5640  
Db 5581 TCCATGCAATTTGGGAGATGTGTGAGGACCTGTGTGGTACCCGAGAGTGGTGTGGACA 5640  
Qy 5641 GTGTAGCACTTACCAGTCCAGGAGCTGGACACCTACCTGATATACCCAGATCCCCACA 5700  
Db 5641 GTGTAGCACTTACCAGTCCAGGAGCTGGACACCTACCTGATATACCCAGATCCCCACA 5700  
Qy 5701 GCCACTACTGA 5711  
Db 5701 GCCACTACTGA 5711

RESULT 5  
AR112809  
LOCUS AR112809 5711 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 3 from patent US 6130322.  
ACCESSION AR112809  
VERSION AR112809.1 GI:14092709  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 5711)  
AUTHORS Murphy, P.D., Allen, A.C.P., Alvares, C.P., Critz, B.S., Olson, S.J.,  
Thurber, D. and Zeng, B.  
TITLE Coding sequences of the human BRCA1 gene  
JOURNAL Patent: US 6130322-A 3 10-OCT-2000;  
FEATURES  
source location/Qualifiers  
1..5711  
/organism="unknown"  
BASE COUNT 1953 a 1098 c 1277 g 1383 t  
ORIGIN

Query Match 100.0%; Score 5709.4; DB 6; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGCTCGCTGAGACTTCTGGACCCCGACAGGCTGTGGGTCTTCAGATAAAGTGGGCC 60  
Db 1 AGCTCGCTGAGACTTCTGGACCCCGACAGGCTGTGGGTCTTCAGATAAAGTGGGCC 60  
Qy 61 CCTCGCTCAGAGGCGCTTCAACCTCTGCTCTGGGTAAAGTTCAATTGGAACAGAAAGAAA 120  
Db 61 CCTCGCTCAGAGGCGCTTCAACCTCTGCTCTGGGTAAAGTTCAATTGGAACAGAAAGAAA 120  
Qy 121 TGGATTTATCTGCTCTTCGGCTTGAAGAGTACAAATGTCAATTAATGCTATGAGAAA 180  
Db 121 TGGATTTATCTGCTCTTCGGCTTGAAGAGTACAAATGTCAATTAATGCTATGAGAAA 180  
Qy 181 TCTTAGAGTGTCCATCTGTCTGAGTGTGATCAAGGAACCTGTCTCCACAAGTGTGACC 240  
Db 181 TCTTAGAGTGTCCATCTGTCTGAGTGTGATCAAGGAACCTGTCTCCACAAGTGTGACC 240  
Qy 241 ACATATTTTGCAATTTTGCATGCTGAACTTCTCAACAGAGAAAGGGCTTTCACAGT 300  
Db 241 ACATATTTTGCAATTTTGCATGCTGAACTTCTCAACAGAGAAAGGGCTTTCACAGT 300  
Qy 301 GTCCTTTATGTAAGATGATATAACCAAAAGGAGCTTACAGAAAGTACGAGATTTAGTC 360  
Db 301 GTCCTTTATGTAAGATGATATAACCAAAAGGAGCTTACAGAAAGTACGAGATTTAGTC 360  
Qy 361 AACTTGTGTGAAGAGCTATTGAAATCATTTTGTGCTTTTTCAGCTTGACACAGGTTTGGAGT 420  
Db 361 AACTTGTGTGAAGAGCTATTGAAATCATTTTGTGCTTTTTCAGCTTGACACAGGTTTGGAGT 420  
Qy 421 ATGCAACAGCTATATAATTTTGCAAAAAGGAAATAAATCTCTCTCTGAAATCTAAAAAGATG 480

Db 421 ATGCAACAGCTATATAATTTTGCAAAAAGGAAATAAATCTCTCTGAAATCTAAAAAGATG 480  
Qy 481 AAGTTTCTATCATCTCAAAAGTATGGCTACAGAAACCGTGCAGAAAGCTTCTACAGAGTG 540  
Db 481 AAGTTTCTATCATCTCAAAAGTATGGCTACAGAAACCGTGCAGAAAGCTTCTACAGAGTG 540  
Qy 541 AACCCGAAATTCCTTCTTCAGGAAAACCACTCTCAGTGTCAAATCTCTAACTTGGAA 600  
Db 541 AACCCGAAATTCCTTCTTCAGGAAAACCACTCTCAGTGTCAAATCTCTAACTTGGAA 600  
Qy 601 CTGTGAGAACTCTGAGAGCAAAAGCAGCGGATACAACTCAAAAGACGTCTGTCTACATTG 660  
Db 601 CTGTGAGAACTCTGAGAGCAAAAGCAGCGGATACAACTCAAAAGACGTCTGTCTACATTG 660  
Qy 661 AATTGGGATCTGATTCTTCTGAAGATACCGTTAATAAGGCAACTTATTGCAAGTGTGGAG 720  
Db 661 AATTGGGATCTGATTCTTCTGAAGATACCGTTAATAAGGCAACTTATTGCAAGTGTGGAG 720  
Qy 721 ATCAAGAAATTTGTTACAAATCAACCCCTCAAGGAAACCGGATGAAATCAGTTTGGATTCTG 780  
Db 721 ATCAAGAAATTTGTTACAAATCAACCCCTCAAGGAAACCGGATGAAATCAGTTTGGATTCTG 780  
Qy 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGACGGATGTAAACAAATCTGAACATCATCAAC 840  
Db 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGACGGATGTAAACAAATCTGAACATCATCAAC 840  
Qy 841 CCAGTAATAATGATTTTGAACACCACTCAGAAAGCGTGCAGCTGAGAGGCATCCAGAAAGT 900  
Db 841 CCAGTAATAATGATTTTGAACACCACTCAGAAAGCGTGCAGCTGAGAGGCATCCAGAAAGT 900  
Qy 901 ATCAGGGTAGTCTCTGTTTCAAACTTGTGAGCCATGTGGCAACAATACTCATGCCA 960  
Db 901 ATCAGGGTAGTCTCTGTTTCAAACTTGTGAGCCATGTGGCAACAATACTCATGCCA 960  
Qy 961 GCTCATTTACAGCATGAGAACAGCAAGTTTATTCTACTAAGACAGAAATGAATGTAGAAA 1020  
Db 961 GCTCATTTACAGCATGAGAACAGCAAGTTTATTCTACTAAGACAGAAATGAATGTAGAAA 1020  
Qy 1021 AGGCTGAATTTCTGTAATAAAGCAACAGCTGCTGTAGCAAGGAGCAACATCAACAGAT 1080  
Db 1021 AGGCTGAATTTCTGTAATAAAGCAACAGCTGCTGTAGCAAGGAGCAACATCAACAGAT 1080  
Qy 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGCGGACTCCAGCAGCAAGAAAGGATG 1140  
Db 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGCGGACTCCAGCAGCAAGAAAGGATG 1140  
Qy 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGGAATTAAGCAGAAACTGCCATGCT 1200  
Db 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGGAATTAAGCAGAAACTGCCATGCT 1200  
Qy 1201 CAGAGAACTCTAGAGATCTGAGAGTCTTCTTGGATAACACTAAATAGCAGCATTCAGA 1260  
Db 1201 CAGAGAACTCTAGAGATCTGAGAGTCTTCTTGGATAACACTAAATAGCAGCATTCAGA 1260  
Qy 1261 AAGTTAATGAGTGGTTTTCCAGAAAGTGAATGAACTGTTAGGTTCTGATGACTCAGATG 1320  
Db 1261 AAGTTAATGAGTGGTTTTCCAGAAAGTGAATGAACTGTTAGGTTCTGATGACTCAGATG 1320  
Qy 1321 GGGAGTCTGAATCAAAATGCGAAAGTGTGATGATTTGGAGCTTCTAAATGAGGTAGATG 1380  
Db 1321 GGGAGTCTGAATCAAAATGCGAAAGTGTGATGATTTGGAGCTTCTAAATGAGGTAGATG 1380  
Qy 1381 AATATTTCTGTTCTTTCAGAGAAATATGACTTACTGGCCAGTGATCCTCATGAGGCTTTAA 1440  
Db 1381 AATATTTCTGTTCTTTCAGAGAAATATGACTTACTGGCCAGTGATCCTCATGAGGCTTTAA 1440  
Qy 1441 TATGTAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGAGTAAATATTGAAGACAAAATAT 1500  
Db 1441 TATGTAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGAGTAAATATTGAAGACAAAATAT 1500  
Qy 1501 TTGGGAAAACCTATCGGAAGAGGCAAGCCCTCCCAACTTAAGCCATGTAACTGAAAATC 1560  
Db 1501 TTGGGAAAACCTATCGGAAGAGGCAAGCCCTCCCAACTTAAGCCATGTAACTGAAAATC 1560

Db 1501 TTGGAAACCTATCGGAAGAGGCAAGCCTCCCAACTTAAGCCATGTAACTGAAATC 1560  
Qy 1561 TAAATTATAGGAGCATTTCTTACTGAGCCACAGATAATAACAGAGCGTCCCTCACAATA 1620  
Db 1561 TAAATTATAGGAGCATTTCTTACTGAGCCACAGATAATAACAGAGCGTCCCTCACAATA 1620  
Qy 1621 AATTAAAGCGTAAAGGAGACCTACATCAGGCGTTCATCCTCGAGGATTTTATCAAGAAAG 1680  
Db 1621 AATTAAAGCGTAAAGGAGACCTACATCAGGCGTTCATCCTCGAGGATTTTATCAAGAAAG 1680  
Qy 1681 CAGATTTGGCAGTTCAAAAGACTCCTGAAATGATAAATCAGGGAATTAACCAAAAGGAGC 1740  
Db 1681 CAGATTTGGCAGTTCAAAAGACTCCTGAAATGATAAATCAGGGAATTAACCAAAAGGAGC 1740  
Qy 1741 AGAATGGTCAAGTGAATGATTAATTAATAGTGTGATGAGAAATAAACAAGAGGTGATT 1800  
Db 1741 AGAATGGTCAAGTGAATGATTAATTAATAGTGTGATGAGAAATAAACAAGAGGTGATT 1800  
Qy 1801 CTATTGAGATGAGAAATAATCTTAACCAATAGAAATCACTCGAATAAGAAATCTGCTTCA 1860  
Db 1801 CTATTGAGATGAGAAATAATCTTAACCAATAGAAATCACTCGAATAAGAAATCTGCTTCA 1860  
Qy 1861 AAACGAAAGCTGAACCTATTAAGAGCAGATTAAGCAATATGGAATCTGAAATTAATATCC 1920  
Db 1861 AAACGAAAGCTGAACCTATTAAGAGCAGATTAAGCAATATGGAATCTGAAATTAATATCC 1920  
Qy 1921 ACAATTCAAAGACACCTAAAGAAATAGGCTGAGGAGAGTCTTACCAAGGCATATTC 1980  
Db 1921 ACAATTCAAAGACACCTAAAGAAATAGGCTGAGGAGAGTCTTACCAAGGCATATTC 1980  
Qy 1981 ATGCGCTTGAACCTAGTAGTCACTAGTAAATCTTAAGCCACCTAAITGTACTGAAITGCAAA 2040  
Db 1981 ATGCGCTTGAACCTAGTAGTCACTAGTAAATCTTAAGCCACCTAAITGTACTGAAITGCAAA 2040  
Qy 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATAAAGAAAAAAGTACAACTGCAAGTCA 2100  
Db 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATAAAGAAAAAAGTACAACTGCAAGTCA 2100  
Qy 2101 GGCAACAGAGAAACCTTACAACTCATGGAAGTAAAGAACTGCAACTGGAGCCCAAGAGA 2160  
Db 2101 GGCAACAGAGAAACCTTACAACTCATGGAAGTAAAGAACTGCAACTGGAGCCCAAGAGA 2160  
Qy 2161 GTAAACAGCCAAATGAACAGACAGTAAAGACATGACAGTGAATCTTCCAGAGCTGA 2220  
Db 2161 GTAAACAGCCAAATGAACAGACAGTAAAGACATGACAGTGAATCTTCCAGAGCTGA 2220  
Qy 2221 AGTTAAACAAATGACCTGGTCTTTTACTAGTGTTCAAATACAGTGAATTAAGAAAT 2280  
Db 2221 AGTTAAACAAATGACCTGGTCTTTTACTAGTGTTCAAATACAGTGAATTAAGAAAT 2280  
Qy 2281 TTGTCAATCTTAGCCTTCCAGAGAGAGAAAGAGAACTAGAGAACTAGTAAAGTGT 2340  
Db 2281 TTGTCAATCTTAGCCTTCCAGAGAGAGAAAGAGAACTAGAGAACTAGTAAAGTGT 2340  
Qy 2341 CTAAATATGCTGAAGACCCCAAGATCTATGTTAAGTGAGAGAAAGGTTTTGCAAACTG 2400  
Db 2341 CTAAATATGCTGAAGACCCCAAGATCTATGTTAAGTGAGAGAAAGGTTTTGCAAACTG 2400  
Qy 2401 AAAGATCTGAGAGTAGCAGTATTTTACTGTGTACCTGGTATCTGATTTGGCACTCAGG 2460  
Db 2401 AAAGATCTGAGAGTAGCAGTATTTTACTGTGTACCTGGTATCTGATTTGGCACTCAGG 2460  
Qy 2461 AAAGTATCTGTTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAACAGAACCAATTAAT 2520  
Db 2461 AAAGTATCTGTTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAACAGAACCAATTAAT 2520  
Qy 2521 GTGTGAGTCAAGTGTGAGCAATTTGAAACCCCAAGGCACTAATTCATGTTGTTTCCAAAG 2580  
Db 2521 GTGTGAGTCAAGTGTGAGCAATTTGAAACCCCAAGGCACTAATTCATGTTGTTTCCAAAG 2580  
Qy 2581 ATATAGAAATGACACAGAGGCTTTAAGTATCCATTTGGGACATGAATTAACCAAGTC 2640  
Db 2581 ATATAGAAATGACACAGAGGCTTTAAGTATCCATTTGGGACATGAATTAACCAAGTC 2640

Qy 2641 GGGAAACAGCATAGAAATGGAAGAAAGTGAACCTTGATGCTCAGTATTTGCAGAAATACAT 2700  
Db 2641 GGGAAACAGCATAGAAATGGAAGAAAGTGAACCTTGATGCTCAGTATTTGCAGAAATACAT 2700  
Qy 2701 TCAAGGTTTTCAAGCGCCAGTCATTTGCTCTGTTTTCAAAATCCAGGAAATGCAAGAGG 2760  
Db 2701 TCAAGGTTTTCAAGCGCCAGTCATTTGCTCTGTTTTCAAAATCCAGGAAATGCAAGAGG 2760  
Qy 2761 AATGTGCAACATTTCTTGCCCACTCTGCGGTCTTTAAAGAAACAAAGTCCAAAAGTCACTT 2820  
Db 2761 AATGTGCAACATTTCTTGCCCACTCTGCGGTCTTTAAAGAAACAAAGTCCAAAAGTCACTT 2820  
Qy 2821 TTGAATCTGAACAAAGAGAAATCAAGGAAAGATGATCTTAATATCAAGCCTCTAC 2880  
Db 2821 TTGAATCTGAACAAAGAGAAATCAAGGAAAGATGATCTTAATATCAAGCCTCTAC 2880  
Qy 2881 AGACAGTTAATATACATCTGAGGCTTTCTGTTGGTTCAGAAAGATAAGCCAGTTGATA 2940  
Db 2881 AGACAGTTAATATACATCTGAGGCTTTCTGTTGGTTCAGAAAGATAAGCCAGTTGATA 2940  
Qy 2941 ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTTGCTCTATCATCTCAGTTCAAGGCA 3000  
Db 2941 ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTTGCTCTATCATCTCAGTTCAAGGCA 3000  
Qy 3001 ACCGAACTGAGCTCATTTACTCCAAATAAATCAAGCTTTTACAAACCCCATATCGTATAC 3060  
Db 3001 ACCGAACTGAGCTCATTTACTCCAAATAAATCAAGCTTTTACAAACCCCATATCGTATAC 3060  
Qy 3061 CACCACCTTTTCCCATCAAGTCAATTTGTTAAAACTAAATGTAAGAAAAATCTGTAGAGG 3120  
Db 3061 CACCACCTTTTCCCATCAAGTCAATTTGTTAAAACTAAATGTAAGAAAAATCTGTAGAGG 3120  
Qy 3121 AAAACTTTGAGGAACATTTCAATGTACCTGAAAGAGAAATGGAAGATGAGAACATTTCCAA 3180  
Db 3121 AAAACTTTGAGGAACATTTCAATGTACCTGAAAGAGAAATGGAAGATGAGAACATTTCCAA 3180  
Qy 3181 GTACAGTGAGCACAATTTAGCGGTAAATCAATTAAGAGAAATGTTTTTAAAGGAGCCAGCT 3240  
Db 3181 GTACAGTGAGCACAATTTAGCGGTAAATCAATTAAGAGAAATGTTTTTAAAGGAGCCAGCT 3240  
Qy 3241 CAAGCAATATTAATGAAGTAGGTTTCCAGTACTTAATGAAGTGGCTCCAGTATTAATGAAA 3300  
Db 3241 CAAGCAATATTAATGAAGTAGGTTTCCAGTACTTAATGAAGTGGCTCCAGTATTAATGAAA 3300  
Qy 3301 TAGGTTCCAGTGATGAAACATTTCAAGCAGAACCTAGGTAGAAAACAGAGGCCCCAAATTTGA 3360  
Db 3301 TAGGTTCCAGTGATGAAACATTTCAAGCAGAACCTAGGTAGAAAACAGAGGCCCCAAATTTGA 3360  
Qy 3361 ATGCTATGCTTAGATTAGGGTTTTTGCACCTCGAGGTCTATAAACAAAGTCTTCTCGGAA 3420  
Db 3361 ATGCTATGCTTAGATTAGGGTTTTTGCACCTCGAGGTCTATAAACAAAGTCTTCTCGGAA 3420  
Qy 3421 GTAAATGTAAAGCATCTCGAAATAAAAAGCAAGAAATGAAGAAAGTAGTTTCAAGCTGTTA 3480  
Db 3421 GTAAATGTAAAGCATCTCGAAATAAAAAGCAAGAAATGAAGAAAGTAGTTTCAAGCTGTTA 3480  
Qy 3481 ATACAGATTTCTCTCCATATCTGATTTTCAAGTAACTTAGAACAGCCTATGCGGAAGTAGTC 3540  
Db 3481 ATACAGATTTCTCTCCATATCTGATTTTCAAGTAACTTAGAACAGCCTATGCGGAAGTAGTC 3540  
Qy 3541 ATGCATCTCAGGTTTTGTTCTGAGACACCTGATCAGCTGTTAGATGATGTTGGAATAAAGG 3600  
Db 3541 ATGCATCTCAGGTTTTGTTCTGAGACACCTGATGATGATGTTGGAATAAAGG 3600  
Qy 3601 AAGATACTAGTTTTGCTGAAAATGACATTAAGGAAAAGTTCTGCTGTTTTTAGCAAAAGCG 3660  
Db 3601 AAGATACTAGTTTTGCTGAAAATGACATTAAGGAAAAGTTCTGCTGTTTTTAGCAAAAGCG 3660  
Qy 3661 TCCAGAGAGGAGAGCTTAGCAGGAGTCCAGGCTTTTACCCCATACATTTGGCTCAGG 3720  
Db 3661 TCCAGAGAGGAGAGCTTAGCAGGAGTCCAGGCTTTTACCCCATACATTTGGCTCAGG 3720

Qy	3721	GTACCAAGAGGGGCAAGAAATAGAGTCTCAGAAAGAGAACTTATCTAGTAGGAGATG	3780
Db	3721	GTATCCGAAGAGGGGCCAAGAAATAGAGTCTCAGAAAGAGAACTTATCTAGTAGGAGATG	3780
Qy	3781	AAGAGCTTCCCTGCTTCCACACACTTGTATTGTTGTAAGTAAACAATATACCTTCTCAGT	3840
Db	3781	AAGAGCTTCCCTGCTTCCACACACTTGTATTGTTGTAAGTAAACAATATACCTTCTCAGT	3840
Qy	3841	CTACTAGGCATPAGCACCGTTGCTACCGAGTGTCTGCTTAAGAAACACAGAGAGAAATTTAT	3900
Db	3841	CTACTAGGCATPAGCACCGTTGCTACCGAGTGTCTGCTTAAGAAACACAGAGAGAAATTTAT	3900
Qy	3901	TATCATTTGAAGATAGCTTAAATGACTGCGAGTACCAAGGTAAATATGCGAAAGCATCTC	3960
Db	3901	TATCATTTGAAGATAGCTTAAATGACTGCGAGTACCAAGGTAAATATGCGAAAGCATCTC	3960
Qy	3961	AGGAACATCACTTAGTGAGGAAACAAATGTTCTGCTAGCTTCTTTTCTTCAAGTGCA	4020
Db	3961	AGGAACATCACTTAGTGAGGAAACAAATGTTCTGCTAGCTTCTTTTCTTCAAGTGCA	4020
Qy	4021	GTGAATTTGGAAGACTTGACTGCAATACAAACACCCAGGATCCCTTCTGATTGGTTCTT	4080
Db	4021	GTGAATTTGGAAGACTTGACTGCAATACAAACACCCAGGATCCCTTCTGATTGGTTCTT	4080
Qy	4081	CCAAACAAATGAGGCATCAGTCTGAAAGCCAGGAGTTGCTGAGTGACAGGAATTGG	4140
Db	4081	CCAAACAAATGAGGCATCAGTCTGAAAGCCAGGAGTTGCTGAGTGACAGGAATTGG	4140
Qy	4141	TTTCAGATGATGAAGAGGAGGACGGCTTGGAGAGAAATATCAAGAGAGCAAAAGCA	4200
Db	4141	TTTCAGATGATGAAGAGGAGGACGGCTTGGAGAGAAATATCAAGAGAGCAAAAGCA	4200
Qy	4201	TGGAATTCAAATCTTAGTGGAAGCAGCATCTGGGTGTGAGAGTGAAACAAAGGCTCTCTGAAG	4260
Db	4201	TGGAATTCAAATCTTAGTGGAAGCAGCATCTGGGTGTGAGAGTGAAACAAAGGCTCTCTGAAG	4260
Qy	4261	ACTGCTCAGGCTATCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGATACCATGC	4320
Db	4261	ACTGCTCAGGCTATCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGATACCATGC	4320
Qy	4321	AACATACCTGATAAAGCTCCAGCAGGAAATGGCTGAAGCTGCTGTAGAACAGC	4380
Db	4321	AACATACCTGATAAAGCTCCAGCAGGAAATGGCTGAAGCTGCTGTAGAACAGC	4380
Qy	4381	ATGGGAGCCAGCTTCTAAACAGCTTACCTTCCATATAAGTGACTCTCTGCTGCCCTTCAGG	4440
Db	4381	ATGGGAGCCAGCTTCTAAACAGCTTACCTTCCATATAAGTGACTCTCTGCTGCCCTTCAGG	4440
Qy	4441	ACCTGCGAAATCCAGAACAAAGCAGCATCAGAAAAAGCAGTATTAACTTCAAGAAAAAGTA	4500
Db	4441	ACCTGCGAAATCCAGAACAAAGCAGCATCAGAAAAAGCAGTATTAACTTCAAGAAAAAGTA	4500
Qy	4501	GTGAATACCTTATAGCCAGNATCCAGAGGCTTTCTGCTGACAGTGTGAGTGCTG	4560
Db	4501	GTGAATACCTTATAGCCAGNATCCAGAGGCTTTCTGCTGACAGTGTGAGTGCTG	4560
Qy	4561	CAGATAGTCTTACCAAGTAAATAAAGAAACAGAGTGGAAGGTATCCCTTCTTAAT	4620
Db	4561	CAGATAGTCTTACCAAGTAAATAAAGAAACAGAGTGGAAGGTATCCCTTCTTAAT	4620
Qy	4621	GCCCATCATTAGATGATGGTGTACATGCAAGTGTCTGGAGTCTTCAAGAAATAGAA	4680
Db	4621	GCCCATCATTAGATGATGGTGTACATGCAAGTGTCTGGAGTCTTCAAGAAATAGAA	4680
Qy	4681	ACTACCCATCTCAGAGAGGCTCATTAAAGTGTGTTGATGTGGAGGAGCAACAGCTGGAAG	4740
Db	4681	ACTACCCATCTCAGAGAGGCTCATTAAAGTGTGTTGATGTGGAGGAGCAACAGCTGGAAG	4740
Qy	4741	AGTCTGGGCCACAGATTTGACGAAACATCTTACTTTGCCAAGGCAAGATCTAGAGGAA	4800
Db	4741	AGTCTGGGCCACAGATTTGACGAAACATCTTACTTTGCCAAGGCAAGATCTAGAGGAA	4800
Qy	4801	CCCCTTACCTGGAACTGGAATCAGCCCTCTTCTCTGATGACCCCTGAAATCTGATCCTTCTG	4860

Db	4801	CCCCTTACCTGGAACTGGAATCAGCCCTCTTCTCTGATGACCCCTGAAATCTGATCCTTCTG	4860
Qy	4861	AAGACAGAGCCCCAGAGTCAAGTCTGTTGGCAACATACCATCTTCAACCTCTCATTTGA	4920
Db	4861	AAGACAGAGCCCCAGAGTCAAGTCTGTTGGCAACATACCATCTTCAACCTCTCATTTGA	4920
Qy	4921	AAGTTCCTCCAAATTTGAAAGTTGCAAGATCTGCCAGGGTCCAGCTGCTCATACTACTG	4980
Db	4921	AAGTTCCTCCAAATTTGAAAGTTGCAAGATCTGCCAGGGTCCAGCTGCTCATACTACTG	4980
Qy	4981	ATACTGCTGGTATATGCAATGGAAGAAAGTGTGACGAGGAGAGCCAGAAATGACAG	5040
Db	4981	ATACTGCTGGTATATGCAATGGAAGAAAGTGTGACGAGGAGAGCCAGAAATGACAG	5040
Qy	5041	CTTCAACAGAAAGGGTCAACAAAGAAATGTCCATGGTGGTGTCTGGGCTGACCCAGAG	5100
Db	5041	CTTCAACAGAAAGGGTCAACAAAGAAATGTCCATGGTGGTGTCTGGGCTGACCCAGAG	5100
Qy	5101	AATTTATGCTCGTGTCAAGTTTGCAGAAAAACCAACATCATCTTTAACTAATCTAATTA	5160
Db	5101	AATTTATGCTCGTGTCAAGTTTGCAGAAAAACCAACATCATCTTTAACTAATCTAATTA	5160
Qy	5161	CTGAGAGACTACTCATGTTGTTATGAAAAACAGATGCTGAGTTTGTGTGTAACGGACAC	5220
Db	5161	CTGAGAGACTACTCATGTTGTTATGAAAAACAGATGCTGAGTTTGTGTGTAACGGACAC	5220
Qy	5221	TGAAATATTTTCTAGGAATTTGCGGAGGAAAAATGGGTAGTTAGTCTATTTCTGGGTGACCC	5280
Db	5221	TGAAATATTTTCTAGGAATTTGCGGAGGAAAAATGGGTAGTTAGTCTATTTCTGGGTGACCC	5280
Qy	5281	AGTCTATTAAAGAAAGAAAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGGAGATGTGG	5340
Db	5281	AGTCTATTAAAGAAAGAAAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGGAGATGTGG	5340
Qy	5341	TCAATGGAAGAAACCAAGGTTCCAAAGGAGCAAGAGATCCAGAGCAGAAAGATCT	5400
Db	5341	TCAATGGAAGAAACCAAGGTTCCAAAGGAGCAAGAGATCCAGAGCAGAAAGATCT	5400
Qy	5401	TCAGGGGCTAGAAAACTGTTGCTATGCGGCCCTTCCACCAATGCCCCACAGATCAACTGG	5460
Db	5401	TCAGGGGCTAGAAAACTGTTGCTATGCGGCCCTTCCACCAATGCCCCACAGATCAACTGG	5460
Qy	5461	AATGGATGTTACAGCTGTGTGGTCTTCTGTGGTGAAGAGAGCTTTTCATTTACCCCTTG	5520
Db	5461	AATGGATGTTACAGCTGTGTGGTCTTCTGTGGTGAAGAGAGCTTTTCATTTACCCCTTG	5520
Qy	5521	GCACAGTGTCCACCCAAATTTGTGGTGTGAGCCAGATGCGCTGGACAGAGGACAAATGGCT	5580
Db	5521	GCACAGTGTCCACCCAAATTTGTGGTGTGAGCCAGATGCGCTGGACAGAGGACAAATGGCT	5580
Qy	5581	TCCATGCAATTTGGGACAGATGTGTGGGACCTCTGTGGTGAAGAGAGTGGGTGTTGACAC	5640
Db	5581	TCCATGCAATTTGGGACAGATGTGTGGGACCTCTGTGGTGAAGAGAGTGGGTGTTGACAC	5640
Qy	5641	GTGTAGCACTTACAGTGCAGAGCTGGACACCTACCTGATACCCAGATCCCCCACA	5700
Db	5641	GTGTAGCACTTACAGTGCAGAGCTGGACACCTACCTGATACCCAGATCCCCCACA	5700
Qy	5701	GCCACTACTGA 5711	
Db	5701	GCCACTACTGA 5711	

## RESULT 6

AR007334.

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

5711 bp

DNA

linear

PAT 04-DEC-1998

Sequence 3 from patent US 5750400.

AR007334

AR007334

GI:3966818

Unknown.

Unknown.

Unclassified.									
REFERENCE	1 (bases 1 to 5711)								
AUTHORS	Murphy, P.D., Allen, A.C., Alvares, C.P., Critz, B.S., Olson, S.J., Schelter, D.B. and Zeng, B.								
TITLE	Coding sequences of the human BRCA1 gene								
JOURNAL	Patent: US 5750400-A 3 12-MAY-1998;								
FEATURES	Location/Qualifiers								
source	1..5711								
BASE COUNT	1956 a 1098 c 1274 g 1383 t								
ORIGIN									
Query Match 99.8%; Score 5701.4; DB 6; Length 5711;									
Best Local Similarity 99.9%; Pred. No. 0;									
Matches 5705; Conservative 0; Mismatches 6; Indels 0; Gaps 0;									
QY	1	AGCTCGCTGAGACTTCTGGACCCGCGCACACAGGCTGTGGGGTTCTCAGATAA	CTGGGCC	60					
DB	1	AGCTCGCTGAGACTTCTGGACCCCGCACACAGGCTGTGGGGTTCTCAGATAA	CTGGGCC	60					
QY	61	CCTGGCTCAGGAGGCTTCCACCTCTGCTCTGGGTAAAGTTCAATTGAAACAGAAAGAAA	120						
DB	61	CCTGGCTCAGGAGGCTTCCACCTCTGCTCTGGGTAAAGTTCAATTGAAACAGAAAGAAA	120						
QY	121	TGGATTTATCTGCTCTCGCGTTGAAGAAATGTCATTAATGCTATGCA	AAAA	180					
DB	121	TGGATTTATCTGCTCTCGCGTTGAAGAAATGTCATTAATGCTATGCA	AAAA	180					
QY	181	TCCTAGAGTGCCTCTGCTCTGGAGTTGATCAAGAACCTGTCTCCA	AAAGTGTGACC	240					
DB	181	TCCTAGAGTGCCTCTGCTCTGGAGTTGATCAAGAACCTGTCTCCA	AAAGTGTGACC	240					
QY	241	ACATATTTTGCAAAATTTTGATGCTGAACTTCTCAACAGAAAGGGGCTT	CACAGT	300					
DB	241	ACATATTTTGCAAAATTTTGATGCTGAACTTCTCAACAGAAAGGGGCTT	CACAGT	300					
QY	301	GTCTTTTATGTAAGAAATGATATAACCAAAAGGAGCTTACAGAAAGTAC	GAGATTTAGTC	360					
DB	301	GTCTTTTATGTAAGAAATGATATAACCAAAAGGAGCTTACAGAAAGTAC	GAGATTTAGTC	360					
QY	361	AACCTGTTGAAGAGCTATTGAAATCATTTGTGCTTTTACGCTTGAC	AGTTGGAGT	420					
DB	361	AACCTGTTGAAGAGCTATTGAAATCATTTGTGCTTTTACGCTTGAC	AGTTGGAGT	420					
QY	421	ATGCAAAACAGCTATAATTTTGCAAAAAGGAAATAACTCTCCTGAA	CATCTAAAGATG	480					
DB	421	ATGCAAAACAGCTATAATTTTGCAAAAAGGAAATAACTCTCCTGAA	CATCTAAAGATG	480					
QY	481	AAAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCAAAG	AGACTTCTACAGAGTG	540					
DB	481	AAAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCAAAG	AGACTTCTACAGAGTG	540					
QY	541	AACCCGAAATCCTTCTTGAGGAAACAGTCTCAGTGTCCAACTCT	TAACTTGAA	600					
DB	541	AACCCGAAATCCTTCTTGAGGAAACAGTCTCAGTGTCCAACTCT	TAACTTGAA	600					
QY	601	CTGTGAGAACTCTCAGGACAAAGCAGCGGTACAACTCTCAAA	AGACCTGTGTACATTG	660					
DB	601	CTGTGAGAACTCTCAGGACAAAGCAGCGGTACAACTCTCAAA	AGACCTGTGTGTACATTG	660					
QY	661	AATTGGGATCTGATTTCTTGAAGATACCGTTAATAAGGCAACTT	ATTGCAAGTGTGGAG	720					
DB	661	AATTGGGATCTGATTTCTTGAAGATACCGTTAATAAGGCAACTT	ATTGCAAGTGTGGAG	720					
QY	721	ATCAAGATTTGTACAAATCAACCTCAAGAACCGGATGAAATC	AGTTTGAATTTCTG	780					
DB	721	ATCAAGATTTGTACAAATCAACCTCAAGAACCGGATGAAATC	AGTTTGAATTTCTG	780					
QY	781	CAAAAAGGCTGCTTGTGAAATTTTCTGAGCGGATGTAACAA	ATCTCATCAAC	840					
DB	781	CAAAAAGGCTGCTTGTGAAATTTTCTGAGCGGATGTAACAA	ATCTCATCAAC	840					
QY	841	CCAGTAATATGATTTGAACCACTGAGAAAGCGTGCAGCTG	AGAGGCATCCGAAAGT	900					

DB	841	CCAGTAATATGATTTTGAACCACTGAGAAAGCGTGAGCTG	AGAGGCATCCGAAAGT	900					
QY	901	ATCAGGGTAGTTCCTGTTTCAAACTTGCATGTGGAGCCATGT	GGCACAATACTCATGCCA	960					
DB	901	ATCAGGGTAGTTCCTGTTTCAAACTTGCATGTGGAGCCATGT	GGCACAATACTCATGCCA	960					
QY	961	GCTCATTTACAGCATGAGAACAGCAGTTTATTTACTCTACT	AAAGACAGAAATGATGTAGAAA	1020					
DB	961	GCTCATTTACAGCATGAGAACAGCAGTTTATTTACTCTACT	AAAGACAGAAATGATGTAGAAA	1020					
QY	1021	AGGCTGAATTCGTATAATAAAGCAACAGCCTGCTTAGCA	AGGAGGCAACATACACAGAT	1080					
DB	1021	AGGCTGAATTCGTATAATAAAGCAACAGCCTGCTTAGCA	AGGAGGCAACATACACAGAT	1080					
QY	1081	GGGCTGGAAGTAAGGAAACATGTAATGATAGGCGGACT	CCCAGCACAGAAAAAGGTAG	1140					
DB	1081	GGGCTGGAAGTAAGGAAACATGTAATGATAGGCGGACT	CCCAGCACAGAAAAAGGTAG	1140					
QY	1141	ATCTGAATGCTGATCCCTCTGTGAGAGAAAGAAATGGA	ATAAGCAGAAATCTGCATGCT	1200					
DB	1141	ATCTGAATGCTGATCCCTCTGTGAGAGAAAGAAATGGA	ATAAGCAGAAATCTGCATGCT	1200					
QY	1201	CAGAGAAATCCTAGAGATACCTGAAGATGTTCTTGGATA	ACACTAAATAGCAGCAATTCAGA	1260					
DB	1201	CAGAGAAATCCTAGAGATACCTGAAGATGTTCTTGGATA	ACACTAAATAGCAGCAATTCAGA	1260					
QY	1261	AAAGTTAATGAGTGGTTTTCCAGAAAGTGAATGAACT	GTGTAGGTTTGTAGTCAATGATG	1320					
DB	1261	AAAGTTAATGAGTGGTTTTCCAGAAAGTGAATGAACT	GTGTAGGTTTGTAGTCAATGATG	1320					
QY	1321	GGGAGTCTGAATCAAAATGCCCAGAGTGTGATGTTGG	AGCGTTCTAAATGAGGTAGATG	1380					
DB	1321	GGGAGTCTGAATCAAAATGCCCAGAGTGTGATGTTGG	AGCGTTCTAAATGAGGTAGATG	1380					
QY	1381	AAATATCTGCTTCTCAGAGAAATAGACTTACTTGGC	CAGTGATCTCATGAGGCTTTAA	1440					
DB	1381	AAATATCTGCTTCTCAGAGAAATAGACTTACTTGGC	CAGTGATCTCATGAGGCTTTAA	1440					
QY	1441	TATGTAAAGTGAAGAGTTCACTCCAAATCAGTAGAG	ATAATATTGAAGACAAAATAT	1500					
DB	1441	TATGTAAAGTGAAGAGTTCACTCCAAATCAGTAGAG	ATAATATTGAAGACAAAATAT	1500					
QY	1501	TTGGGAAACCTATCGGAAGAGCGCTCCCACTTAA	GCCATGTAACCTGAAATC	1560					
DB	1501	TTGGGAAACCTATCGGAAGAGCGCTCCCACTTAA	GCCATGTAACCTGAAATC	1560					
QY	1561	TAATTTATAGGAGCATTTGTTACTGAGCCACAGAT	ATAATACAGAGCGTCCCCTCACAAATA	1620					
DB	1561	TAATTTATAGGAGCATTTGTTACTGAGCCACAGAT	ATAATACAGAGCGTCCCCTCACAAATA	1620					
QY	1621	AATTAAGCGTTAAAGAGACCTACATCAGGCTTCA	TCTGAGGATTTTATCAAGAAAG	1680					
DB	1621	AATTAAGCGTTAAAGAGAGACCTACATCAGGCTTCA	TCTGAGGATTTTATCAAGAAAG	1680					
QY	1681	CAGATTTGGCAGTCTCAAGAGCTCCCTGAAATG	ATAATCAGGAACTAAACCAACGAGC	1740					
DB	1681	CAGATTTGGCAGTCTCAAGAGCTCCCTGAAATG	ATAATCAGGAACTAAACCAACGAGC	1740					
QY	1741	AGATGGTCAAGTGATGAATATTACTAATAGTGGT	CATGAGATAATAACCAAAAGGTCATT	1800					
DB	1741	AGATGGTCAAGTGATGAATATTACTAATAGTGGT	CATGAGATAATAACCAAAAGGTCATT	1800					
QY	1801	CTATTGAGATGAGAAAAATCTTAACCCAAATAGA	ATACATCTCGAAAAAGAAATCTGCTTTCA	1860					
DB	1801	CTATTGAGATGAGAAAAATCTTAACCCAAATAGA	ATACATCTCGAAAAAGAAATCTGCTTTCA	1860					
QY	1861	AAACGAAAGCTGACCTATAAGCAGCAGATATAG	CATATGGAACCTCGAATTTAAATATCC	1920					
DB	1861	AAACGAAAGCTGACCTATAAGCAGCAGATATAG	CATATGGAACCTCGAATTTAAATATCC	1920					
QY	1921	ACAATTTCAAAGCACCTTAAAGAAATAGGCTG	AGGAGGAGTCTTCTTACCGGCATATTC	1980					

Db 1921 ACAATTCAAAAGCACCTAAAGAAATAGGCTGAGGAGGAAGTCTTCTACAGGCATATTC 1980  
Qy 1981 ATGCGCTTGAACCTAGTAGTCAAGTGAAGAACTTAAGCCCACTTAATGTGTACTGAATTCGAAA 2040  
Db 1981 ATGCGCTTGAACCTAGTAGTCAAGTGAAGAACTTAAGCCCACTTAATGTGTACTGAATTCGAAA 2040  
Qy 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATAAGAAAGAAAGAAAGTACAAACCAATGCCAGTCA 2100  
Db 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATAAGAAAGAAAGAAAGTACAAACCAATGCCAGTCA 2100  
Qy 2101 GGCAACAGCAAGAACTTCAACCTCATGTGAAGAGTAAAGAACTTCAACCTGGAGCCCAAGAGA 2160  
Db 2101 GGCAACAGCAAGAACTTCAACCTCATGTGAAGAGTAAAGAACTTCAACCTGGAGCCCAAGAGA 2160  
Qy 2161 GTAAACAGCCAAATGAACAGACAAGTAAAGACATGACAGTGATATTTTCCAGAGCTGA 2220  
Db 2161 GTAAACAGCCAAATGAACAGACAAGTAAAGAACTTCAACCTGGAGCCCAAGAGA 2220  
Qy 2221 AGTTAAACAAATGCCACCTGGTCTTTTACTAAGTGTTCAAATACCAGTGAACCTTAAAGAT 2280  
Db 2221 AGTTAAACAAATGCCACCTGGTCTTTTACTAAGTGTTCAAATACCAGTGAACCTTAAAGAT 2280  
Qy 2281 TTGTCAATCCTAGCTTCCAAGAGAGAAAGAAAGAGAACTAGAAACAGTTTAAAGTGT 2340  
Db 2281 TTGTCAATCCTAGCTTCCAAGAGAGAAAGAAAGAGAACTAGAAACAGTTTAAAGTGT 2340  
Qy 2341 CTAATAATGTCTGAAGACCCCAAGATCTCATGTTAAAGTGGAGAAAGGGTTTTCGAAACTG 2400  
Db 2341 CTAATAATGTCTGAAGACCCCAAGATCTCATGTTAAAGTGGAGAAAGGGTTTTCGAAACTG 2400  
Qy 2401 AAAGATCTGTAGAGATGACGATATTTCACTGGTACCTGGTACTGATTTATGGCACTCAGG 2460  
Db 2401 AAAGATCTGTAGAGATGACGATATTTCACTGGTACTCCTGGTACTGATTTATGGCACTCAGG 2460  
Qy 2461 AAAGTATCTCTGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAACAGAACCAATTAAT 2520  
Db 2461 AAAGTATCTCTGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAACAGAACCAATTAAT 2520  
Qy 2521 GTGTGAGTCACTGTGAGCACTTTGAAAACCCCAAGGCACTAATCATGGTTGTTCCAAAG 2580  
Db 2521 GTGTGAGTCACTGTGAGCACTTTGAAAACCCCAAGGCACTAATCATGGTTGTTCCAAAG 2580  
Qy 2581 ATAATAGAAATGACACAGAGGCTTTAAGTATCCATTGGGACATGAAGTTAAACACAGTC 2640  
Db 2581 ATAATAGAAATGACACAGAGGCTTTAAGTATCCATTGGGACATGAAGTTAAACACAGTC 2640  
Qy 2641 GGGAAACAGCATAGAAATGAGAAAGTGAATCTGATGCTCAGTATTTGAGAGATACAT 2700  
Db 2641 GGGAAACAGCATAGAAATGAGAAAGTGAATCTGATGCTCAGTATTTGAGAGATACAT 2700  
Qy 2701 TCAAGGTTTCAAAGCCGAGTCATTTGCTCTGTGTTTCAAATCCAGGAAATGCAGAGAGG 2760  
Db 2701 TCAAGGTTTCAAAGCCGAGTCATTTGCTCTGTGTTTCAAATCCAGGAAATGCAGAGAGG 2760  
Qy 2761 AATGTGCAACATCTCTGCCACTCTGGGTCTTTAAAGAAAACAAAGTCCAAAAGTCACTT 2820  
Db 2761 AATGTGCAACATCTCTGCCACTCTGGGTCTTTAAAGAAAACAAAGTCCAAAAGTCACTT 2820  
Qy 2821 TTGAATGTGAACAAAGAGAAATCAAGAGAAATGAGTCTTAATATCAAGCCTGTAC 2880  
Db 2821 TTGAATGTGAACAAAGAGAAATCAAGAGAAATGAGTCTTAATATCAAGCCTGTAC 2880  
Qy 2881 AGACAGTTTAATATCACTCAGGCTTCTGTGTTGTTGGTTCAGAAAGATAGCCAGTTGATA 2940  
Db 2881 AGACAGTTTAATATCACTCAGGCTTCTGTGTTGTTGGTTCAGAAAGATAGCCAGTTGATA 2940  
Qy 2941 ATGCCAAATGTAGTATCAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTTCAGAGGCA 3000  
Db 2941 ATGCCAAATGTAGTATCAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTTCAGAGGCA 3000  
Qy 3001 ACGAACTGGACTCATTTACTCAAAATAAACATGGAATTTTACAAACCCCATATCGTATAC 3060  
Db 3001 ACGAACTGGACTCATTTACTCAAAATAAACATGGAATTTTACAAACCCCATATCGTATAC 3060

Qy 3061 CACCACITTTTCCCATCAAGTCATTTGTTTAAACCTAAATGTAAAGAAAATCTGCTAGAGG 3120  
Db 3061 CACCACITTTTCCCATCAAGTCATTTGTTTAAACCTAAATGTAAAGAAAATCTGCTAGAGG 3120  
Qy 3121 AAAACTTTTGAGGACATTTCAATGTCACTGAAGAGAAATGGGAATTCAGAACATTTCCAA 3180  
Db 3121 AAAACTTTTGAGGACATTTCAATGTCACTGAAGAGAAATGGGAATTCAGAACATTTCCAA 3180  
Qy 3181 GTACAGTCAGCACAAATTTAGCCGTAATTAACATTTAGAGAAAATGTTTTTAAAGGAGCCAGCT 3240  
Db 3181 GTACAGTCAGCACAAATTTAGCCGTAATTAACATTTAGAGAAAATGTTTTTAAAGGAGCCAGCT 3240  
Qy 3241 CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA 3300  
Db 3241 CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA 3300  
Qy 3301 TAGGTTCCAGTGATGAAGCAATTTCAAGCAGAACTAGGTAGAAACAGAGGGCCAAATTTGA 3360  
Db 3301 TAGGTTCCAGTGATGAAGCAATTTCAAGCAGAACTAGGTAGAAACAGAGGGCCAAATTTGA 3360  
Qy 3361 ATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGGTCTATAAAACAAAGTCTTCTCGAAA 3420  
Db 3361 ATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGGTCTATAAAACAAAGTCTTCTCGAAA 3420  
Qy 3421 GTAAATTTGAAGCACTCTGAAAATAAAAAAGCAAGAAATATGAAGAAAGTAGTTTCAAGACTGTTA 3480  
Db 3421 GTAAATTTGAAGCACTCTGAAAATAAAAAAGCAAGAAATATGAAGAAAGTAGTTTCAAGACTGTTA 3480  
Qy 3481 ATACAGATTTCTCTCCATATCTGATTTTCAAGATACTTTAGAACAGCCCTATGGGAAGTAGTC 3540  
Db 3481 ATACAGATTTCTCTCCATATCTGATTTTCAAGATACTTTAGAACAGCCCTATGGGAAGTAGTC 3540  
Qy 3541 ATGCATCTCAGGTTGTTCTGAGACACCTGATGACCTGTTAGATGATGTTGCAATTAAGG 3600  
Db 3541 ATGCATCTCAGGTTGTTCTGAGACACCTGATGACCTGTTAGATGATGTTGCAATTAAGG 3600  
Qy 3601 AAGTACTAGTTTGTGCAAAATGACATTAAGGAAAGTCTGCTGTTTTTATAGCAAAAGCG 3660  
Db 3601 AAGTACTAGTTTGTGCAAAATGACATTAAGGAAAGTCTGCTGTTTTTATAGCAAAAGCG 3660  
Qy 3661 TCCAGAGAGGAGCTTTAGCAGGAGTCTTAGCCCTTTTCCACCATACACATTTGGCTCAGG 3720  
Db 3661 TCCAGAGAGGAGCTTTAGCAGGAGTCTTAGCCCTTTTCCACCATACACATTTGGCTCAGG 3720  
Qy 3721 GTTACCAAGAGGGGCCAAGAAATTTAGAGTCTCAGAGAGAACTTATCTAGTGAGGATG 3780  
Db 3721 GTTACCAAGAGGGGCCAAGAAATTTAGAGTCTCAGAGAGAACTTATCTAGTGAGGATG 3780  
Qy 3781 AAGAGCTTCCCTGCTTCCAAACACTTTGTTATTTGGTAAAGTAAACAATATACCTTCTCAGT 3840  
Db 3781 AAGAGCTTCCCTGCTTCCAAACACTTTGTTATTTGGTAAAGTAAACAATATACCTTCTCAGT 3840  
Qy 3841 CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGTCTAAGAAACACAGAGAGAAATTTAT 3900  
Db 3841 CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGTCTAAGAAACACAGAGAGAAATTTAT 3900  
Qy 3901 TATCATTTGAAGATAGCTTAAATGACCTGACGTACACAGTAAATTTGGCAAGGCACTCTC 3960  
Db 3901 TATCATTTGAAGATAGCTTAAATGACCTGACGTACACAGTAAATTTGGCAAGGCACTCTC 3960  
Qy 3961 AGGAACATCACTTGTAGTGAGGAAACAAAATGTTCTGCTAGCTGTTTTTCTTCCAGATGCA 4020  
Db 3961 AGGAACATCACTTGTAGTGAGGAAACAAAATGTTCTGCTAGCTGTTTTTCTTCCAGATGCA 4020  
Qy 4021 GTGAATTTGGAAGACTTGACTGCAATTAACAAACCCAGGATCTTCTTGTGATTTGTTCTT 4080  
Db 4021 GTGAATTTGGAAGACTTGACTGCAATTAACAAACCCAGGATCTTCTTGTGATTTGTTCTT 4080  
Qy 4081 CCAACCAATTCAGGCATCAGTCTGAAAGCCAGGAGTTGGTCTGCTGACAGAGAAATGG 4140  
Db 4081 CCAACCAATTCAGGCATCAGTCTGAAAGCCAGGAGTTGGTCTGCTGACAGAGAAATGG 4140



4141 TTTTCAGATGATGAAGAGAGAAACGGCTTGGAGAAAAATAATCAAGAGAGCAAAAGCA 4200  
Db  
4141 TTTTCAGATGATGAAGAGAGAAACGGCTTGGAGAAAAATAATCAAGAGAGCAAAAGCA 4200  
Qy  
4201 TGGATTCAAACCTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAAACAAGCCTCTCTGAAG 4260  
Db  
4201 TGGATTCAAACCTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAAACAAGCCTCTCTGAAG 4260  
Qy  
4261 ACTGCTCAGGGCTATCCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGATACCATGC 4320  
Db  
4261 ACTGCTCAGGGCTATCCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGATACCATGC 4320  
Qy  
4321 AACATAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACTAGAAAGCTGTGTAGAACAGC 4380  
Db  
4321 AACATAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACTAGAAAGCTGTGTAGAACAGC 4380  
Qy  
4381 ATGGAGAGCAGCTTCTAACAGTACCTTCCATCATTAAGTGACTCTTCTGCCCTTGAGG 4440  
Db  
4381 ATGGAGAGCAGCTTCTAACAGTACCTTCCATCATTAAGTGACTCTTCTGCCCTTGAGG 4440  
Qy  
4441 ACCTGCGAAATCCAGAACAAAGCAGCATCAGAAAAAGCAGTATTAACCTTCAGAAAAAGTA 4500  
Db  
4441 ACCTGCGAAATCCAGAACAAAGCAGCATCAGAAAAAGCAGTATTAACCTTCAGAAAAAGTA 4500  
Qy  
4501 GTGAATACCTTATAAGCCAGAAATCCAGAAAGCCCTTTCTGCTGACAAAGTTTCAGGTGTCTG 4560  
Db  
4501 GTGAATACCTTATAAGCCAGAAATCCAGAAAGCCCTTTCTGCTGACAAAGTTTCAGGTGTCTG 4560  
Qy  
4561 CAGATAGTCTACAGTAAATAAAGAACAGAGGTGAAAGTCAATCCCTTCTAAAT 4620  
Db  
4561 CAGATAGTCTACCAAGTAAATAAAGAACAGAGGTGAAAGTCAATCCCTTCTAAAT 4620  
Qy  
4621 GCCCATCATTAGATAGTAGGTGATACATGACAGTGTCTCTGGAGTCTTCAGAAATAGAA 4680  
Db  
4621 GCCCATCATTAGATAGTAGGTGATACATGACAGTGTCTCTGGAGTCTTCAGAAATAGAA 4680  
Qy  
4681 ACTACCCATCTCAAGAGGAGCTCAATTAAGTGTGTGAGTGGAGGAGCAACAGCTGGAAG 4740  
Db  
4681 ACTACCCATCTCAAGAGGAGCTCAATTAAGTGTGTGAGTGGAGGAGCAACAGCTGGAAG 4740  
Qy  
4741 AGTCTGGGCCACAGATTGACGAAACATCTTACCTGCAAGGCAAGATCTAGAGGAA 4800  
Db  
4741 AGTCTGGGCCACAGATTGACGAAACATCTTACCTGCAAGGCAAGATCTAGAGGAA 4800  
Qy  
4801 CCCCTTACTGGAATCTGGAATCAGCTCTCTCTGATGACCCCTGAATCTGATCCTCTG 4860  
Db  
4801 CCCCTTACTGGAATCTGGAATCAGCTCTCTCTGATGACCCCTGAATCTGATCCTCTG 4860  
Qy  
4861 AAGACAGAGCCCCAGAGTCAGCTCGTGTGGCAACATACCATCTTCAACCTCTGCATTGA 4920  
Db  
4861 AAGACAGAGCCCCAGAGTCAGCTCGTGTGGCAACATACCATCTTCAACCTCTGCATTGA 4920  
Qy  
4921 AAGTTCGCCAATTTGAAGTTGCGAATCTGCCAGAGTCCAGCTGCTCATACTACTG 4980  
Db  
4921 AAGTTCGCCAATTTGAAGTTGCGAATCTGCCAGAGTCCAGCTGCTCATACTACTG 4980  
Qy  
4981 ATACTGCTGGGTATAATGCAATGGAAGAAAGTGTGAGCAGGAGAAAGCCAGAAATGACAG 5040  
Db  
4981 ATACTGCTGGGTATAATGCAATGGAAGAAAGTGTGAGCAGGAGAAAGCCAGAAATGACAG 5040  
Qy  
5041 CTTCAACAGAAAGGGTCAACAAAAAGAAATGTCATGTTGGTGTCTGGGCTGACCCAGAAAG 5100  
Db  
5041 CTTCAACAGAAAGGGTCAACAAAAAGAAATGTCATGTTGGTGTCTGGGCTGACCCAGAAAG 5100  
Qy  
5101 AATTATGCTGCTGATACAGTTTGGCAGAAACACCATCATCACTTTAACTTAATCTAATTA 5160  
Db  
5101 AATTATGCTGCTGATACAGTTTGGCAGAAACACCATCATCACTTTAACTTAATCTAATTA 5160  
Qy  
5161 CTGAAGAGACTACTCATCTGTTATGAAACAGAGTGTGAGTTGTGTGTAACGGACAC 5220  
Db  
5161 CTGAAGAGACTACTCATCTGTTATGAAACAGAGTGTGAGTTGTGTGTAACGGACAC 5220  
Qy  
5221 TGAATAATTTTCTAGGAATTCGCGGAGGAAATGGGTAGTTAGCTATTTTCTGGGTGACCC 5280

Db 5221 TGAATAATTTTCTAGGAATTCGCGGAGGAAATGGGTAGTTAGCTATTTTCTGGGTGACCC 5280  
Qy 5281 AGTCTATTAAGAAAGAAAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGAGATGTGG 5340  
Db 5281 AGTCTATTAAGAAAGAAAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGAGATGTGG 5340  
Qy 5341 TCATGGAAGAAACCAACCAAGGTCCAAAGCGAGCAAGAGATCCAGAGCAAGAAAGATCT 5400  
Db 5341 TCAATGGAAGAAACCAACCAAGGTCCAAAGCGAGCAAGAGATCCAGAGCAAGAAAGATCT 5400  
Qy 5401 TCAGGGGCTAGAAATCTGTTGCTATGGGCCCTTCAACCAATGCCACAGATCAACTGG 5460  
Db 5401 TCAGGGGCTAGAAATCTGTTGCTATGGGCCCTTCAACCAATGCCACAGATCAACTGG 5460  
Qy 5461 AATGGATGGTACAGCTGTGTGGTCTCTGTGTGGAAGGAGCTTTTCATTCACCTTTG 5520  
Db 5461 AATGGATGGTACAGCTGTGTGGTCTCTGTGTGGAAGGAGCTTTTCATTCACCTTTG 5520  
Qy 5521 GCACAGGTGTCCACCCCAATTTGTTGCTGTGAGCCAGATGCTTGACAGAGGACAAATGGCT 5580  
Db 5521 GCACAGGTGTCCACCCCAATTTGTTGCTGTGAGCCAGATGCTTGACAGAGGACAAATGGCT 5580  
Qy 5581 TCCATGCAATTTGGGCAGATGTGTGAGGCACCTGTGTGTGACCCGAGAGTGGGTGTGGACA 5640  
Db 5581 TCCATGCAATTTGGGCAGATGTGTGAGGCACCTGTGTGTGACCCGAGAGTGGGTGTGGACA 5640  
Qy 5641 GTGTAGCACTTACCACTGCGAGGAGCTGGACACCTACCTGATACCCCAAGATCCCAACA 5700  
Db 5641 GTGTAGCACTTACCACTGCGAGGAGCTGGACACCTACCTGATACCCCAAGATCCCAACA 5700  
Qy 5701 GCCACTACTGA 5711  
Db 5701 GCCACTACTGA 5711

RESULT 7  
AR112810  
LOCUS AR112810 5711 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 5 from patent US 6130322.  
ACCESSION AR112810  
VERSION AR112810.1 GI:14092710  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 5711)  
AUTHORS Murphy, P.D., Allen, A.C.P., Alvares, C.P., Critz, B.S., Olson, S.J.,  
Thurber, D. and Zeng, B.  
TITLE Coding sequences of the human BRCA1 gene  
JOURNAL Patent: US 6130322-A 5 10-OCT-2000;  
FEATURES Location/Qualifiers  
source 1. 5711  
BASE COUNT 1956 a 1098 c 1274 g 1383 t  
ORIGIN

Query Match 99.8%; Score 5701.4; DB 6; Length 5711;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 5705; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AGCTCGCTGAGACTTCTCTGACCCCGCAGCAGGCTGTGGGGTTTCTCAGATAACTGGGCC 60  
Db 1 AGCTCGCTGAGACTTCTCTGACCCCGCAGCAGGCTGTGGGGTTTCTCAGATAACTGGGCC 60  
Qy 61 CCTGCGCTCAGGAGGCTTCCACCTCTGCTGTGGTAAAGTTCATTGGAACAGAGAA 120  
Db 61 CCTGCGCTCAGGAGGCTTCCACCTCTGCTGTGGTAAAGTTCATTGGAACAGAGAA 120  
Qy 121 TGAATTTATCTGCTTCTCGGCTTGAGAGAGTACAAAATGTCAATATGCTATGCAAAAA 180  
Db 121 TGAATTTATCTGCTTCTCGGCTTGAGAGAGTACAAAATGTCAATATGCTATGCAAAAA 180



181 QY TCTTAGAGTGCCCATCTGTCTGGAGTTGATCAAGGAACCTGTCTCCACAAGTGTGACC 240  
181 Db TCTTAGAGTGCCCATCTGTCTGGAGTTGATCAAGGAACCTGTCTCCACAAGTGTGACC 240  
241 QY ACATATTTTGGCAAAATTTTGCATGCTGAACTTCTCAACCAAGAAAGGGGCTTCCAGT 300  
241 Db ACATATTTTGGCAAAATTTTGCATGCTGAACTTCTCAACCAAGAAAGGGGCTTCCAGT 300  
301 QY GTCCCTTTATGTAAGATGATATAACCAAAAGGAGCCTACAAGAAAGTACGAGATTTAGTC 360  
301 Db GTCCCTTTATGTAAGATGATATAACCAAAAGGAGCCTACAAGAAAGTACGAGATTTAGTC 360  
361 QY AACTTTTGAAGAGCTATGAAATCATTTGTGCTTTTTCAGCTTCAACAGGTTTGGAGT 420  
361 Db AACTTTTGAAGAGCTATGAAATCATTTGTGCTTTTTCAGCTTCAACAGGTTTGGAGT 420  
421 QY ATGCAACAGCTATAATTTTCCAAAAGGAGAAATTAACCTCTCTGAAACATCTAAAGATG 480  
421 Db ATGCAACAGCTATAATTTTCCAAAAGGAGAAATTAACCTCTCTGAAACATCTAAAGATG 480  
481 QY AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAAGACTTCTACAGAGTG 540  
481 Db AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAAGACTTCTACAGAGTG 540  
541 QY AACCCGAAAATCCTTCTCTGAGGAAACCAAGTCTCAGTGTCCAACTCTTAACCTTGAA 600  
541 Db AACCCGAAAATCCTTCTCTGAGGAAACCAAGTCTCAGTGTCCAACTCTTAACCTTGAA 600  
601 QY CTGTGAGAACTCTGAGGAAACCAAGCGGATACAACTCAAGACGCTCTCTACATTTG 660  
601 Db CTGTGAGAACTCTGAGGAAACCAAGCGGATACAACTCAAGACGCTCTCTACATTTG 660  
661 QY AATTGGGATCTGATTTCTGAGATACCGTTTAATGAGCAACTTATTGCGAGTGGGAG 720  
661 Db AATTGGGATCTGATTTCTGAGATACCGTTTAATGAGCAACTTATTGCGAGTGGGAG 720  
721 QY ATCAAGAAATGTTTACAATCAACCTCAAGGAAACCAAGGATGAAATCATGTTGGATCTG 780  
721 Db ATCAAGAAATGTTTACAATCAACCTCAAGGAAACCAAGGATGAAATCATGTTGGATCTG 780  
781 QY CAAAAGAGGCTGCTTGTGAAATTTCTGAGCGGATGTAACAATTAATCAATCATCAAC 840  
781 Db CAAAAGAGGCTGCTTGTGAAATTTCTGAGCGGATGTAACAATTAATCAATCATCAAC 840  
841 QY CCAGTAATAATGATTTGAACCACTGAGAGCGTGACAGTCCAGAGGATCCAGAAAAGT 900  
841 Db CCAGTAATAATGATTTGAACCACTGAGAGCGTGACAGTCCAGAGGATCCAGAAAAGT 900  
901 QY ATCAGGCTAGTTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCAAAAATCTCATGCCA 960  
901 Db ATCAGGCTAGTTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCAAAAATCTCATGCCA 960  
961 QY GCTCAATTCAGCATGAGAACAGCAGTTTATTAATCACTAAGAGACAGATGATGAGAAA 1020  
961 Db GCTCAATTCAGCATGAGAACAGCAGTTTATTAATCACTAAGAGACAGATGATGAGAAA 1020  
1021 QY AGGCTGAATCTGTAATAAGCAACAGCCTGGCTTACGAGGAGCCAAACATACAGAT 1080  
1021 Db AGGCTGAATCTGTAATAAGCAACAGCCTGGCTTACGAGGAGCCAAACATACAGAT 1080  
1081 QY GGGCTGGAAGTAAAGAAACATGTAATGATAGCGGACTCCAGCAGAGAAAAAGGTAG 1140  
1081 Db GGGCTGGAAGTAAAGAAACATGTAATGATAGCGGACTCCAGCAGAGAAAAAGGTAG 1140  
1141 QY ATCTGAATGCTGATCCCTGCTGTGAGAGAAAAGATGGAATTAAGCAGAAAACCTGCCATGCT 1200  
1141 Db ATCTGAATGCTGATCCCTGCTGTGAGAGAAAAGATGGAATTAAGCAGAAAACCTGCCATGCT 1200  
1201 QY CAGAGAACTCTAGATACTGAAGATGTTCTTGGATACACTAATAGCAGCATTCAGA 1260  
1201 Db CAGAGAACTCTAGATACTGAAGATGTTCTTGGATACACTAATAGCAGCATTCAGA 1260  
1261 QY AAGTTAAATGAGTGGTGTTCACAGAAAGTATGAACTGTTAGTGTCTGATGACTCACATGATG 1320

1261 Db AAGTTAAATGAGTGGTGTTCACAGAAAGTATGAACTGTTAGGTTCTGATGACTCACATGATG 1320  
1321 QY GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGATTATGGAGCTTCTAAATGAGGTAGATG 1380  
1321 Db GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGATTATGGAGCTTCTAAATGAGGTAGATG 1380  
1381 QY AATATCTGGTTCTTCAGAGAAAATAGACTTACTTGGCCAGTGATCCTCATGAGGCTTTAA 1440  
1381 Db AATATCTGGTTCTTCAGAGAAAATAGACTTACTTGGCCAGTGATCCTCATGAGGCTTTAA 1440  
1441 QY TATGTAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGAGTAATATTGAGAGCAAAAATAT 1500  
1441 Db TATGTAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGAGTAATATTGAGAGCAAAAATAT 1500  
1501 QY TTGGGAAAAACCTATCGGAAAGAGGCAAGCCCTCCCAACTTAAGCCATGTAATCAAAAATC 1560  
1501 Db TTGGGAAAAACCTATCGGAAAGAGGCAAGCCCTCCCAACTTAAGCCATGTAATCAAAAATC 1560  
1561 QY TAATATAGGAGCAATTTGTTACTGAGCCACAGATAATAACAAGAGGCTCCCTCACAATA 1620  
1561 Db TAATATAGGAGCAATTTGTTACTGAGCCACAGATAATAACAAGAGGCTCCCTCACAATA 1620  
1621 QY AATTAAAGCGTAAAGAGGACCTACATCAGGCTTCTCTGAGGATTTTATCAAGAAAG 1680  
1621 Db AATTAAAGCGTAAAGAGGACCTACATCAGGCTTCTCTGAGGATTTTATCAAGAAAG 1680  
1681 QY CAGATTTGGCAGTTTCAAAAGACTCTGAAATGATAAATCAGGGAACCTAACCAACGGAGC 1740  
1681 Db CAGATTTGGCAGTTTCAAAAGACTCTGAAATGATAAATCAGGGAACCTAACCAACGGAGC 1740  
1741 QY AGAATGGTCAAGTGATGAATTAATTAATAGTGTGATGAGAAATAAAACAAAAGGTGAT 1800  
1741 Db AGAATGGTCAAGTGATGAATTAATTAATAGTGTGATGAGAAATAAAACAAAAGGTGAT 1800  
1801 QY CTATTCAAGATGAGAAAATCCTTAACCAATAGAACTCACTCGAAAAGAAATCTGCTTCA 1860  
1801 Db CTATTCAAGATGAGAAAATCCTTAACCAATAGAACTCACTCGAAAAGAAATCTGCTTCA 1860  
1861 QY AAAACGAAGCTGAACCTTATAAGCAGCAGTAAAGCAATATGGAACCTCAAAATTAATATCC 1920  
1861 Db AAAACGAAGCTGAACCTTATAAGCAGCAGTAAAGCAATATGGAACCTCAAAATTAATATCC 1920  
1921 QY ACAATTTCAAAAGCACCTTAAAGAAATAGGCTGAGGAGAAAGTCTTCTACAGGCAATTC 1980  
1921 Db ACAATTTCAAAAGCACCTTAAAGAAATAGGCTGAGGAGAAAGTCTTCTACAGGCAATTC 1980  
1981 QY ATGGCTTGAACCTAGTAGTGAATTAATTAAGCCACCTTAATTTGATGTAATTTGCAAA 2040  
1981 Db ATGGCTTGAACCTAGTAGTGAATTAATTAAGCCACCTTAATTTGATGTAATTTGCAAA 2040  
2041 QY TTGATAGTTGTTCTAGCAGTGAAGATAAAAGAAAAAAGTACAAACCAATGCCAGTCA 2100  
2041 Db TTGATAGTTGTTCTAGCAGTGAAGATAAAAGAAAAAAGTACAAACCAATGCCAGTCA 2100  
2101 QY GGCACAGCAGAAAACCTCAACTCATGGAAGTAAAGAAACCTGCAACTGGAGCAGAAAGA 2160  
2101 Db GGCACAGCAGAAAACCTCAACTCATGGAAGTAAAGAAACCTGCAACTGGAGCAGAAAGA 2160  
2161 QY GTAAACAGCCAAATGAACAGACAAGTAAAGACATGACAGTGATATCTTCCAGAGCTGA 2220  
2161 Db GTAAACAGCCAAATGAACAGACAAGTAAAGACATGACAGTGATATCTTCCAGAGCTGA 2220  
2221 QY AGTTTAAACAAATGCACTGCTGTTCTTTACTTAAGTGTTCAAATCAGTGAACCTTAAAGAT 2280  
2221 Db AGTTTAAACAAATGCACTGCTGTTCTTTACTTAAGTGTTCAAATCAGTGAACCTTAAAGAT 2280  
2281 QY TTGTCAAATCTAGCCTTCCAGAGAGAAAAGAGAGAAAACCTAGAAAACAGTTAAAGTGT 2340  
2281 Db TTGTCAAATCTAGCCTTCCAGAGAGAAAAGAGAGAAAACCTAGAAAACAGTTAAAGTGT 2340  
2341 QY CTAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGGTTTTCGAAAAC 2400

Db 2341 CTAATAATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGGTTTTGCAAACTG 2400  
Qy 2401 AAAGATCTGTAGAGTAGTACAGTATTTCACTGGTACCTGTACTGATTATGSCACTCAGG 2460  
Db 2401 AAAGATCTGTAGAGTAGTACAGTATTTCACTGGTACCTGTACTGATTATGSCACTCAGG 2460  
Qy 2461 AAAGATCTCGTTACTGGAAGTTAGCACTCTAGGGAAGGCCAAAAACAGAACCAATAAAT 2520  
Db 2461 AAAGATCTCGTTACTGGAAGTTAGCACTCTAGGGAAGGCCAAAAACAGAACCAATAAAT 2520  
Qy 2521 GTGTGAGTCAGTGTGACAGCATTTGAAACCCCAAGGACCTAATTCATGGTTGTTCCAAAG 2580  
Db 2521 GTGTGAGTCAGTGTGACAGCATTTGAAACCCCAAGGACCTAATTCATGGTTGTTCCAAAG 2580  
Qy 2581 ATAATAGAAATGACACAGAGGCTTTAAGTATCCATTGGGACATGAAGTTAAACACAGTC 2640  
Db 2581 ATAATAGAAATGACACAGAGGCTTTAAGTATCCATTGGGACATGAAGTTAAACACAGTC 2640  
Qy 2641 GGGAAACAAGCATAGAAATGGAAGAAAGTGAACCTTGATGCTCAGTATTTGCGAGAAATACAT 2700  
Db 2641 GGGAAACAAGCATAGAAATGGAAGAAAGTGAACCTTGATGCTCAGTATTTGCGAGAAATACAT 2700  
Qy 2701 TCAAGGTTTCAAAGGCCAGTCATTTGCTCTGTTTTCAAATCCAGGAAATGCAGAGG 2760  
Db 2701 TCAAGGTTTCAAAGGCCAGTCATTTGCTCTGTTTTCAAATCCAGGAAATGCAGAGG 2760  
Qy 2761 AATGTCAACATCTCTGCCCACTCTGGTCTCTTAAAGAAACAAGTCCAAAGTCACTT 2820  
Db 2761 AATGTCAACATCTCTGCCCACTCTGGTCTCTTAAAGAAACAAGTCCAAAGTCACTT 2820  
Qy 2821 TTGAATGTGAACAAAGGAAGAAATCAAGAAAGAAATGAGTCTAATATCAAGGCTGTAC 2880  
Db 2821 TTGAATGTGAACAAAGGAAGAAATCAAGAAAGAAATGAGTCTAATATCAAGGCTGTAC 2880  
Qy 2881 AGACAGTTAATATCATCTCAGGCTTTCTGTTGGTTCAGAAAGATAAGCCAGTTGATA 2940  
Db 2881 AGACAGTTAATATCATCTCAGGCTTTCTGTTGGTTCAGAAAGATAAGCCAGTTGATA 2940  
Qy 2941 ATGCCAAATGATCAAGAGGCTCTAGGTTTTGCTATCATCTCAGTTCCAGAGGCA 3000  
Db 2941 ATGCCAAATGATCAAGAGGCTCTAGGTTTTGCTATCATCTCAGTTCCAGAGGCA 3000  
Qy 3001 ACGAACTGGAGCTCACTTACTCCAAATAAACATGGAATTTTACAAACCCATATCGTATAC 3060  
Db 3001 ACGAACTGGAGCTCACTTACTCCAAATAAACATGGAATTTTACAAACCCATATCGTATAC 3060  
Qy 3061 CACCACTTTTCCCATCAAGTCATTTGTTAAAACCTAATGTAAGAAATCTGCTAGAGG 3120  
Db 3061 CACCACTTTTCCCATCAAGTCATTTGTTAAAACCTAATGTAAGAAATCTGCTAGAGG 3120  
Qy 3121 AAAAATTTGAGGAACATTCATGTCACTGAAAGAGAAATGGGAAATGAGAACATTCCAA 3180  
Db 3121 AAAAATTTGAGGAACATTCATGTCACTGAAAGAGAAATGGGAAATGAGAACATTCCAA 3180  
Qy 3181 GTACAGTGAGCACAAATAGCCGTAATAACATTAGAGAAATGTTTTTAAAGAGCCAGCT 3240  
Db 3181 GTACAGTGAGCACAAATAGCCGTAATAACATTAGAGAAATGTTTTTAAAGAGCCAGCT 3240  
Qy 3241 CAAGCAATTAATTAAGTAGGTTCCAGTACTAATAGAGTGGGCTCCAGTATTAATGAAA 3300  
Db 3241 CAAGCAATTAATTAAGTAGGTTCCAGTACTAATAGAGTGGGCTCCAGTATTAATGAAA 3300  
Qy 3301 TAGGTTCCAGTGATGAACAACTCAAGCAGAACTAGGTAGNAAACAGAGGGCCAAATGGA 3360  
Db 3301 TAGGTTCCAGTGATGAACAACTCAAGCAGAACTAGGTAGNAAACAGAGGGCCAAATGGA 3360  
Qy 3361 ATGCTATGCTTAGATTAGGGGTTTTGCAACTGAGGCTATAAAACAAAGTCTTCCCTGAAA 3420  
Db 3361 ATGCTATGCTTAGATTAGGGGTTTTGCAACTGAGGCTATAAAACAAAGTCTTCCCTGAAA 3420  
Qy 3421 GTAATTGAGCATCTCGAAATAAAAAAGCAAGAAATATGAAGAGTAGTTTCAGACTGTTA 3480  
Db 3421 GTAATTGAGCATCTCGAAATAAAAAAGCAAGAAATATGAAGAGTAGTTTCAGACTGTTA 3480

Qy 3481 ATACAGATTTCTCTCCATATCTGATTTTCAGATACTTTAGAACAGCCTATGGNAGTAGTC 3540  
Db 3481 ATACAGATTTCTCTCCATATCTGATTTTCAGATACTTTAGAACAGCCTATGGNAGTAGTC 3540  
Qy 3541 ATGCATCTCAGGTTTGTCTTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGG 3600  
Db 3541 ATGCATCTCAGGTTTGTCTTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGG 3600  
Qy 3601 AAGATACCTAGTTTGTCTGAAAAATGACATTAAGGAAAGTTCTGCTGTTTTTAGCAAAAAGCG 3660  
Db 3601 AAGATACCTAGTTTGTCTGAAAAATGACATTAAGGAAAGTTCTGCTGTTTTTAGCAAAAAGCG 3660  
Qy 3661 TCCAGAGAGGAGGCTTAGCAGGAGTCTTAGCCCTTTTCCATACACATTTGCTCAGG 3720  
Db 3661 TCCAGAGAGGAGGCTTAGCAGGAGTCTTAGCCCTTTTCCATACACATTTGCTCAGG 3720  
Qy 3721 GTTACCGAAGAGGGGCCCAAGAAATTTAGAGTCTCAGAGAGAACTTATCTAGTCAGAGATG 3780  
Db 3721 GTTACCGAAGAGGGGCCCAAGAAATTTAGAGTCTCAGAGAGAACTTATCTAGTCAGAGATG 3780  
Qy 3781 AAGAGCTTCCCTGCTTCCAAACACTTGTATTTGGTAAAGTAAACAATATACCTTCTCAGT 3840  
Db 3781 AAGAGCTTCCCTGCTTCCAAACACTTGTATTTGGTAAAGTAAACAATATACCTTCTCAGT 3840  
Qy 3841 CTACTAGGCATAGCACCGTGTCTACCGAGTGTCTGTCTAAGAACACAGAGAGAAATTTAT 3900  
Db 3841 CTACTAGGCATAGCACCGTGTCTACCGAGTGTCTGTCTAAGAACACAGAGAGAAATTTAT 3900  
Qy 3901 TATCATTTGAAGAAATAGCTTAAATGACTGCAGTAAACAGGTAATATTTGGCAAGGCATCTC 3960  
Db 3901 TATCATTTGAAGAAATAGCTTAAATGACTGCAGTAAACAGGTAATATTTGGCAAGGCATCTC 3960  
Qy 3961 AGGAACATCACTTGTAGTGAGGAAACAAAATGTTCTGTCTAGCTGTTTTTCTTCACAGTGCA 4020  
Db 3961 AGGAACATCACTTGTAGTGAGGAAACAAAATGTTCTGTCTAGCTGTTTTTCTTCACAGTGCA 4020  
Qy 4021 GTGAATTTGGAGAGCTTGCATGCAAAATAACAACCCAGGATCCCTTCTGATTTGGTCTT 4080  
Db 4021 GTGAATTTGGAGAGCTTGCATGCAAAATAACAACCCAGGATCCCTTCTGATTTGGTCTT 4080  
Qy 4081 CCAACAAATAGGAGCATCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGCAAGGAAATGG 4140  
Db 4081 CCAACAAATAGGAGCATCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGCAAGGAAATGG 4140  
Qy 4141 TTTCAGATGATGAAGAAAGAGGAAACGGGCTTTGGAAGAAAAATAATCAAGAGAGCAAAAGCA 4200  
Db 4141 TTTCAGATGATGAAGAAAGAGGAAACGGGCTTTGGAAGAAAAATAATCAAGAGAGCAAAAGCA 4200  
Qy 4201 TGGATTCAAAATTTAGGTGAAGCAGCATCTCGGTGTGAGAGTGAAACAGCGCTCTCTGAAG 4260  
Db 4201 TGGATTCAAAATTTAGGTGAAGCAGCATCTCGGTGTGAGAGTGAAACAGCGCTCTCTGAAG 4260  
Qy 4261 ACTGCTCAGGCTATCTCTCAGAGTGACATTTTAAACCTCAGCAGAGGATACCATGC 4320  
Db 4261 ACTGCTCAGGCTATCTCTCAGAGTGACATTTTAAACCTCAGCAGAGGATACCATGC 4320  
Qy 4321 AACATAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACCTAGAACTGTGTAGAACAGC 4380  
Db 4321 AACATAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACCTAGAACTGTGTAGAACAGC 4380  
Qy 4381 ATGGGAGCCAGCTTCTTAAACAGTACCTTCCATCATTAAGTGACTCTCTGCCCTTTCAGG 4440  
Db 4381 ATGGGAGCCAGCTTCTTAAACAGTACCTTCCATCATTAAGTGACTCTCTGCCCTTTCAGG 4440  
Qy 4441 ACCTGCGAAATCCAGAAACAGACATCAGAAAAAGCAGTATTAACCTTCACAGAAAAAGTA 4500  
Db 4441 ACCTGCGAAATCCAGAAACAGACATCAGAAAAAGCAGTATTAACCTTCACAGAAAAAGTA 4500  
Qy 4501 GTGAATACCTTATAAGCCAGAAATCCAGAAAGCCCTTTCTGCTGACAGAGTTGAGTGTCTG 4560  
Db 4501 GTGAATACCTTATAAGCCAGAAATCCAGAAAGCCCTTTCTGCTGACAGAGTTGAGTGTCTG 4560

Qy 4561 CAGATAGTTCTACAGTAAATAAAGAACAGAGAGTGGAAAGTCAATCCCTTCTAAAT 4620  
Db |||||||  
Qy 4561 CAGATAGTTCTACAGTAAATAAAGAACAGAGAGTGGAAAGTCAATCCCTTCTAAAT 4620  
Db |||||||  
Qy 4621 GCCCATCATAGATGATAGTGGTACATGACAGTGTCTCTGGAGTCTTCAGAAATAGAA 4680  
Db |||||||  
Qy 4621 GCCCATCATAGATGATAGTGGTACATGACAGTGTCTCTGGAGTCTTCAGAAATAGAA 4680  
Db |||||||  
Qy 4681 ACTACCATCTCAAGAGGAGCTCAATTAAGTGTGTGATGGAGGACACAGCTGGAAG 4740  
Db |||||||  
Qy 4681 ACTACCATCTCAAGAGGAGCTCAATTAAGTGTGTGATGGAGGACACAGCTGGAAG 4740  
Db |||||||  
Qy 4741 AGTCTGGGCCACAGATTTGACGAAACATCTTACTTGCACAGGCAAGATCTAGAGGAA 4800  
Db |||||||  
Qy 4741 AGTCTGGGCCACAGATTTGACGAAACATCTTACTTGCACAGGCAAGATCTAGAGGAA 4800  
Db |||||||  
Qy 4801 CCCCTTACCTGGATCTGGAATCAGCCTCTTCTCTGATGACCCCTGAATCTGATCCTTCTG 4860  
Db |||||||  
Qy 4801 CCCCTTACCTGGATCTGGAATCAGCCTCTTCTCTGATGACCCCTGAATCTGATCCTTCTG 4860  
Db |||||||  
Qy 4861 AAGACAGAGCCCCAGAGTCAGCTCGTGTGTGCAACATACCATCTTCAACCTCTGCAATGA 4920  
Db |||||||  
Qy 4861 AAGACAGAGCCCCAGAGTCAGCTCGTGTGTGCAACATACCATCTTCAACCTCTGCAATGA 4920  
Db |||||||  
Qy 4921 AAGTTCCCAATTTGAAAGTTGCAAGATCTGCCAGAGTCCAGCTGCTCTACTACTG 4980  
Db |||||||  
Qy 4921 AAGTTCCCAATTTGAAAGTTGCAAGATCTGCCAGAGTCCAGCTGCTCTACTACTG 4980  
Db |||||||  
Qy 4981 ATACTGCTGGGTATTAATGCAATGGAAGAAAGTGTGAGCAGGGAAGCCAGAAATGACAG 5040  
Db |||||||  
Qy 4981 ATACTGCTGGGTATTAATGCAATGGAAGAAAGTGTGAGCAGGGAAGCCAGAAATGACAG 5040  
Db |||||||  
Qy 5041 CTTCAACAGAAAGGTCACAAAGAAATGTCATGCTGGTGTCTGGCTGACCCAGAGAG 5100  
Db |||||||  
Qy 5041 CTTCAACAGAAAGGTCACAAAGAAATGTCATGCTGGTGTCTGGCTGACCCAGAGAG 5100  
Db |||||||  
Qy 5101 AATTTATGCTCGTGTACAAAGTTTGCAGAAACACCAATCACTTTAACTAATCTAATTA 5160  
Db |||||||  
Qy 5101 AATTTATGCTCGTGTACAAAGTTTGCAGAAACACCAATCACTTTAACTAATCTAATTA 5160  
Db |||||||  
Qy 5161 CTGAAGAGACTACTCATGTTGTATGAAAACAGATGCTGAGTTGTGTGTAACGGACAC 5220  
Db |||||||  
Qy 5161 CTGAAGAGACTACTCATGTTGTATGAAAACAGATGCTGAGTTGTGTGTAACGGACAC 5220  
Db |||||||  
Qy 5221 TGAATAATTTCTAGGAATTCGGGAGGAAATGGTGTAGTTAGTTATTTCTGGGTGACCC 5280  
Db |||||||  
Qy 5221 TGAATAATTTCTAGGAATTCGGGAGGAAATGGTGTAGTTAGTTATTTCTGGGTGACCC 5280  
Db |||||||  
Qy 5281 AGTCTATTAAAGAAAGAAATGCTGAAATGAGCATGATTTTGAAGTCAAGAGAGATGTGG 5340  
Db |||||||  
Qy 5281 AGTCTATTAAAGAAAGAAATGCTGAAATGAGCATGATTTTGAAGTCAAGAGAGATGTGG 5340  
Db |||||||  
Qy 5341 TCAATGGAAGAAACACCAAGGTCAGAGGAGCAAGAGATCCAGAGCAGAAAGATCT 5400  
Db |||||||  
Qy 5341 TCAATGGAAGAAACACCAAGGTCAGAGGAGCAAGAGATCCAGAGCAGAAAGATCT 5400  
Db |||||||  
Qy 5401 TCAGGGGCTAGAAATCTGTTGCTATGGGCCCTTCAACCAACATGCCACAGATCAACTGG 5460  
Db |||||||  
Qy 5401 TCAGGGGCTAGAAATCTGTTGCTATGGGCCCTTCAACCAACATGCCACAGATCAACTGG 5460  
Db |||||||  
Qy 5461 AATGATGGTACAGCTGTGTGTGCTCTGTGGTGAAGAGCTTTTCATCTACCCCTTG 5520  
Db |||||||  
Qy 5461 AATGATGGTACAGCTGTGTGTGCTCTGTGGTGAAGAGCTTTTCATCTACCCCTTG 5520  
Db |||||||  
Qy 5521 GCACAGGTGTCCACCAATTTGTTGGTGTGTCAGGCAAGATGCTTGGACAGAGCAATGGCT 5580  
Db |||||||  
Qy 5521 GCACAGGTGTCCACCAATTTGTTGGTGTGTCAGGCAAGATGCTTGGACAGAGCAATGGCT 5580  
Db |||||||  
Qy 5581 TCCATGCAATTTGGGCAGATGTGTAGGCAACCTGTGTGACCCGAGAGTGGTGTGGACA 5640  
Db |||||||  
Qy 5581 TCCATGCAATTTGGGCAGATGTGTAGGCAACCTGTGTGACCCGAGAGTGGTGTGGACA 5640  
Db |||||||  
Qy 5641 GTGTAGCACTCTACAGTGCCAGGAGCTGGACACCTACTGATACCCAGATCCCCCACA 5700

Db 5641 GTGTAGCACTCTACAGTCCAGAGCTGGACACCTACTGATACCCAGATCCCCCACA 5700  
Qy |||||||  
Db 5701 GCCACTACTGA 5711  
Qy |||||||  
Db 5701 GCCACTACTGA 5711  
Qy |||||||  
RESULT 8  
AR033056  
LOCUS AR033056 5711 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 1 from patent US 5869245.  
ACCESSION AR033056  
VERSION AR033056.1 GI:5948661  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 5711)  
AUTHORS Yeung,A.T.  
TITLE Mismatch endonuclease and its use in identifying mutations in  
targeted polynucleotide strands  
JOURNAL Patent: US 5869245-A 1 09-FEB-1999;  
FEATURES Location/Qualifiers  
source 1..5711  
BASE COUNT 1956 a 1099 c 1274 g 1382 t  
ORIGIN  
Query Match 99.8%; Score 5699.8; DB 6; Length 5711;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 5704; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
Qy 1 AGCTCGCTGAGACTTCCTGGACCCCGACACAGGCTGTGGGGTTTCTCAGATAAAGTGGGCC 60  
Db |||||||  
Qy 1 AGCTCGCTGAGACTTCCTGGACCCCGACACAGGCTGTGGGGTTTCTCAGATAAAGTGGGCC 60  
Db |||||||  
Qy 61 CCTCGCTCAGGAGGCTTCACTCTGCTGCTGGTAAAGTTCAATGTTGAAACAGAAAGAAA 120  
Db |||||||  
Qy 61 CCTCGCTCAGGAGGCTTCACTCTGCTGCTGGTAAAGTTCAATGTTGAAACAGAAAGAAA 120  
Db |||||||  
Qy 121 TGGATTTATCTGCTCTCGGCTGACAGAGTACAAAATGCTAATTAATGCTATGCAAGAAA 180  
Db |||||||  
Qy 121 TGGATTTATCTGCTCTCGGCTGACAGAGTACAAAATGCTAATTAATGCTATGCAAGAAA 180  
Db |||||||  
Qy 181 TCTTAGAGTGCCCATCTGCTGAGTTGATCAAGGAACCTGTCTCCACAAAGTGTGACC 240  
Db |||||||  
Qy 181 TCTTAGAGTGCCCATCTGCTGAGTTGATCAAGGAACCTGTCTCCACAAAGTGTGACC 240  
Db |||||||  
Qy 241 ACATATTTTGCAAAATTTTGCAATGCTGAACTTCTCAACAGAGAAAGGGCTTCCACAGT 300  
Db |||||||  
Qy 241 ACATATTTTGCAAAATTTTGCAATGCTGAACTTCTCAACAGAGAAAGGGCTTCCACAGT 300  
Db |||||||  
Qy 301 GTCCTTTATGTAAGATGATATAACCAAGAGGCTTACAGAAAGTACAGATTTAGTTC 360  
Db |||||||  
Qy 301 GTCCTTTATGTAAGATGATATAACCAAGAGGCTTACAGAAAGTACAGATTTAGTTC 360  
Db |||||||  
Qy 361 AACTTTGTTGAAGAGCTATTGAAAATCATTTGTGCTTTTTCAGCTTGCACACAGTGTGGAGT 420  
Db |||||||  
Qy 361 AACTTTGTTGAAGAGCTATTGAAAATCATTTGTGCTTTTTCAGCTTGCACACAGTGTGGAGT 420  
Db |||||||  
Qy 421 ATGCAAAACAGCTATAATTTTGCAAAAAGGAAAAATACTCTCTGTAACATCTTAAAGATG 480  
Db |||||||  
Qy 421 ATGCAAAACAGCTATAATTTTGCAAAAAGGAAAAATACTCTCTGTAACATCTTAAAGATG 480  
Db |||||||  
Qy 481 AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCAAAAGACTTCTACAGAGTG 540  
Db |||||||  
Qy 481 AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCAAAAGACTTCTACAGAGTG 540  
Db |||||||  
Qy 541 AACCCGAAAATCCTTCTTGGCAGGAAACCTGTCTCAGTGTCCAACTCTCTAACCTTTGAA 600  
Db |||||||  
Qy 541 AACCCGAAAATCCTTCTTGGCAGGAAACCTGTCTCAGTGTCCAACTCTCTAACCTTTGAA 600  
Db |||||||

QY 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCTCAAAAGACGCTGTGTACATTTG 660  
DB 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCTCAAAAGACGCTGTGTACATTTG 660  
QY 661 AATTGGGATCTGATTTCTGAGAGTACCGTTAATAAGGCAACTTATTGCGAGTGTGGAG 720  
DB 661 AATTGGGATCTGATTTCTGAGAGTACCGTTAATAAGGCAACTTATTGCGAGTGTGGAG 720  
QY 721 ATCAAGAAATGTTTACAAATCAACCTCAAGGAACCCAGGGATGAAATCAGTTTGGATTTCTG 780  
DB 721 ATCAAGAAATGTTTACAAATCAACCTCAAGGAACCCAGGGATGAAATCAGTTTGGATTTCTG 780  
QY 781 CAAAAAGGCTGCTTGTGAAATTTCTGAGACGGATGTAACAAATCTCAACATCATCAAC 840  
DB 781 CAAAAAGGCTGCTTGTGAAATTTCTGAGACGGATGTAACAAATCTCAACATCATCAAC 840  
QY 841 CCAGTAAATGATTTGAAACCACTGAGAGCGGTGACGCTGAGAGGATCCAGAAAGT 900  
DB 841 CCAGTAAATGATTTGAAACCACTGAGAGCGGTGACGCTGAGAGGATCCAGAAAGT 900  
QY 901 ATCAGGCTAGTCTGTTTCAACCTTGCATGTGGAGCCATGTGGCACAATACTCATGCCA 960  
DB 901 ATCAGGCTAGTCTGTTTCAACCTTGCATGTGGAGCCATGTGGCACAATACTCATGCCA 960  
QY 961 GCTCATTAACAGCATGAGAACAGCAGTTTATTACTCACTAATAAGACAGATGAATGTAGAA 1020  
DB 961 GCTCATTAACAGCATGAGAACAGCAGTTTATTACTCACTAATAAGACAGATGAATGTAGAA 1020  
QY 1021 AGGCTGAATTTCTGTAATAAAGCAAAAGCTGTGGCTTAGCAAGGCGCAACATTAACAGAT 1080  
DB 1021 AGGCTGAATTTCTGTAATAAAGCAAAAGCTGTGGCTTAGCAAGGCGCAACATTAACAGAT 1080  
QY 1081 GGGCTGGAAGTAAGCAACATGTAATGATGGCGGACTCCAGCAGCAGCAAAAGGCTAG 1140  
DB 1081 GGGCTGGAAGTAAGCAACATGTAATGATGGCGGACTCCAGCAGCAGCAAAAGGCTAG 1140  
QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGGAATAAGCAGAAACTGCCATGCT 1200  
DB 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGGAATAAGCAGAAACTGCCATGCT 1200  
QY 1201 CAGAGAACTCTAGAGATACTGAAGATGTTCTTGATTAACACTAAATAGCAGCATTCAGA 1260  
DB 1201 CAGAGAACTCTAGAGATACTGAAGATGTTCTTGATTAACACTAAATAGCAGCATTCAGA 1260  
QY 1261 AAGTTAATGAGTGTGTTTCCAGAGAGTGAATGAATGTTAGGTTCTGATGACCTCAATGATG 1320  
DB 1261 AAGTTAATGAGTGTGTTTCCAGAGAGTGAATGAATGTTAGGTTCTGATGACCTCAATGATG 1320  
QY 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGTAATTGGAGCTTCTAAATGAGGTAGATG 1380  
DB 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGTAATTGGAGCTTCTAAATGAGGTAGATG 1380  
QY 1381 AATATCTGTTTCTAGAGAAATAGACTTACTTGGCCAGTGATCTCTCATGAGGCTTTAA 1440  
DB 1381 AATATCTGTTTCTCTAGAGAAATAGACTTACTTGGCCAGTGATCTCTCATGAGGCTTTAA 1440  
QY 1441 TATGTAAAGTGAAGAGTTCACCTCCAAATCAGTAGAGAGTAAATTTGAAGACAAATAT 1500  
DB 1441 TATGTAAAGTGAAGAGTTCACCTCCAAATCAGTAGAGAGTAAATTTGAAGACAAATAT 1500  
QY 1501 TTGGGAAAACTATCGGAAGAGGCAAGCCCTCCCAACTTAAGCCATGTAATCTGAAATC 1560  
DB 1501 TTGGGAAAACTATCGGAAGAGGCAAGCCCTCCCAACTTAAGCCATGTAATCTGAAATC 1560  
QY 1561 TAATTTAGGAGCATTTGTTTACTGAGGCAAGATAAATCAAGAGCGTCCCTCTCAAAATA 1620  
DB 1561 TAATTTAGGAGCATTTGTTTACTGAGGCAAGATAAATCAAGAGCGTCCCTCTCAAAATA 1620  
QY 1621 AATTTAAAGCGTAAAGGAGACCTACATCAGGCTTCTCATCTGAGGATTTTATCAAGAAAG 1680  
DB 1621 AATTTAAAGCGTAAAGGAGACCTACATCAGGCTTCTCATCTGAGGATTTTATCAAGAAAG 1680  
QY 1681 CAGATTTGGCAGTTTCAAAAGACTCTCTGAAATGATAAATCAGGGAACCTAAACCAACGGAGC 1740

DB 1681 CAGATTTGGCAGTTTCAAAAGACTCTCTGAAATGATAAATCAGGGAACCTAAACCAACGGAGC 1740  
QY 1741 AGAATGTCAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1800  
DB 1741 AGAATGTCAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1800  
QY 1801 CTATTTCAAGATGAGAAATCTTAACCAATAGAAATCACTCGAAAGAAAGATCTGCTTTCA 1860  
DB 1801 CTATTTCAAGATGAGAAATCTTAACCAATAGAAATCACTCGAAAGAAAGATCTGCTTTCA 1860  
QY 1861 AAACGAAAGCTGAAACCTTAAAGCAGCAGTAAAGCAATATGGAATCTGAAATTAATATCC 1920  
DB 1861 AAACGAAAGCTGAAACCTTAAAGCAGCAGTAAAGCAATATGGAATCTGAAATTAATATCC 1920  
QY 1921 ACAATTTCAAAAGCACTTAAAGAAATAGGCTGAGGAGGAAGTCTTTACAGGCAATATTC 1980  
DB 1921 ACAATTTCAAAAGCACTTAAAGAAATAGGCTGAGGAGGAAGTCTTTACAGGCAATATTC 1980  
QY 1981 ATGCGCTTGAACCTAGTGTAGTAAATCTTAAGCCCACTTAATTTGACTGAATTTGCAAA 2040  
DB 1981 ATGCGCTTGAACCTAGTGTAGTAAATCTTAAGCCCACTTAATTTGACTGAATTTGCAAA 2040  
QY 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATAAGAAAAAGTACAAACCAATGCCAGTCA 2100  
DB 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATAAGAAAAAGTACAAACCAATGCCAGTCA 2100  
QY 2101 GGCAACAGAGAAACCTTAACCTAATGGAAGTAAAGAACTGCAACTGGAGCCCAAGAGA 2160  
DB 2101 GGCAACAGAGAAACCTTAACCTAATGGAAGTAAAGAACTGCAACTGGAGCCCAAGAGA 2160  
QY 2161 GTAAACAGCCAAATGAACAGACAGTAAGACATGACAGTGATCTTTCCAGAGCTGA 2220  
DB 2161 GTAAACAGCCAAATGAACAGACAGTAAGACATGACAGTGATCTTTCCAGAGCTGA 2220  
QY 2221 AGTTAAACAAATGCACTGCTGTTTCTTAAGTCTTCAAAATACCAGTGAACTTAAAGAAAT 2280  
DB 2221 AGTTAAACAAATGCACTGCTGTTTCTTAAGTCTTCAAAATACCAGTGAACTTAAAGAAAT 2280  
QY 2281 TTGTCATCTAGCCTTCCAGAGAGAGAAAGAGAGAACTAGAGAACTAGAGAACTAGAGTGT 2340  
DB 2281 TTGTCATCTAGCCTTCCAGAGAGAGAAAGAGAGAACTAGAGAACTAGAGAACTAGAGTGT 2340  
QY 2341 CTAAATATGTCGAGAGCCCAAGATCTCATGTTAAGTGAGAGAGGTTTTCAGAACTG 2400  
DB 2341 CTAAATATGTCGAGAGCCCAAGATCTCATGTTAAGTGAGAGAGGTTTTCAGAACTG 2400  
QY 2401 AAAGATCTGTAGAGAGTAGCAGTATTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2460  
DB 2401 AAAGATCTGTAGAGAGTAGCAGTATTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2460  
QY 2461 AAAGTATCTGTTTACTGGAAGTTAGCAGTCTAGGGAAGGCAAAACAGAACTAAAT 2520  
DB 2461 AAAGTATCTGTTTACTGGAAGTTAGCAGTCTAGGGAAGGCAAAACAGAACTAAAT 2520  
QY 2521 GTGTGAGTGTGAGAGCTTGAAGAACTTGAAGAACTTGAAGAACTTGAAGAACTTGAAGAACT 2580  
DB 2521 GTGTGAGTGTGAGAGCTTGAAGAACTTGAAGAACTTGAAGAACTTGAAGAACTTGAAGAACT 2580  
QY 2581 AATAAGAAATGACACAGAAAGGCTTAAAGTATCCATTTGGGACATGAAAGTTAAACACAGTCT 2640  
DB 2581 AATAAGAAATGACACAGAAAGGCTTAAAGTATCCATTTGGGACATGAAAGTTAAACACAGTCT 2640  
QY 2641 GGGAAACAGCATAGAAATGGAAGAAAGTGAATTTGATGCTCAGTATTTGAGAAATACAT 2700  
DB 2641 GGGAAACAGCATAGAAATGGAAGAAAGTGAATTTGATGCTCAGTATTTGAGAAATACAT 2700  
QY 2701 TCAGGTTTCAAGGCGCAGTCTATTTGCTCTGTTTCCAAATCCAGGAAATCCAGAGAGG 2760  
DB 2701 TCAGGTTTCAAGGCGCAGTCTATTTGCTCTGTTTCCAAATCCAGGAAATCCAGAGAGG 2760  
QY 2761 AATGTGCAACATTTCTGCGCCACTCTGGGCTCTTAAAGAAACAAAGTCCAAAGTCACTTT 2820

Db 2761 AATGTGCAACATTCTCTGCCCACTCTGGGTCTTTAAGAAACAAGTCCAAAAGTCACCTT 2820  
Qy 2821 TTGAATGTGAACAAAAGGAAGAAATCAAGAAAGAAATAGATCTAAATATCAAGCCTGTAC 2880  
Db 2821 TTGAATGTGAACAAAAGGAAGAAATCAAGAAAGAAATAGATCTAAATATCAAGCCTGTAC 2880  
Qy 2881 AGACAGTAAATATCACTGCAGGCTTCTCTGTGGTGGTGCAGAAAGATAAGCCAGTGTGATA 2940  
Db 2881 AGACAGTAAATATCACTGCAGGCTTCTCTGTGGTGGTGCAGAAAGATAAGCCAGTGTGATA 2940  
Qy 2941 ATGCCAAATGTAGTATCAAGAGGAGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGGCA 3000  
Db 2941 ATGCCAAATGTAGTATCAAGAGGAGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGGCA 3000  
Qy 3001 ACAGAACTGGACTCATTTACTCCAAATAAATGAGTCTTTTACAAAACCCATATCGTATAC 3060  
Db 3001 ACAGAACTGGACTCATTTACTCCAAATAAATGAGTCTTTTACAAAACCCATATCGTATAC 3060  
Qy 3061 CACCACCTTTTCCCATCAAGTCATTTGTAAACCTAAATGTAAAGAAATCTGCTAGAGG 3120  
Db 3061 CACCACCTTTTCCCATCAAGTCATTTGTAAACCTAAATGTAAAGAAATCTGCTAGAGG 3120  
Qy 3121 AAAAATTTGAGCAACATTCATGTCACTGAAAGAAATGGGAAATGAGAAATTCCTCAA 3180  
Db 3121 AAAAATTTGAGCAACATTCATGTCACTGAAAGAAATGGGAAATGAGAAATTCCTCAA 3180  
Qy 3181 GTACAGTGAGCAAAATTAGCCGTAAATACATTAGAGAAATTTTAAAGGAGCCAGCT 3240  
Db 3181 GTACAGTGAGCAAAATTAGCCGTAAATACATTAGAGAAATTTTAAAGGAGCCAGCT 3240  
Qy 3241 CAAGCAATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGCTCCAGTATTATGAAA 3300  
Db 3241 CAAGCAATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGCTCCAGTATTATGAAA 3300  
Qy 3301 TAGGTTCCAGTGATGAACAACTTCAAGCAGAACTAGGTAGAAACAGAGGGCCAAAATTGA 3360  
Db 3301 TAGGTTCCAGTGATGAACAACTTCAAGCAGAACTAGGTAGAAACAGAGGGCCAAAATTGA 3360  
Qy 3361 ATGCTATGCTTAGATTAGGGTTTTGCAACTGAGGCTTATAAACAAGTCTTCTCTGAA 3420  
Db 3361 ATGCTATGCTTAGATTAGGGTTTTGCAACTGAGGCTTATAAACAAGTCTTCTCTGAA 3420  
Qy 3421 GTAATGTAGCATCTCGAAATATAAAGCAAGAAATATGAAGAGTAGTTCAGACTGTTA 3480  
Db 3421 GTAATGTAGCATCTCGAAATATAAAGCAAGAAATATGAAGAGTAGTTCAGACTGTTA 3480  
Qy 3481 ATACAGATTTCTCTCCATATCTGATTTTCCAGATAACTTAGAACAGCCTATGGGAAGTAGTC 3540  
Db 3481 ATACAGATTTCTCTCCATATCTGATTTTCCAGATAACTTAGAACAGCCTATGGGAAGTAGTC 3540  
Qy 3541 ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTTTAGATGATGGTGAATAAAGG 3600  
Db 3541 ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTTTAGATGATGGTGAATAAAGG 3600  
Qy 3601 AAGATCTAGTTTGTCTGAAATATGACATTAAGGAAAGTTCTGCTGTTTTTATAGCAAAAGCG 3660  
Db 3601 AAGATCTAGTTTGTCTGAAATATGACATTAAGGAAAGTTCTGCTGTTTTTATAGCAAAAGCG 3660  
Qy 3661 TCCAGAGGAGGAGCTTAGCAGGAGTCTAGCCCTTTTACCACATACATTTGGCTCAGG 3720  
Db 3661 TCCAGAGGAGGAGCTTAGCAGGAGTCTAGCCCTTTTACCACATACATTTGGCTCAGG 3720  
Qy 3721 GTTACCGAAGAGGGGCCAAGAAATTAGAGTCTCTAGAGAGAACTTATCTAGTGAGGATG 3780  
Db 3721 GTTACCGAAGAGGGGCCAAGAAATTAGAGTCTCTAGAGAGAACTTATCTAGTGAGGATG 3780  
Qy 3781 AAGAGCTTCCCTGCTTCCAAACATTTGTTATTGTTGTAAGTAACAAATATACCTTCTCAGT 3840  
Db 3781 AAGAGCTTCCCTGCTTCCAAACATTTGTTATTGTTGTAAGTAAGTAACAAATATACCTTCTCAGT 3840  
Qy 3841 CTACTAGGCATAGCAACCGTTGCTACCGAGTGTCTGTCTAAGAAACAGAGAGAGATTTAT 3900  
Db 3841 CTACTAGGCATAGCAACCGTTGCTACCGAGTGTCTGTCTAAGAAACAGAGAGAGATTTAT 3900

Qy 3901 TATCATTTGAAGATAGCTTTAAATGACTGACGTAAACAGGTAAATATTGGCAAGGCATCTC 3960  
Db 3901 TATCATTTGAAGATAGCTTTAAATGACTGACGTAAACAGGTAAATATTGGCAAGGCATCTC 3960  
Qy 3961 AGGAACATCACTTGTAGTGAGGAAACAAAATGTTCTGTAGCTTGTCTTTCTTTCACAGTGCA 4020  
Db 3961 AGGAACATCACTTGTAGTGAGGAAACAAAATGTTCTGTAGCTTGTCTTTCTTTCACAGTGCA 4020  
Qy 4021 GTGAATTTGGAAGACTTGACTGCAAAATACAAACACCCAGGATCCTTTCTTGATTTGGTCTT 4080  
Db 4021 GTGAATTTGGAAGACTTGACTGCAAAATACAAACACCCAGGATCCTTTCTTGATTTGGTCTT 4080  
Qy 4081 CCAAAACAAATGAGGCATCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGACAAGGAATTTGG 4140  
Db 4081 CCAAAACAAATGAGGCATCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGACAAGGAATTTGG 4140  
Qy 4141 TTTCCAGATGATGAAGAAAGAGGAAACGGCTTTGGAAGAAAATAATCAAGAGAGCAAAAGCA 4200  
Db 4141 TTTCCAGATGATGAAGAAAGAGGAAACGGCTTTGGAAGAAAATAATCAAGAGAGCAAAAGCA 4200  
Qy 4201 TGGATTCAAACCTTAGGTGAAGCAGCATCTGGGTCTGAGAGTGAACCAAGCGTCTCTGAAG 4260  
Db 4201 TGGATTCAAACCTTAGGTGAAGCAGCATCTGGGTCTGAGAGTGAACCAAGCGTCTCTGAAG 4260  
Qy 4261 ACTGCTCAGGCTATCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGGATACCATGC 4320  
Db 4261 ACTGCTCAGGCTATCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGGATACCATGC 4320  
Qy 4321 AACATACCTTGATAAAGCTCCAGCAGGAAATGGCTGAACTAGAGCTGTGTTAGAACAGC 4380  
Db 4321 AACATACCTTGATAAAGCTCCAGCAGGAAATGGCTGAACTAGAGCTGTGTTAGAACAGC 4380  
Qy 4381 ATGGGAGCCAGCTTTCTAAACAGCTACCTTCCATCATAAAGTGACTCTCTGCCCCCTTGAAG 4440  
Db 4381 ATGGGAGCCAGCTTTCTAAACAGCTACCTTCCATCATAAAGTGACTCTCTGCCCCCTTGAAG 4440  
Qy 4441 ACCTGCGAAATCCAGAACAAAGCAGCATCAGAAAAAGCAGATTAACCTTTCACAGAAAAAGTA 4500  
Db 4441 ACCTGCGAAATCCAGAACAAAGCAGCATCAGAAAAAGCAGATTAACCTTTCACAGAAAAAGTA 4500  
Qy 4501 GTGAATACCTTATTAAGCCAGAAATCCAGAAAGCCTTTCTGCTGACAAAGTTTCAGGTTGCTG 4560  
Db 4501 GTGAATACCTTATTAAGCCAGAAATCCAGAAAGCCTTTCTGCTGACAAAGTTTCAGGTTGCTG 4560  
Qy 4561 CAGATAGTTCTACCAAGTAAATAAAGAACAGAGTGAAGAGGTCTATCCCTTCTAAAT 4620  
Db 4561 CAGATAGTTCTACCAAGTAAATAAAGAACAGAGTGAAGAGGTCTATCCCTTCTAAAT 4620  
Qy 4621 GCCCATCATTAAGATGATGGTGTACATGCAAGTTGCTCTGGGAGTCTTCAGAAATAGAA 4680  
Db 4621 GCCCATCATTAAGATGATGGTGTACATGCAAGTTGCTCTGGGAGTCTTCAGAAATAGAA 4680  
Qy 4681 ACTACCATCTCAAGAGGAGCTCAATTAAGTTGTTGATGTCGAGAGCAACAGCTGGAG 4740  
Db 4681 ACTACCATCTCAAGAGGAGCTCAATTAAGTTGTTGATGTCGAGAGCAACAGCTGGAG 4740  
Qy 4741 AGTCTGGGCCACAGATTTTGAAGGAAACATCTTACTTCCCAAGGCAAGATCTAGAGGAA 4800  
Db 4741 AGTCTGGGCCACAGATTTTGAAGGAAACATCTTACTTCCCAAGGCAAGATCTAGAGGAA 4800  
Qy 4801 CCCCTTACCTGGAATCTGGAATCAGCCCTTCTCTGATGACCCCTGAAATCTGATCCTTCTG 4860  
Db 4801 CCCCTTACCTGGAATCTGGAATCAGCCCTTCTCTGATGACCCCTGAAATCTGATCCTTCTG 4860  
Qy 4861 AAGCAGAGCCCCAGAGTCAGCTGTGTTGGCAACATACCATCTTCAACCTCTGCATTGA 4920  
Db 4861 AAGCAGAGCCCCAGAGTCAGCTGTGTTGGCAACATACCATCTTCAACCTCTGCATTGA 4920  
Qy 4921 AAGTTCCTCCAAATGAAAGTTTCAGAACTGCCCCAGGGTCCAGCTGCTCTCATCTACTG 4980  
Db 4921 AAGTTCCTCCAAATGAAAGTTTCAGAACTGCCCCAGGGTCCAGCTGCTCTCATCTACTG 4980





Qy	961	GCTCATTACAGCATGAGAACAGACAGTGTATTAATCTACTAAGACAGAAATGAATGTAGAAA	1020
Db			
Qy	961	GCTCATTACAGCATGAGAACAGACAGTGTATTAATCTACTAAGACAGAAATGAATGTAGAAA	1020
Db			
Qy	1021	AGGCTGAATCTGTAAATAAAGACAAACAGCTGGCTTAGCAAGGAGCCACATTAACAGAT	1080
Db			
Qy	1021	AGGCTGAATCTGTAAATAAAGACAAACAGCTGGCTTAGCAAGGAGCCACATTAACAGAT	1080
Db			
Qy	1081	GGGCTGGAAGTAAGGAAACATGTAATGATAGGCGGACTCCAGACAGAAAAAAGGTAG	1140
Db			
Qy	1081	GGGCTGGAAGTAAGGAAACATGTAATGATAGGCGGACTCCAGACAGAAAAAAGGTAG	1140
Db			
Qy	1141	ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGGAATTAAGCAGAAAACTGCCATGCT	1200
Db			
Qy	1201	CAGAGAACTCTAGAGATCTGAGAGATGTTCTTGGATAAACATTAATAGCAGCAATTCAGA	1260
Db			
Qy	1201	CAGAGAACTCTAGAGATCTGAGAGATGTTCTTGGATAAACATTAATAGCAGCAATTCAGA	1260
Db			
Qy	1261	AAGTTAATGATGTTTTCAGAGAGTGAATGAATCTGTTAGGTTCTGATGACTCAATCATG	1320
Db			
Qy	1261	AAGTTAATGATGTTTTCAGAGAGTGAATGAATCTGTTAGGTTCTGATGACTCAATCATG	1320
Db			
Qy	1321	GGGAGTCTGAATCAAATGCCAAAGTAGCTGATGTAATTTGGAGCTTCTAAATGAGGTAGATG	1380
Db			
Qy	1381	AATATCTGTTCTTTCAGAGAAATAGACTTACTTGGCCAGTGAATCTCATGAGGCTTTAA	1440
Db			
Qy	1441	TATGTAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGAGTAATTTGAAGACAAAAATAT	1500
Db			
Qy	1441	TATGTAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGAGTAATTTGAAGACAAAAATAT	1500
Db			
Qy	1501	TTGGGAAAACTTATCGGAAGAGGCAAGCCCTCCCAACTTAAGCCATGTAATCGAAATC	1560
Db			
Qy	1561	TAATTTAGGAGCAATTTGTACTGAGGCAAGATAATTAAGAGCGTCCCTTCAAAATA	1620
Db			
Qy	1561	TAATTTAGGAGCAATTTGTACTGAGGCAAGATAATTAAGAGCGTCCCTTCAAAATA	1620
Db			
Qy	1621	AATTAAGCGTAAAGAGAGCTACATCAGGCTTCTCATCTGAGGATTTTATCAAGAAAG	1680
Db			
Qy	1621	AATTAAGCGTAAAGAGAGCTACATCAGGCTTCTCATCTGAGGATTTTATCAAGAAAG	1680
Db			
Qy	1681	CAGATTTGGCAGTTCAAAAGACTCTGAAATGATAAATCAGGGAATTAACCAACGGAGC	1740
Db			
Qy	1681	CAGATTTGGCAGTTCAAAAGACTCTGAAATGATAAATCAGGGAATTAACCAACGGAGC	1740
Db			
Qy	1741	AGAAATGCTAAGTGAATTAATTAATAGTGTGATGAGAAATAAACAAGAGTGAAT	1800
Db			
Qy	1741	AGAAATGCTAAGTGAATTAATTAATAGTGTGATGAGAAATAAACAAGAGTGAAT	1800
Db			
Qy	1801	CTATTCAGATGAGAAAAATCCTAACCCATAGAACTCACTCGAAAAAGAAATCTGCTTTCA	1860
Db			
Qy	1801	CTATTCAGATGAGAAAAATCCTAACCCATAGAACTCACTCGAAAAAGAAATCTGCTTTCA	1860
Db			
Qy	1861	AAACGAAAGCTGAACCTTATAGCAGCAGTATAAGCAATATGGAATCGAAATTAATATCC	1920
Db			
Qy	1861	AAACGAAAGCTGAACCTTATAGCAGCAGTATAAGCAATATGGAATCGAAATTAATATCC	1920
Db			
Qy	1921	ACAAATCAAAAGCACCTAAAAAGAAATAGGCTGAGGAGGAAGTCTTCTACAGGCAATTC	1980
Db			
Qy	1981	ATGGCTTTGAATAGTAGTGAATTAATCTAAGCCACCTAAATGTACTGAATTTGCAAA	2040
Db			
Qy	1981	ATGGCTTTGAATAGTAGTGAATTAATCTAAGCCACCTAAATGTACTGAATTTGCAAA	2040
Db			

Qy	2041	TTGATAGTTGTTCTTAGCAGTGAAGAGATAAAGAAAAAAGTACAACCAATGCCAGTCA	2100
Db			
Qy	2041	TTGATAGTTGTTCTTAGCAGTGAAGAGATAAAGAAAAAAGTACAACCAATGCCAGTCA	2100
Db			
Qy	2101	GGCAGCAGCAAAACCTTACACTCATGGAAGGTAAAGAACCTGCAACTGGAGCCCAAGAGA	2160
Db			
Qy	2101	GGCAGCAGCAAAACCTTACACTCATGGAAGGTAAAGAACCTGCAACTGGAGCCCAAGAGA	2160
Db			
Qy	2161	GTAAACAAGCCAAATGAATGAAACAGACAAGTAAAGACATGACAGCGATACITTTCCAGAGCTGA	2220
Db			
Qy	2161	GTAAACAAGCCAAATGAATGAAACAGACAAGTAAAGACATGACAGCGATACITTTCCAGAGCTGA	2220
Db			
Qy	2221	AGTTAACAATGACACCTGGTTCTTTTACTAAGTGTTCAAATATCCAGTGAACCTTAAGAAT	2280
Db			
Qy	2221	AGTTAACAATGACACCTGGTTCTTTTACTAAGTGTTCAAATATCCAGTGAACCTTAAGAAT	2280
Db			
Qy	2281	TTGTCAATCTAGCCTTCCAAAGAGAGAAAAAGAGAGAACTAGAAAAAGTTTAAAGTGT	2340
Db			
Qy	2281	TTGTCAATCTAGCCTTCCAAAGAGAGAAAAAGAGAGAACTAGAAAAAGTTTAAAGTGT	2340
Db			
Qy	2341	CTAATAATGCTGAAGACCCCAAGATCTCATGTTTAACTGGAGAAAGGTTTTCGAAACTG	2400
Db			
Qy	2341	CTAATAATGCTGAAGACCCCAAGATCTCATGTTTAACTGGAGAAAGGTTTTCGAAACTG	2400
Db			
Qy	2401	AAAGATCTGAGAGAGTAGCAGTATTTTCACTGGTACTGGTACTGATTTATGGCACTCAGG	2460
Db			
Qy	2401	AAAGATCTGAGAGAGTAGCAGTATTTTCACTGGTACTGGTACTGATTTATGGCACTCAGG	2460
Db			
Qy	2461	AAAGTATCTGTTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAACAGAACCAATTAAT	2520
Db			
Qy	2461	AAAGTATCTGTTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAACAGAACCAATTAAT	2520
Db			
Qy	2521	GTGTGAGTCAAGTGTGACGACATTTGAAACCCCAAGGACCTAAATTCATGGTTTGTCCAAAG	2580
Db			
Qy	2521	GTGTGAGTCAAGTGTGACGACATTTGAAACCCCAAGGACCTAAATTCATGGTTTGTCCAAAG	2580
Db			
Qy	2581	ATAATAGAAATGACACAGAAAGGCTTTAAAGTATCCATTTGGGACATGAAGTTTAAACACAGTC	2640
Db			
Qy	2581	ATAATAGAAATGACACAGAAAGGCTTTAAAGTATCCATTTGGGACATGAAGTTTAAACACAGTC	2640
Db			
Qy	2641	GGGAAACAAGCATAGAAATGGAAGAAAGTGAAGAAAGTGAAGTTCAGTATTTGAGAAATACAT	2700
Db			
Qy	2641	GGGAAACAAGCATAGAAATGGAAGAAAGTGAAGAAAGTGAAGTTCAGTATTTGAGAAATACAT	2700
Db			
Qy	2701	TCAGAGTTTCAAAGCGCCAGTCATTTCCTCTGTTTCAAATCCAGGAAATCCAGAAAGAGG	2760
Db			
Qy	2701	TCAGAGTTTCAAAGCGCCAGTCATTTCCTCTGTTTCAAATCCAGGAAATCCAGAAAGAGG	2760
Db			
Qy	2761	AATGTGCAACATTTCTGCCCCACTCTGGGTCCTTTAAAGAAACAAAGTCCAAAAGTCACTT	2820
Db			
Qy	2761	AATGTGCAACATTTCTGCCCCACTCTGGGTCCTTTAAAGAAACAAAGTCCAAAAGTCACTT	2820
Db			
Qy	2821	TTGAAATGTGAACAAAGGAGAAATCAAGGAAGAAATGAGTCTTAATATCAAGCCTGTAC	2880
Db			
Qy	2821	TTGAAATGTGAACAAAGGAGAAATCAAGGAAGAAATGAGTCTTAATATCAAGCCTGTAC	2880
Db			
Qy	2881	AGACAGTTTAATATACACTGACAGGCTTTCTGTTGGTTCAGAAAGATAAGCCAGTTGATA	2940
Db			
Qy	2881	AGACAGTTTAATATACACTGACAGGCTTTCTGTTGGTTCAGAAAGATAAGCCAGTTGATA	2940
Db			
Qy	2941	ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTTCTATCATCTCAGTTCCAGAGGCA	3000
Db			
Qy	2941	ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTTCTATCATCTCAGTTCCAGAGGCA	3000
Db			
Qy	3001	ACGAAATCTGAGTCAATTTACTTCCAAATAAATCAATGAGCTTTTACAAAAACCATATCGTATAC	3060
Db			
Qy	3001	ACGAAATCTGAGTCAATTTACTTCCAAATAAATCAATGAGCTTTTACAAAAACCATATCGTATAC	3060
Db			
Qy	3061	CACCACATTTTCCCATCAAGTCATTGTTTAACTAAATGTAAGAAAAATCTGCTAGAGG	3120
Db			
Qy	3061	CACCACATTTTCCCATCAAGTCATTGTTTAACTAAATGTAAGAAAAATCTGCTAGAGG	3120
Db			
Qy	3121	AAAACTTTGAGGAACATTTCAATGTCTCAGCTGAAAGAGAAATGGGAAATGAGAAACATTTCCA	3180



Db 3121 AAAAATTGGAGAAACATTCATATGTCACCTGAAAGAGAAATGGGAAATGAGAAACATTCCAA 3180  
QY GTACAGTGAGACAAATAGCCGTATTAACATTAAGAGAAATGTTTTAAAGAGCCAGCT 3240  
Db 3181 GTACAGTGAGACAAATAGCCGTATTAACATTAAGAGAAATGTTTTAAAGAGCCAGCT 3240  
QY CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA 3300  
Db 3241 CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA 3300  
QY TAGGTTCCAGTGATGAAAACATTAAGAGAAATAGGTTAGAAAACAGAGGGCCAAAATGGA 3360  
Db 3301 TAGGTTCCAGTGATGAAAACATTAAGAGAAATAGGTTAGAAAACAGAGGGCCAAAATGGA 3360  
QY ATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGGCTCTAATAACAAAGTCTTCTCTGAA 3420  
Db 3361 ATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGGCTCTAATAACAAAGTCTTCTCTGAA 3420  
QY GTAATTTGAAGCATCTGAAAATAAAAAAGCAAGAAATATGAAGAGTAGTTCCAGACTGTTA 3480  
Db 3421 GTAATTTGAAGCATCTGAAAATAAAAAAGCAAGAAATATGAAGAGTAGTTCCAGACTGTTA 3480  
QY ATACAGATTTCTCTCCATATCTGATTTAGATAAATCTAGAAACAGCCATATGGAAAGTAGTC 3540  
Db 3481 ATACAGATTTCTCTCCATATCTGATTTAGATAAATCTAGAAACAGCCATATGGAAAGTAGTC 3540  
QY ATGATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGG 3600  
Db 3541 ATGATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGG 3600  
QY AAGATCTAGTTTGTCTGAAAATGACATTAAGGAAAGTTCTGCTGTTTTAGCAAAAGCG 3660  
Db 3601 AAGATCTAGTTTGTCTGAAAATGACATTAAGGAAAGTTCTGCTGTTTTAGCAAAAGCG 3660  
QY AAGATCTAGTTTGTCTGAAAATGACATTAAGGAAAGTTCTGCTGTTTTAGCAAAAGCG 3660  
TCCAAGAGGAGAGCTTAGCAGGAGTCTAGCCCTTTACCCCATACACATTTGCTCAGG 3720  
QY GTTACCGNAGAGGGCCCAAGAAATAGAGTCTCTCAGAGAGAACTTATCTAGTAGGATG 3780  
Db 3721 GTTACCGNAGAGGGCCCAAGAAATAGAGTCTCTCAGAGAGAACTTATCTAGTAGGATG 3780  
QY AAGAGCTTCCCTGCTTCCAACACTTGTATTGTTGTTAAAGTAAACAAATATACCTTCTCAGT 3840  
Db 3781 AAGAGCTTCCCTGCTTCCAACACTTGTATTGTTGTTAAAGTAAACAAATATACCTTCTCAGT 3840  
QY CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGTCTAAGAAACACAGAGGAGAAATTTAT 3900  
Db 3841 CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGTCTAAGAAACACAGAGGAGAAATTTAT 3900  
QY TATCATTTGAGAAATAGCTTAATGACTGCAGTACAGGTAATTTGGCAAGGCATCTC 3960  
Db 3901 TATCATTTGAGAAATAGCTTAATGACTGCAGTACAGGTAATTTGGCAAGGCATCTC 3960  
QY AGGAACATCACCTTAGTGAGGAAACAAAATGCTGCTAGCTGCTTTTCTTCCAGTGCA 4020  
Db 3961 AGGAACATCACCTTAGTGAGGAAACAAAATGCTGCTAGCTGCTTTTCTTCCAGTGCA 4020  
QY GTGAATTTGGAAGACTTGATGCAAAATCAAAACACCCAGGATCCCTTTCTGATTGGTTCTT 4080  
Db 4021 GTGAATTTGGAAGACTTGATGCAAAATCAAAACACCCAGGATCCCTTTCTGATTGGTTCTT 4080  
QY CCAACAAATGAGGCATCAGTCTGAAGCCNAGGAGTTGCTCTAGTGACNAGGAATGG 4140  
Db 4081 CCAACAAATGAGGCATCAGTCTGAAGCCNAGGAGTTGCTCTAGTGACNAGGAATGG 4140  
QY TTTTCAAGATGATGAAAGAGGAAACGGGCTTGGAGAAATAAATCAAGAGAGCAAAAGCA 4200  
Db 4141 TTTTCAAGATGATGAAAGAGGAAACGGGCTTGGAGAAATAAATCAAGAGAGCAAAAGCA 4200  
QY TGGATTCAAACTTAGGTGAGCAGCATCTGGGTGTGAGAGTGAAACAAAGCGTCTCTGAAG 4260

Db 4201 TGGATTCAAACTTAGGTGAGCAGCATCTGGGTGTGAGAGTGAAACAAAGCGTCTCTGAAG 4260  
QY ACTGCTCAGGGCTATCTCTCAGAGTGACATTTTTAAACACTCAGCAGAGGATACCAATGC 4320  
Db 4261 ACTGCTCAGGGCTATCTCTCAGAGTGACATTTTTAAACACTCAGCAGAGGATACCAATGC 4320  
QY AACATAAACCCTGATATAAGCTCCAGCAGGAAATGGCTGAACTAGAAAGCTGTGTAGAACAGC 4380  
Db 4321 AACATAAACCCTGATATAAGCTCCAGCAGGAAATGGCTGAACTAGAAAGCTGTGTAGAACAGC 4380  
QY ATGGGAGCAGCCCTTTAAACAGCTTACCTTCCATCATATAAGTGAATCTCTCTGCCCTTGAGG 4440  
Db 4381 ATGGGAGCAGCCCTTTAAACAGCTTACCTTCCATCATATAAGTGAATCTCTCTGCCCTTGAGG 4440  
QY ACCTGCCAAATCCAGAACAAAGCAGATCAGAAAAGCAGATTAATTAATTCACAGAAAAGTA 4500  
Db 4441 ACCTGCCAAATCCAGAACAAAGCAGATCAGAAAAGCAGATTAATTAATTCACAGAAAAGTA 4500  
QY GTGAATACCCCTTATAAGCCAGAAATCCAGAAAGCCCTTTCTGCTGACAAAGTTTGGAGGTGCTG 4560  
Db 4501 GTGAATACCCCTTATAAGCCAGAAATCCAGAAAGCCCTTTCTGCTGACAAAGTTTGGAGGTGCTG 4560  
QY CAGATAGTTCTACAGTAAATAAAGAAACAGAGAGTGGAAAGTCAATCCCTTCTTAAT 4620  
Db 4561 CAGATAGTTCTACAGTAAATAAAGAAACAGAGAGTGGAAAGTCAATCCCTTCTTAAT 4620  
QY GCCCATCATTAGATGATAGGTGTACATGACAGTCTCTGCGAGTCTTTCAGAAATGAA 4680  
Db 4621 GCCCATCATTAGATGATAGGTGTACATGACAGTCTCTGCGAGTCTTTCAGAAATGAA 4680  
QY ACTACCCATCTCAAGAGGAGCTCATTAAGGTGTTGATGTGGAGAGCAACAGCTGGAAG 4740  
Db 4681 ACTACCCATCTCAAGAGGAGCTCATTAAGGTGTTGATGTGGAGAGCAACAGCTGGAAG 4740  
QY AGTCTGGGCCACACAGATTTGACGGAAACATCTTACTTGCACAAAGGCAAGATCTAGAGGAA 4800  
Db 4741 AGTCTGGGCCACACAGATTTGACGGAAACATCTTACTTGCACAAAGGCAAGATCTAGAGGAA 4800  
QY CCCCTTACCTTGGATCTGGAATCAGCCTCTCTCTGATGACCCCTGAATCTGATCCTTCTG 4860  
Db 4801 CCCCTTACCTTGGATCTGGAATCAGCCTCTCTCTGATGACCCCTGAATCTGATCCTTCTG 4860  
QY AAGACAGAGCCCAAGAGTCTGCTGTGGCAACATACCATCTTCAACCTCTGCATTTGA 4920  
Db 4861 AAGACAGAGCCCAAGAGTCTGCTGTGGCAACATACCATCTTCAACCTCTGCATTTGA 4920  
QY AAGTTCCCAATTAAGAAAGTTGACAGAAATCTGCCAGGGTCCAGCTGTCTCATACTACTG 4980  
Db 4921 AAGTTCCCAATTAAGAAAGTTGACAGAAATCTGCCAGGGTCCAGCTGTCTCATACTACTG 4980  
QY ATACTGCTGGGTATAATGCAATGGAAGAAAGTGTGACGAGGAGAAAGCCAGAAATGACAG 5040  
Db 4981 ATACTGCTGGGTATAATGCAATGGAAGAAAGTGTGACGAGGAGAAAGCCAGAAATGACAG 5040  
QY CTTCAACAGAAAGGGTCAACAAAGAAATGTCCATGTTGGTGTCTGGGCTGACCCCAAGAG 5100  
Db 5041 CTTCAACAGAAAGGGTCAACAAAGAAATGTCCATGTTGGTGTCTGGGCTGACCCCAAGAG 5100  
QY AATTTATGCTGCTGATCAAGTTTGCAGAAAACCAACATCATCTTAACTAATCTAATTA 5160  
Db 5101 AATTTATGCTGCTGATCAAGTTTGCAGAAAACCAACATCATCTTAACTAATCTAATTA 5160  
QY CTGAGAGACTACTCATGTTGTTATGAAACAGATGCTGAGTTGTGTGTGAAACGGACAC 5220  
Db 5161 CTGAGAGACTACTCATGTTGTTATGAAACAGATGCTGAGTTGTGTGTGAAACGGACAC 5220  
QY TGAATAATTTTCTAGGAAATTCGGGAGGAAATGGGTAGTTAGCTATTTCTGGGTGACCC 5280  
Db 5221 TGAATAATTTTCTAGGAAATTCGGGAGGAAATGGGTAGTTAGCTATTTCTGGGTGACCC 5280  
QY AGTCTATTAAGAAAGAAATGCTGAAATGAGCATGATTTTGAAGTCAAGAGGAGATGTGG 5340  
Db 5281 AGTCTATTAAGAAAGAAATGCTGAAATGAGCATGATTTTGAAGTCAAGAGGAGATGTGG 5340

Qy	5341	TCATGGAAGAAACACCAAGGTCCAAAGCGAGCAAGAAATCCAGGACAGAAAGATCT	5400	5'UTR
Db	5341	TCATGGAAGAAACACCAAGGTCCAAAGCGAGCAAGAAATCCAGGACAGAAAGATCT	5400	exon
Qy	5401	TCAGGGGGCTAGAAATCTGTTGCTATGGCCCTTCCACCAATCCACCATGCAACTGG	5460	exon
Db	5401	TCAGGGGGCTAGAAATCTGTTGCTATGGCCCTTCCACCAATCCACCATGCAACTGG	5460	exon
Qy	5461	AATGATGGTACAGCTGTGTGCTGCTTCTGTGGTGAAGAGCTTTCATTCACCCCTTG	5520	CDS
Db	5461	AATGATGGTACAGCTGTGTGCTGCTTCTGTGGTGAAGAGCTTTCATTCACCCCTTG	5520	
Qy	5521	GCACAGGTGCCACCAATTGTTGTGTCAGCAGATGCTGTGACAGAGACAAATGGCT	5580	
Db	5521	GCACAGGTGCCACCAATTGTTGTGTCAGCAGATGCTGTGACAGAGACAAATGGCT	5580	
Qy	5581	TCCATGAATGGGCAGATGTGAGGACCTGTGTTGACCCGAGAGTGGTGTGGACA	5640	
Db	5581	TCCATGAATGGGCAGATGTGAGGACCTGTGTTGACCCGAGAGTGGTGTGGACA	5640	
Qy	5641	GTGTAGCACTCTACAGTCCAGGAGCTGGACACTTACCTGATACCCAGATCCCCACA	5700	
Db	5641	GTGTAGCACTCTACAGTCCAGGAGCTGGACACTTACCTGATACCCAGATCCCCACA	5700	
Qy	5701	GCCACTACTGA	5711	
Db	5701	GCCACTACTGA	5711	
RESULT 10				
HSU14680				
LOCUS				
DEFINITION Homo sapiens breast and ovarian cancer susceptibility (BRCA1) mRNA, complete cds.				
ACCESSION U14680				
VERSION U14680.1 GI:555931				
KEYWORDS				
SOURCE Homo sapiens (human)				
ORGANISM				
REFERENCE 1 (bases 1 to 5711)				
AUTHORS Miki, Y., Swensen, J., Shattuck-Eidens, D., Futreal, P.A., Harshman, K., Tavtigian, S., Liu, Q., Cochran, C., Bennett, L.M., Ding, W., Bell, R., Rosenthal, J., Hussey, C., Tran, T., McClure, M., Frye, C., Hattier, T., Phelps, R., Haugen-Strano, A., Katcher, H., Yakumo, K., Gholami, Z., Shaffer, D., Stone, S., Bayer, S., Wray, C., Bogden, R., Dayananth, P., Ward, J., Tonin, P., Narod, S., Bristow, P.K., Norris, F.H., Helvering, L., Morrison, P., Rostock, P., Lai, M., Barrett, J.C., Lewis, C., Neuhausen, S., Cannon-Albright, L., Goldgar, D., Wiseman, R., Kamb, A. and Skolnick, M.H.				
TITLE A strong candidate for the breast and ovarian cancer susceptibility gene BRCA1				
JOURNAL Science 266 (5182), 66-71 (1994)				
MEDLINE 95025896				
PUBMED 7545954				
REFERENCE 2 (bases 1 to 5711)				
AUTHORS Skolnick, M.H.				
TITLE Direct Submission				
JOURNAL Submitted (14-SEP-1994) Mark H. Skolnick, Myriad Genetics Inc. and the University of Utah, 421 Wakara Way, Suite 201, Salt Lake City, UT 84108, USA				
FEATURES				
source				
1. .5711				
/organism="Homo sapiens"				
/mol_type="mRNA"				
/db_xref="taxon:9606"				
/chromosome="17"				
/map="17q21; spans D17S855"				
/note="For sequence of alternatively spliced exon 4, see GenBank Accession Number U15595"				
1. .5711				
gene				

/gene="BRCA1"  
1. .119  
/gene="BRCA1"  
1. .100  
/gene="BRCA1"  
/number=1  
101. .199  
/gene="BRCA1"  
/number=2  
120. .5711  
/gene="BRCA1"  
/note="influences susceptibility to breast and ovarian cancer"  
/codon\_start=1  
/product="breast and ovarian cancer susceptibility"  
/protein\_id="AAA73985.1"  
/db\_xref="GI:555932"  
/translation="MDLSALRVEQNVINAMOKILEPCICLELIEKPVSTKCDHIFC  
KFMKLNNKKGSPQCPKCNIDITKRSLSQESTRFSQIVBELLLKICAFQDITGLEVA  
NSYFAKKNNSEPHLKDEVI IQSMGYRRNRAKLLQSEPNLSQTSLSVQLSNUG  
TVRLTKRIQPKTSVYIELGSDSESDVTNKATYCSVGDQELLQITPQSTRDEISL  
DSAKKAACEFSEDTVTNTEHHQPSNNDLNTTEKAAERHPEKYQGSVSNLHVPCT  
NTHASSLOHENSLLLTKDRMVEKAEFCNKSQOPGLARSOHNRWAGSKETCNDRTTP  
STKKYDLNADPLCEKERNKQKLPCSENPRDTEDPWITLNSSIQKNWFSRSDDEL  
LGDDHDSSESENAKVADVLDVNLNEVDEYSGSEKIDLLASDPHEALICKSERVHSK  
SVESNIEDKIFGKTYRKASLPNLSHVTENLIIGAFVTEPQIIQERPLTNKLRKRRP  
TSGLHPEDFIKADLAVQKTPPMINQNTQEQNMVNTNSGHNKTGDSIQNEK  
NPPIESLEKESAFKTKAEPISSSISSNLELNIHNSKPKNLRKRSRTHIHALE  
LVVSRNLSPNCTELOIDSCSSSEI KKKYNOMPVHRNLOLMGKPEPATGAKSN  
KPNQTSKRHDSITFPELKLITNAPGSTKCSNTSELKFEVNPISI,PREKEKLETKVY  
SNAEDPKLMLSGERVLTQERSVSSISLVPGTDYGTQBSISLLESTVLGKATPE  
NKVSCAAEFENPKGLIHGCSKONRDETFKYPGLGHEVNHRSRETSIEMSESLDAQY  
LQNTFKVKSQSFAPFNPNGNAEECAATFAHSGSLKKQSPKVTFECEKEENQKNE  
SNTPQVNTNITAGFVVGQKDPVNAKSIKGGSRFCILSSQFRGNETGLITPNKHG  
LQNPVRIPLPIKSPVTKCKKNLLEENFEHSMSPEREMGNENIPSTVSTSRNN  
IRENVKEASSNNINEVSGSINIGSDDENIQALGNRGPKNAMRLGV  
LQPEVYKQSLPNSGNRHPETKQIEYEVVQTVNTDFSLISDNLEQPMGSHASQVC  
SETPDDLLDGEIKEDTFAENDIKESSAVFSKVQKGLSRSPSPFTHLAQYRR  
GAKLSEENLSEDEBELFCQHLFKVNNIPSPQSTRSHVATECLSKNTENLLS  
KKNLNDNQVILAKASQBHLSEETKCSALFSSQSELEDITANTNTQDPFLGS  
SKMRHQSQGVCLSDKELVSDDEERGTLSENNQEQSDMSNLGAASCESETSV  
SEPCSLSSQSDILITTOQRTMQHNLKIQEMAELEAVLEQHSQSPNSVPSISDS  
SALEDLKNPQSTSEKAVLSQKSSEYPIQNPGLSADKFEVSADSTSKNKGPGVE  
RSFSPKCPKSDLDWMHSCSGSLQNRNPSPQELIKYVDVEEQLESQGHDLTETS  
LQPDQLEGTPLYLESIGLSFSDPESDPSDRAPEARVGNIPSTSAKLPQLKVAES  
AQSPAAATTTDTAGYNAMESVREKPELTASTERVNKRSMVMVSGLTPEFMLVYKF  
ARKHHITLNLITEETHVVMKTDAAEFVCERTLKYFLGIAGGKVVSVFWYDQSIKER  
KMLNEHDFEVRGVDVNGNRHQPKARESQRKIFRGLEICCGYFFTNMPTDQLEWV  
QLCGASVKSLSSTLTGTGVHPIVVQPDADNEDNGFHAIGQMCEAPVVTREWLDVS  
ALYQCQSLDYLIPQIPSHY"  
200. .253  
/gene="BRCA1"  
/number=3  
254. .331  
/gene="BRCA1"  
/number=5  
332. .420  
/gene="BRCA1"  
/number=6  
421. .560  
/gene="BRCA1"  
/number=7  
561. .665  
/gene="BRCA1"  
/number=8  
666. .712  
/gene="BRCA1"  
/number=9  
713. .788  
/gene="BRCA1"  
/number=10  
789. .4215  
/gene="BRCA1"



Qy	1501	TTGGGAAAACTTATCGGAAGAGCGAAGCCCTCCCAACTTAAAGCCATGTAACTGAAAATC	1560
Dd	1501	TTGGGAAAACTTATCGGAAGAGCGAAGCCCTCCCAACTTAAAGCCATGTAACTGAAAATC	1560
Qy	1561	TAATTTATGAGGCAATTTGTTACTGAGCCACAGATAATACAGAGCGTCCCTCACAATA	1620
Dd	1561	TAATTTATGAGGCAATTTGTTACTGAGCCACAGATAATACAGAGCGTCCCTCACAATA	1620
Qy	1621	AAATTAAGCGGTAAAGGAGACCTACATCAGGCGCTTCATCTGAGGATTTTATCAAGAAAG	1680
Dd	1621	AAATTAAGCGGTAAAGGAGACCTACATCAGGCGCTTCATCTGAGGATTTTATCAAGAAAG	1680
Qy	1681	CAGATTTGGCAGTTCAAAAGACTCCTGAAATGATAAATACAGGAACTAAACAAACGGAGC	1740
Dd	1681	CAGATTTGGCAGTTCAAAAGACTCCTGAAATGATAAATACAGGAACTAAACAAACGGAGC	1740
Qy	1741	AGATGCTCAAGTCATGATTAATTAATAGTGTGCTGATGAGATAAACAAGGTCATTT	1800
Dd	1741	AGATGCTCAAGTCATGATTAATTAATAGTGTGCTGATGAGATAAACAAGGTCATTT	1800
Qy	1801	CTATTCAAGATGAGAAAAATCCTAACCAATAGAAATCACTCGAAAAAGAACTCTGTTTCA	1860
Dd	1801	CTATTCAAGATGAGAAAAATCCTAACCAATAGAAATCACTCGAAAAAGAAATCTGTTTCA	1860
Qy	1861	AAACGAAAGCTGAACCTATTAAGCAGCAGTATAAGCAATATGGAATCGAAATTAATATCC	1920
Dd	1861	AAACGAAAGCTGAACCTATTAAGCAGCAGTATAAGCAATATGGAATCGAAATTAATATCC	1920
Qy	1921	ACAAATCAAAAGCACTTAAAGAAATAGGCTGAGGAGGAGTCTTACACAGGCAATATTC	1980
Dd	1921	ACAAATCAAAAGCACTTAAAGAAATAGGCTGAGGAGGAGTCTTACACAGGCAATATTC	1980
Qy	1981	ATGCGCTGAACTAGTACAGTAAATCTAAAGCCACCTAAATTTGACTGAAATGCAAA	2040
Dd	1981	ATGCGCTGAACTAGTACAGTAAATCTAAAGCCACCTAAATTTGACTGAAATGCAAA	2040
Qy	2041	TTGATAGTTGTTCTAGCAGTGAAGAGATAAAGAAAAAAGTACAAACCAATGCCAGTCA	2100
Dd	2041	TTGATAGTTGTTCTAGCAGTGAAGAGATAAAGAAAAAAGTACAAACCAATGCCAGTCA	2100
Qy	2101	GGCAGCAGAAAACCTACAACTATGGAAGTAAAGAAACCTGCAACCTGGAAGCCAAAGA	2160
Dd	2101	GGCAGCAGAAAACCTACAACTATGGAAGTAAAGAAACCTGCAACCTGGAAGCCAAAGA	2160
Qy	2161	GTACACGCCAAATGACACAGATTAAGACATGACAGTGATCTTCCACAGCTGA	2220
Dd	2161	GTACACGCCAAATGACACAGATTAAGACATGACAGTGATCTTCCACAGCTGA	2220
Qy	2221	AGTTAAACAAATGCACTGTTCTTTTACTAAGTGTTCAAATACCAAGTGAACCTTAAAGAT	2280
Dd	2221	AGTTAAACAAATGCACTGTTCTTTTACTAAGTGTTCAAATACCAAGTGAACCTTAAAGAT	2280
Qy	2281	TTGTCAATCTCTAGCCTTCCAAAGAGAGAAAGAGAGAAACTAGAAACAGTAAAGTGT	2340
Dd	2281	TTGTCAATCTCTAGCCTTCCAAAGAGAGAAAGAGAGAAACTAGAAACAGTAAAGTGT	2340
Qy	2341	CTAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGGTTTGGCAACTG	2400
Dd	2341	CTAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGGTTTGGCAACTG	2400
Qy	2401	AAAGATCTGTAGAGATGAGTATTTTCACTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2460
Dd	2401	AAAGATCTGTAGAGATGAGTATTTTCACTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2460
Qy	2461	AAAGTATCTCGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAACAGAAACCAATAAAT	2520
Dd	2461	AAAGTATCTCGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAACAGAAACCAATAAAT	2520
Qy	2521	GTGTGAGTCAAGTGTGACATTTGAAAACCCCAAGGGAATAATTCATGTTGTTTCCAAAG	2580
Dd	2521	GTGTGAGTCAAGTGTGACATTTGAAAACCCCAAGGGAATAATTCATGTTGTTTCCAAAG	2580

Qy	2581	ATAATAGAAATGACACAGAGGCTTTAAGTATCCATTGGGACATGAAGTTAAACCAAGTC	2640
Dd	2581	ATAATAGAAATGACACAGAGGCTTTAAGTATCCATTGGGACATGAAGTTAAACCAAGTC	2640
Qy	2641	GGGAAACAAAGCATAGAAATGGAAGAAAGTGAACCTTGATGCTCAGTATTTGAGAAATACAT	2700
Dd	2641	GGGAAACAAAGCATAGAAATGGAAGAAAGTGAACCTTGATGCTCAGTATTTGAGAAATACAT	2700
Qy	2701	TCAAGGTTTCAAAGCGCCAGTCATTTGCTCTGTTTCAAATCCAGGAAATGCAAGAGG	2760
Dd	2701	TCAAGGTTTCAAAGCGCCAGTCATTTGCTCTCGTTTCAAATCCAGGAAATGCAAGAGG	2760
Qy	2761	AATGTGCAACATTTCTCTGCCCACCTCTGGGCTTTTAAAGAAACCAAGTCCAAAGTCACTT	2820
Dd	2761	AATGTGCAACATTTCTCTGCCCACCTCTGGGCTTTTAAAGAAACCAAGTCCAAAGTCACTT	2820
Qy	2821	TTGAAATGTGAACAAAGGAAAGAAATCAAGGAAAGAAATGAGTCTAAATCAAGCTGTAC	2880
Dd	2821	TTGAAATGTGAACAAAGGAAAGAAATCAAGGAAAGAAATGAGTCTAAATCAAGCTGTAC	2880
Qy	2881	AGACAGTTAATATCACTGCAAGGCTTTCTCTGTTGTTGTCAGAAAGATAGCCAGTGTGATA	2940
Dd	2881	AGACAGTTAATATCACTGCAAGGCTTTCTCTGTTGTTGTCAGAAAGATAGCCAGTGTGATA	2940
Qy	2941	ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTCTCTATCATCTCAGTTCAGAGGCA	3000
Dd	2941	ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTCTCTATCATCTCAGTTCAGAGGCA	3000
Qy	3001	ACGAAATCGACATCTTACTCCAAATAAATCAATGACATTTTACAAACCCATATCGTATAC	3060
Dd	3001	ACGAAATCGACATCTTACTCCAAATAAATCAATGACATTTTACAAACCCATATCGTATAC	3060
Qy	3061	CACCACATTTTCCCATCAAGTCAATTTGTTAAACCTAAATGTAAGAAAAATCTGCTAGAGG	3120
Dd	3061	CACCACATTTTCCCATCAAGTCAATTTGTTAAACCTAAATGTAAGAAAAATCTGCTAGAGG	3120
Qy	3121	AAAACTTTGAGGAACTTCAATGTCACTGAAAGAGAAATGGGAAATGAGAACTTCAAA	3180
Dd	3121	AAAACTTTGAGGAACTTCAATGTCACTGAAAGAGAAATGGGAAATGAGAACTTCAAA	3180
Qy	3181	GTACAGTGAGCACAATTTAGCCGTAAATCAATAGAGAAATGTTTAAAGGAGCCAGCT	3240
Dd	3181	GTACAGTGAGCACAATTTAGCCGTAAATCAATAGAGAAATGTTTAAAGGAGCCAGCT	3240
Qy	3241	CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA	3300
Dd	3241	CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA	3300
Qy	3301	TAGGTTCCAGTGATGAAAACATTTCAAGCAGAACTTAGGTAGAAAACAGAGGGCCAAATTTGA	3360
Dd	3301	TAGGTTCCAGTGATGAAAACATTTCAAGCAGAACTTAGGTAGAAAACAGAGGGCCAAATTTGA	3360
Qy	3361	ATGCTATGCTTAGATTTAGGGGTTTGGCAACTGAGGCTTATAAACAAGTCTTCTGGA	3420
Dd	3361	ATGCTATGCTTAGATTTAGGGGTTTGGCAACTGAGGCTTATAAACAAGTCTTCTGGA	3420
Qy	3421	GTAAATCTAGCATCTTGAATAAAGCAAGAAATATGAAGAAAGTGTTCAGACTGTTA	3480
Dd	3421	GTAAATCTAGCATCTTGAATAAAGCAAGAAATATGAAGAAAGTGTTCAGACTGTTA	3480
Qy	3481	ATACAGATTTCTCTCCCATATCTGATTTTCAAGTAACTTAGAACAGCCTATGGAAAGTAGTC	3540
Dd	3481	ATACAGATTTCTCTCCCATATCTGATTTTCAAGTAACTTAGAACAGCCTATGGAAAGTAGTC	3540
Qy	3541	ATGCATCTCAGGTTTGTTCAGACACTGATGACCTGTTAGATGATGGTGAATAAAGG	3600
Dd	3541	ATGCATCTCAGGTTTGTTCAGACACTGATGACCTGTTAGATGATGGTGAATAAAGG	3600
Qy	3601	AAGTACTAGTCTGCTGAAAATGACATTAAGGAAAGTCTGCTGTTTAAAGCAAGG	3660
Dd	3601	AAGTACTAGTCTGCTGAAAATGACATTAAGGAAAGTCTGCTGTTTAAAGCAAGG	3660
Qy	3661	TCCAGAGAGGAGGCTTTAGCAGGAGTCTCCTGCCCTTTTCAACCCATACACATTTTGGCTCAGG	3720

Db 3661 TCCAGAAAGGAGAGCTTAGCAGGAGTCTCAGCCCTTTCCACCCATACACATTTGGCTCAGG 3720  
Qy 3721 GTTACCGNAGAGGGCCAGAAATTTAGAGTCTCAGAGAGAACTTATCTAGTGAGGATG 3780  
Db 3721 GTTACCGNAGAGGGCCAGAAATTTAGAGTCTCAGAGAGAACTTATCTAGTGAGGATG 3780  
Qy 3781 AAGAGCTTCCCTGCTCCCAACACTTTTATTGTTGTAAGATAAACAATATACCTTCTCAGT 3840  
Db 3781 AAGAGCTTCCCTGCTCCCAACACTTTTATTGTTGTAAGATAAACAATATACCTTCTCAGT 3840  
Qy 3841 CTACTAGGCATPAGCACCGTTCTACCGAGTGTCTGTCTAAGAACACAGAGGAGAAATTTAT 3900  
Db 3841 CTACTAGGCATPAGCACCGTTCTACCGAGTGTCTGTCTAAGAACACAGAGGAGAAATTTAT 3900  
Qy 3901 TATCATTTGAAGATAGCTTAAATGACTGCACTAACCAGGTAAATTTGGCAAGGCATCTC 3960  
Db 3901 TATCATTTGAAGATAGCTTAAATGACTGCACTAACCAGGTAAATTTGGCAAGGCATCTC 3960  
Qy 3961 AGGAACATCACCTTAGTGAGGAAACAAATCTTCTGCTAGCTTCTTCTTCTCAGTGCA 4020  
Db 3961 AGGAACATCACCTTAGTGAGGAAACAAATCTTCTGCTAGCTTCTTCTTCTCAGTGCA 4020  
Qy 4021 GTGAATTTGGAAGACTTGACTGCAATACAAACACCCAGGATCCTTTCTTGATTGGTCTT 4080  
Db 4021 GTGAATTTGGAAGACTTGACTGCAATACAAACACCCAGGATCCTTTCTTGATTGGTCTT 4080  
Qy 4081 CCAAAACAAATGAGGCATCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGACAAGGAATTGG 4140  
Db 4081 CCAAAACAAATGAGGCATCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGACAAGGAATTGG 4140  
Qy 4141 TTTCCAGATGATGAAGAGAGAAACGGCTTTGGAGAAATAATCAAGAGAGCAAGCA 4200  
Db 4141 TTTCCAGATGATGAAGAGAGAAACGGCTTTGGAGAAATAATCAAGAGAGCAAGCA 4200  
Qy 4201 TGGATTCAAACCTTAGTGAGCAGCATCTGGGTGTGAGAGTGAAACAGCGTCTCTGAG 4260  
Db 4201 TGGATTCAAACCTTAGTGAGCAGCATCTGGGTGTGAGAGTGAAACAGCGTCTCTGAG 4260  
Qy 4261 ACTGCTCAGGCTATCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGATACCATGC 4320  
Db 4261 ACTGCTCAGGCTATCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGATACCATGC 4320  
Qy 4321 AACATACTGATAAAGCTCCAGCAGGAAATGGCTGAACTAGAGCTGTGTTAGAACAGC 4380  
Db 4321 AACATACTGATAAAGCTCCAGCAGGAAATGGCTGAACTAGAGCTGTGTTAGAACAGC 4380  
Qy 4381 ATGGGAGCCAGCCCTTAAACAGCTACCCCTTCCATCATAAGTGACTCTCTGCCCTTGAGG 4440  
Db 4381 ATGGGAGCCAGCCCTTAAACAGCTACCCCTTCCATCATAAGTGACTCTCTGCCCTTGAGG 4440  
Qy 4441 ACCTGCGAATCCAGAACAAAGCAATCAGAAAAGCAGATTAATCTTCAAGAAAAGTA 4500  
Db 4441 ACCTGCGAATCCAGAACAAAGCAATCAGAAAAGCAGATTAATCTTCAAGAAAAGTA 4500  
Qy 4501 GTGAATACCTTAAAGCCAGAAATCCAGAGCCCTTCTGCTGACAAGTTTGAGGTCTG 4560  
Db 4501 GTGAATACCTTAAAGCCAGAAATCCAGAGCCCTTCTGCTGACAAGTTTGAGGTCTG 4560  
Qy 4561 CAGATAGTCTTACCAAGTAAATAAAGAACACAGAGTGGAAGGTCTATCCCTTCTAAAT 4620  
Db 4561 CAGATAGTCTTACCAAGTAAATAAAGAACACAGAGTGGAAGGTCTATCCCTTCTAAAT 4620  
Qy 4621 GCCCATCATTAGATAGTGGTACATGCACTGCTCTGGAGTCTTCAGAAATAGAA 4680  
Db 4621 GCCCATCATTAGATAGTGGTACATGCACTGCTCTGGAGTCTTCAGAAATAGAA 4680  
Qy 4681 ACTACCCATCTCAAGAGAGCTCAATTAAGTTGTTGATGTGGAGGACACAGCTGGAAG 4740  
Db 4681 ACTACCCATCTCAAGAGAGCTCAATTAAGTTGTTGATGTGGAGGACACAGCTGGAAG 4740  
Qy 4741 AGTCTGGGCCACAGATTTGACGGAAACATCTTACTTTGCCAAGGCAAGATCTAGAGGAA 4800

Db 4741 AGTCTGGGCCACAGATTTGACGGAAACATCTTACTTTGCCAAGGCAAGATCTAGAGGAA 4800  
Qy 4801 CCCCTTACCTGGAAATCTGGAAATCAGCCCTTCTCTGATGACCCCTGAATCTGATCCTCTG 4860  
Db 4801 CCCCTTACCTGGAAATCTGGAAATCAGCCCTTCTCTGATGACCCCTGAATCTGATCCTCTG 4860  
Qy 4861 AAGACAGAGCCCCAGAGTCTGAGTCTGTGGCAACATACCATCTTCAACCTCTGCATTTGA 4920  
Db 4861 AAGACAGAGCCCCAGAGTCTGAGTCTGTGGCAACATACCATCTTCAACCTCTGCATTTGA 4920  
Qy 4921 AAGTTCCCAATTTGAAAGTTGCAAGATCTGCCAGGGTCCAGCTGCTCATACTACTG 4980  
Db 4921 AAGTTCCCAATTTGAAAGTTGCAAGATCTGCCAGAGTCCAGCTGCTCATACTACTG 4980  
Qy 4981 ATACTGCTGGGTATTAATGCAATGGAAGAAAGTGTGAGCAGGAGGAAGCAGAAATGACAG 5040  
Db 4981 ATACTGCTGGGTATTAATGCAATGGAAGAAAGTGTGAGCAGGAGGAAGCAGAAATGACAG 5040  
Qy 5041 CTTCAACAGAGAAAGGTCACAAAGAAATGTCATGCTGGTGTCTGGCTCAGCCCAAGAG 5100  
Db 5041 CTTCAACAGAGAAAGGTCACAAAGAAATGTCATGCTGGTGTCTGGCTCAGCCCAAGAG 5100  
Qy 5101 AATTTATGCTCGTGTAACAAGTTTGGCCAGAAAACACACATCCTTAACTAATCTAATTA 5160  
Db 5101 AATTTATGCTCGTGTAACAAGTTTGGCCAGAAAACACACATCCTTAACTAATCTAATTA 5160  
Qy 5161 CTGAAGAGACTACTCATGTTGTTATGAAAAACAGATGCTGAGTTGTGTGTAACGGACAC 5220  
Db 5161 CTGAAGAGACTACTCATGTTGTTATGAAAAACAGATGCTGAGTTGTGTGTAACGGACAC 5220  
Qy 5221 TGAATAATTTTCTAGGAATTTGCGGAGGAAAAATGGGTAGTTAGTCTATTCTTGGGTGACC 5280  
Db 5221 TGAATAATTTTCTAGGAATTTGCGGAGGAAAAATGGGTAGTTAGTCTATTCTTGGGTGACC 5280  
Qy 5281 AGTCTATTAAGAAAGAAAAATGCTGAATGAGCATGATTTTGAAGTCAGAGGAGATGTGG 5340  
Db 5281 AGTCTATTAAGAAAGAAAAATGCTGAATGAGCATGATTTTGAAGTCAGAGGAGATGTGG 5340  
Qy 5341 TCAATGGAAGAAACCAAGGTTCCAAAGGTCGCAAGGAGCAAGAAATCCAGGACAGAAAGATCT 5400  
Db 5341 TCAATGGAAGAAACCAAGGTTCCAAAGGTCGCAAGGAGCAAGAAATCCAGGACAGAAAGATCT 5400  
Qy 5401 TCAGGGGCTAGAAATCTGTTGCTATGCGGCCCTTCCACCAATGCCCCACAGATCAACTGG 5460  
Db 5401 TCAGGGGCTAGAAATCTGTTGCTATGCGGCCCTTCCACCAATGCCCCACAGATCAACTGG 5460  
Qy 5461 AATGGATGTTACAGCTGTGTGGTCTTCTGTGTGTAAGGAGCTTTTCATTCACCCCTTG 5520  
Db 5461 AATGGATGTTACAGCTGTGTGGTCTTCTGTGTGTAAGGAGCTTTTCATTCACCCCTTG 5520  
Qy 5521 GCACAGTGTCCACCAATTTGTGTGTGAGCCAGATGCTTGACAGAGGACAAATGGCT 5580  
Db 5521 GCACAGTGTCCACCAATTTGTGTGTGAGCCAGATGCTTGACAGAGGACAAATGGCT 5580  
Qy 5581 TCCATGCAATTTGGGAGATGTGAGGACCTGTGTGTGAGCCCGAGAGTGGGTGTGGACA 5640  
Db 5581 TCCATGCAATTTGGGAGATGTGAGGACCTGTGTGTGAGCCCGAGAGTGGGTGTGGACA 5640  
Qy 5641 GTGTAGCACTTACAGTGCAGGAGCTGGACACCTACCTGATACCCCGAGATCCCCCACA 5700  
Db 5641 GTGTAGCACTTACAGTGCAGGAGCTGGACACCTACCTGATACCCCGAGATCCCCCACA 5700  
Qy 5701 GCCACTACTGA 5711  
Db 5701 GCCACTACTGA 5711

RESULT 11  
AR070223  
LOCUS  
DEFINITION  
ACCESSION  
VERSION

AR070223 5712 bp DNA linear PAT 18-FEB-2000  
Sequence 1 from patent US 5891857.

AR070223  
AR070223.1 GI:7221111

KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 5712)  
AUTHORS Holt, J.T., Jensen, R.A., King, M.-C., Page, D.L., Szabo, C.I.,  
Jetton, T.L., Robinson-Benton, C.L. and Thompson, M.E.  
TITLE Characterized BRCA1 and BRCA2 proteins and screening and  
therapeutic methods based on characterized BRCA1 and BRCA2 proteins  
JOURNAL Patent: US 5891857-A 1 06-APR-1999;  
FEATURES Location/Qualifiers  
source 1..5712  
BASE COUNT 1956 a 1099 c 1274 g 1383 t  
ORIGIN  
Query Match 99.8%; Score 5699.8; DB 6; Length 5712;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 5704; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
Qy 1 AGCTCGCTGAGACTTCCTGGACCCCGCACACAGGCTGTGGGTTTCTCAGATAAAGTGGGCC 60  
Db 1 AGCTCGCTGAGACTTCCTGGACCCCGCACACAGGCTGTGGGTTTCTCAGATAAAGTGGGCC 60  
Qy 61 CCTGCGCTCAGAGGCTTCACCTCTGCTCTGGGTAAAGTTCAATTGGAAACAGAAAGAAA 120  
Db 61 CCTGCGCTCAGAGGCTTCACCTCTGCTCTGGGTAAAGTTCAATTGGAAACAGAAAGAAA 120  
Qy 121 TGGATTATCTGCTTCGCTTGAAGAGTACAAATGCTCAATTAATGCTATGAGAA 180  
Db 121 TGGATTATCTGCTTCGCTTGAAGAGTACAAATGCTCAATTAATGCTATGAGAA 180  
Qy 181 TCTTAGAGTGCCCATCTGCTGGAGTTGATCAAGAACCTGTCTCCAAAGTGTGACC 240  
Db 181 TCTTAGAGTGCCCATCTGCTGGAGTTGATCAAGAACCTGTCTCCAAAGTGTGACC 240  
Qy 241 ACATATTTTGCAAAATTTTGCATGCTGAAATCTTCTCAACAGAAAGGGCTTTCACAGT 300  
Db 241 ACATATTTTGCAAAATTTTGCATGCTGAAATCTTCTCAACAGAAAGGGCTTTCACAGT 300  
Qy 301 GTCTTTATGTAAGATGATTAACCAAAAGGAGCTTACAGAAAGTACGAGATTTAGTC 360  
Db 301 GTCTTTATGTAAGATGATTAACCAAAAGGAGCTTACAGAAAGTACGAGATTTAGTC 360  
Qy 361 AACTTTTGAAGAGCTATTGAAATCAATTTGTGCTTTTTCAGCTTGACACAGTTTGGAGT 420  
Db 361 AACTTTTGAAGAGCTATTGAAATCAATTTGTGCTTTTTCAGCTTGACACAGTTTGGAGT 420  
Qy 421 ATGCAACAGCTATATTTTGCAGAAAGGAAATTAATCTCTGCAACATCTAAAGATG 480  
Db 421 ATGCAACAGCTATATTTTGCAGAAAGGAAATTAATCTCTGCAACATCTAAAGATG 480  
Qy 481 AAGTTTCTATCATCAAAAGTATGGCTACAGAAACCGTGCCAAAGACTTCTACAGAGTG 540  
Db 481 AAGTTTCTATCATCAAAAGTATGGCTACAGAAACCGTGCCAAAGACTTCTACAGAGTG 540  
Qy 541 AACCCGAAATCTCTCTGAGGAAACCGCTCAGTGCTCAACTCTCTAACCTTGGAA 600  
Db 541 AACCCGAAATCTCTCTGAGGAAACCGCTCAGTGCTCAACTCTCTAACCTTGGAA 600  
Qy 601 CTGTGAGAACTCTGAGGAAACCGGATACAACTCAAAAGACGCTCTGTACATTG 660  
Db 601 CTGTGAGAACTCTGAGGAAACCGGATACAACTCAAAAGACGCTCTGTACATTG 660  
Qy 661 AATTGGGATCTGATTCTTCTGAAGATACCGTTAATAGGCAACTTATTGCAAGTGGGAG 720  
Db 661 AATTGGGATCTGATTCTTCTGAAGATACCGTTAATAGGCAACTTATTGCAAGTGGGAG 720  
Qy 721 ATCAAGATTTGTACAAATCAACCTCAAGAACCCAGGGATGAATCAGTTTGGATCTG 780  
Db 721 ATCAAGATTTGTACAAATCAACCTCAAGAACCCAGGGATGAATCAGTTTGGATCTG 780  
Qy 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGACGGATGTAACAAATACTGAAACATCATCAAC 840

Db 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGACGGATGTAACAAATACTGAAACATCATCAAC 840  
Qy 841 CCAGTAATAATGATTTTCAACACCACTGAGAAGCCTGAGCTGAGAGGATCCAGAAAAGT 900  
Db 841 CCAGTAATAATGATTTTCAACACCACTGAGAAGCCTGAGCTGAGAGGATCCAGAAAAGT 900  
Qy 901 ATCAGGGTAGTCTTCTTTCAAACTTGGATGAGGACCTGAGCAAAATCTCATGCCA 960  
Db 901 ATCAGGGTAGTCTTCTTTCAAACTTGGATGAGGACCTGAGCAAAATCTCATGCCA 960  
Qy 961 GCTCATTTACAGCATGAGAACAGCAGTTTATTACTCATTAAAGACAGATGAATGTAGAAA 1020  
Db 961 GCTCATTTACAGCATGAGAACAGCAGTTTATTACTCATTAAAGACAGATGAATGTAGAAA 1020  
Qy 1021 AGGCTGAATTTCTGTAATAAAGCAACAGCCTGCTTAGCAAGGAGCCAAACATTAACAGT 1080  
Db 1021 AGGCTGAATTTCTGTAATAAAGCAACAGCCTGCTTAGCAAGGAGCCAAACATTAACAGT 1080  
Qy 1081 GGGCTGGAAGTAAGAAACATGTAATGATAGGCGGACTCCAGCACAGAAAAGGTTAG 1140  
Db 1081 GGGCTGGAAGTAAGAAACATGTAATGATAGGCGGACTCCAGCACAGAAAAGGTTAG 1140  
Qy 1141 ATCTGAATGCTGATCCCTCTGTGAGAGAAAGAAATGGAATTAAGCAGAAAAGTGCATGCT 1200  
Db 1141 ATCTGAATGCTGATCCCTCTGTGAGAGAAAGAAATGGAATTAAGCAGAAAAGTGCATGCT 1200  
Qy 1201 CAGAGATCTCTAGAGATCTGAGATGTAAGATGTTCTTGGATAACACTAAATAGCAGATTTCAGA 1260  
Db 1201 CAGAGATCTCTAGAGATCTGAGATGTAAGATGTTCTTGGATAACACTAAATAGCAGATTTCAGA 1260  
Qy 1261 AAGTTAATGATGCTGTTTCCAGAAAGTGAATGAACTGTTAGGTTCTGATGACTCACATGATG 1320  
Db 1261 AAGTTAATGATGCTGTTTCCAGAAAGTGAATGAACTGTTAGGTTCTGATGACTCACATGATG 1320  
Qy 1321 GGGAGTCTGAATCAAAAGTGAATGATGATGTTGAGAGTTCTAAATGAGGTAGATG 1380  
Db 1321 GGGAGTCTGAATCAAAAGTGAATGATGATGTTGAGAGTTCTAAATGAGGTAGATG 1380  
Qy 1381 AATATTCTGTTCTTTCAGAGAAATAGACTTACTTGGCCAGTGATCCTCATGAGGCTTTAA 1440  
Db 1381 AATATTCTGTTCTTTCAGAGAAATAGACTTACTTGGCCAGTGATCCTCATGAGGCTTTAA 1440  
Qy 1441 TATGTAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGAGTAATATTGAAGACAAAATAT 1500  
Db 1441 TATGTAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGAGTAATATTGAAGACAAAATAT 1500  
Qy 1501 TTGGGAAAACTTATCGGAAGAGGCAAGCCTCCCAACTTAAGCCATGTAACCTGAAAAATC 1560  
Db 1501 TTGGGAAAACTTATCGGAAGAGGCAAGCCTCCCAACTTAAGCCATGTAACCTGAAAAATC 1560  
Qy 1561 TAAATTATAGGAGCAATTTTACTGAGCCACAGATAATACAGAGGCTCCCTCACAATA 1620  
Db 1561 TAAATTATAGGAGCAATTTTACTGAGCCACAGATAATACAGAGGCTCCCTCACAATA 1620  
Qy 1621 AATTTAAAGCGTAAAGAGGACCTACATCAGGCTTCTCTCTGAGGATTTTATCAAGAAAG 1680  
Db 1621 AATTTAAAGCGTAAAGAGGACCTACATCAGGCTTCTCTCTGAGGATTTTATCAAGAAAG 1680  
Qy 1681 CAGATTTGGCAGTTCAAAAGACTCCTGAAATGATAAATCAGGGAACCTAACCAACGGAGC 1740  
Db 1681 CAGATTTGGCAGTTCAAAAGACTCCTGAAATGATAAATCAGGGAACCTAACCAACGGAGC 1740  
Qy 1741 AGAATGCTCAAGTGAATTAATTAATAGTGTGATGATGATGATGATGATGATGATGATGAT 1800  
Db 1741 AGAATGCTCAAGTGAATTAATTAATAGTGTGATGATGATGATGATGATGATGATGAT 1800  
Qy 1801 CTATTTCAAGATGAGAAAAATCCTAACCAATAGAAATCACTCGAAAAAGAAATCTGCTTTCA 1860  
Db 1801 CTATTTCAAGATGAGAAAAATCCTAACCAATAGAAATCACTCGAAAAAGAAATCTGCTTTCA 1860  
Qy 1861 AAACGAAAGCTGAAACCTTATAGCAGCAGTAAAGCAATATGGAATCTGAAATTAATATCC 1920



Db 1861 AAACGAAAGCTGAACCTTAATAGCAGCAGTATAAGCAATATATGAACTCGAATTAATAATATCC 1920  
Qy 1921 ACAATTCAAAAGCAGCTAAAAGAAATAGGCTGAGGAGGAAGTCTTCTACCAAGGCATATTC 1980  
Db 1921 ACAATTCAAAAGCAGCTAAAAGAAATAGGCTGAGGAGGAAGTCTTCTACCAAGGCATATTC 1980  
Qy 1981 ATGCGCTTGAACCTAGTCTAGTGAATAATTAAGCCCACTTAATTTGTACTGTAATTCGCAAA 2040  
Db 1981 ATGCGCTTGAACCTAGTCTAGTGAATAATTAAGCCCACTTAATTTGTACTGTAATTCGCAAA 2040  
Qy 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATAAGAAAAAAGTACAAACAAATGCGAGTCA 2100  
Db 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATAAGAAAAAAGTACAAACAAATGCGAGTCA 2100  
Qy 2101 GGCAAGCAGAAACCTCAACCTCATGGAAGTAAAGAACCTGCAACTGGAGCCCAAGAGA 2160  
Db 2101 GGCAAGCAGAAACCTCAACCTCATGGAAGTAAAGAACCTGCAACTGGAGCCCAAGAGA 2160  
Qy 2161 GTAAACAGCCAAATGAACAGACAAGTAAAGACATGACAGTGATATTTCCAGAGCTGA 2220  
Db 2161 GTAAACAGCCAAATGAACAGACAAGTAAAGACATGACAGTGATATTTCCAGAGCTGA 2220  
Qy 2221 AGTTAAACAAATGCACCTGGTCTTTTACTAGTGTCAAATACCAAGTAAAGAAAT 2280  
Db 2221 AGTTAAACAAATGCACCTGGTCTTTTACTAGTGTCAAATACCAAGTAAAGAAAT 2280  
Qy 2281 TTGTCAATCTTAGCTTCCAAAGAGAGAAAGAGAGAACTAGAAACAGTAAAGTGT 2340  
Db 2281 TTGTCAATCTTAGCTTCCAAAGAGAGAAAGAGAGAACTAGAAACAGTAAAGTGT 2340  
Qy 2341 CTAATAATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAAGAGGGTTTTCGAAACTG 2400  
Db 2341 CTAATAATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAAGAGGGTTTTCGAAACTG 2400  
Qy 2401 AAAGATCTGTAGAGATGAGTATTTCACTGGTACCTGGTACTGATATTTGGGCTACAGG 2460  
Db 2401 AAAGATCTGTAGAGATGAGTATTTCACTGGTACCTGGTACTGATATTTGGGCTACAGG 2460  
Qy 2461 AAAGTATCTGTTACTGGAAGTGTAGCACTCTAGGGAAGGCAAAACAGAACCAATAAAT 2520  
Db 2461 AAAGTATCTGTTACTGGAAGTGTAGCACTCTAGGGAAGGCAAAACAGAACCAATAAAT 2520  
Qy 2521 GTGTGAGTCAGTGTGCAGCAATTTGAAAACCCCAAGGCACTAATTCATGGTTGTTCCAAAG 2580  
Db 2521 GTGTGAGTCAGTGTGCAGCAATTTGAAAACCCCAAGGCACTAATTCATGGTTGTTCCAAAG 2580  
Qy 2581 ATAATAGNAATGACACAGAGGCTTTAAGTATCAATTTGGGACATGAAGTTAACACAGTC 2640  
Db 2581 ATAATAGNAATGACACAGAGGCTTTAAGTATCAATTTGGGACATGAAGTTAACACAGTC 2640  
Qy 2641 GGGAAACAGCATAGAAATGAAGAAAGTGAACCTTGATGCTCAGTATTTGAGAGATACAT 2700  
Db 2641 GGGAAACAGCATAGAAATGAAGAAAGTGAACCTTGATGCTCAGTATTTGAGAGATACAT 2700  
Qy 2701 TCAAGGTTTCAAAGCGCCAGTCAATTTGCTCTGTTTCAAATCCAGGAATTCAGAGAGG 2760  
Db 2701 TCAAGGTTTCAAAGCGCCAGTCAATTTGCTCCGTTTCAAATCCAGGAATTCAGAGAGG 2760  
Qy 2761 AATGTGMAACATTTCTGCCCCACTCTGGGCTCTTAAAGAAACAAAGTCCAAAAGTCACTT 2820  
Db 2761 AATGTGMAACATTTCTGCCCCACTCTGGGCTCTTAAAGAAACAAAGTCCAAAAGTCACTT 2820  
Qy 2821 TTGAATGTGAACAAAAGAGAAATCAAGGAAAGAAATGAGTCTAAATATCAAGCCTGTAC 2880  
Db 2821 TTGAATGTGAACAAAAGAGAAATCAAGGAAAGAAATGAGTCTAAATATCAAGCCTGTAC 2880  
Qy 2881 AGACAGTAAATATCACTGCAGGCTTCTGTTGTTGTTGAGAGAAAGTAAAGCAGTGTATA 2940  
Db 2881 AGACAGTAAATATCACTGCAGGCTTCTGTTGTTGTTGAGAGAAAGTAAAGCAGTGTATA 2940  
Qy 2941 ATGCCAAATGTAGTATCAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTTCAGAGGCA 3000  
Db 2941 ATGCCAAATGTAGTATCAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTTCAGAGGCA 3000

Qy 3001 ACGAAACTGGACTCATTTACTCCAAATAAACATGGACTTTTACAAAACCCATATCGTATAC 3060  
Db 3001 ACGAAACTGGACTCATTTACTCCAAATAAACATGGACTTTTACAAAACCCATATCGTATAC 3060  
Qy 3061 CACCACCTTTTCCCATCAAGTCAATTTGTTAAAACTAAATGTAAGAAAAATCTGCTAGAGG 3120  
Db 3061 CACCACCTTTTCCCATCAAGTCAATTTGTTAAAACTAAATGTAAGAAAAATCTGCTAGAGG 3120  
Qy 3121 AAAACTTTGAGGAACATTCATGTCACCTGAAAGAGAAATGGGAATGAGAACATTCCAA 3180  
Db 3121 AAAACTTTGAGGAACATTCATGTCACCTGAAAGAGAAATGGGAATGAGAACATTCCAA 3180  
Qy 3181 GTACAGTGTAGCACAAATTAGCCGTAATAACATTTAGAGAAAAATGTTTTTAAAGGAGCCAGCT 3240  
Db 3181 GTACAGTGTAGCACAAATTAGCCGTAATAACATTTAGAGAAAAATGTTTTTAAAGGAGCCAGCT 3240  
Qy 3241 CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA 3300  
Db 3241 CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA 3300  
Qy 3301 TAGGTTCCAGTGTAGAAAACTTCAAGCAGAACCTAGGTAGAAACAGAGGGCCAAAATTGA 3360  
Db 3301 TAGGTTCCAGTGTAGAAAACTTCAAGCAGAACCTAGGTAGAAACAGAGGGCCAAAATTGA 3360  
Qy 3361 ATGCTATGCTTAGATTTAGGGGTTTTGCAACCTGAGGCTCTATAAACAAAGTCTTCTCTGAA 3420  
Db 3361 ATGCTATGCTTAGATTTAGGGGTTTTGCAACCTGAGGCTCTATAAACAAAGTCTTCTCTGAA 3420  
Qy 3421 GTAAATGTAAGCACTCTGAAATAAAAAAGCAAGAAATATGAAGAGTAGTTCAGACTGTGA 3480  
Db 3421 GTAAATGTAAGCACTCTGAAATAAAAAAGCAAGAAATATGAAGAGTAGTTCAGACTGTGA 3480  
Qy 3481 ATACAGATTTCTCTCCATATCTGATTTTCAAGTAACTTTAGAACAGCCCTATGGGAAGTAGTC 3540  
Db 3481 ATACAGATTTCTCTCCATATCTGATTTTCAAGTAACTTTAGAACAGCCCTATGGGAAGTAGTC 3540  
Qy 3541 ATGCATCTCAGTTGTTCTTGAGACACCTGATGACCTGTTAGATGATGTTGAAATAAAGG 3600  
Db 3541 ATGCATCTCAGTTGTTCTTGAGACACCTGATGACCTGTTAGATGATGTTGAAATAAAGG 3600  
Qy 3601 AAGTACTAGTTTTCGTAATAAAGCAATTAAGGAAAGTCTGCTGTTTTTACGAAAAAGCG 3660  
Db 3601 AAGTACTAGTTTTCGTAATAAAGCAATTAAGGAAAGTCTGCTGTTTTTACGAAAAAGCG 3660  
Qy 3661 TCCAGAGAGGAGGCTTAGCAGGAGTCTAGCCCTTTTCAACCATACACATTTGGCTCAGG 3720  
Db 3661 TCCAGAGAGGAGGCTTAGCAGGAGTCTAGCCCTTTTCAACCATACACATTTGGCTCAGG 3720  
Qy 3721 GTTACCGAAGAGGGCCCAAGAAATTAGAGTCTCAGAAAGAGAACTTATCTAGTGAGGATG 3780  
Db 3721 GTTACCGAAGAGGGCCCAAGAAATTAGAGTCTCAGAAAGAGAACTTATCTAGTGAGGATG 3780  
Qy 3781 AAGAGCTTCCCTGCTTCCAACTTTGTTATTTGGTAAAGTAAACAATATACCTTCTCAGT 3840  
Db 3781 AAGAGCTTCCCTGCTTCCAACTTTGTTATTTGGTAAAGTAAACAATATACCTTCTCAGT 3840  
Qy 3841 CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGCTTAAGAACACAGAGAGAAATTTAT 3900  
Db 3841 CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGCTTAAGAACACAGAGAGAAATTTAT 3900  
Qy 3901 TATCATTTGAAGAAATAGCTTAAATGACTGCAGTAACTACAGGTAATTTGCGAAAGGCATCTC 3960  
Db 3901 TATCATTTGAAGAAATAGCTTAAATGACTGCAGTAACTACAGGTAATTTGCGAAAGGCATCTC 3960  
Qy 3961 AGGAACATCACTTTAGTGAGGAAACAAAATGTTCTGCTAGCTGTTTTTCTTTCACAGTGCA 4020  
Db 3961 AGGAACATCACTTTAGTGAGGAAACAAAATGTTCTGCTAGCTGTTTTTCTTTCACAGTGCA 4020  
Qy 4021 GTGAATTTGGAAGACTTGACTGCAATTAACACACCCAGGATCCCTTCTTGATTTGGTCTT 4080  
Db 4021 GTGAATTTGGAAGACTTGACTGCAATTAACACACCCAGGATCCCTTCTTGATTTGGTCTT 4080



Qy	4081	CCAAACAAATGAGGCGATCAGTCTGAAAGACCGAGGAGTTGGTCTGAGTGA	CAAGGAATTTGG	4141
Db	4081	CCAAACAAATGAGGCGATCAGTCTGAAAGACCGAGGAGTTGGTCTGAGTGA	CAAGGAATTTGG	4140
Qy	4141	TTTCAGATGATGAAGAGGACCGGCTTGGAGAAATATATCAAGAGAGCCAAAGCA		4200
Db	4141	TTTCAGATGATGAAGAGGAAACGGGCTTGGAGAAATATATCAAGAGAGCCAAAGCA		4200
Qy	4201	TGGATTCAAATCTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAAAACGCGTCTCTGAAG		4260
Db	4201	TGGATTCAAATCTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAAAACGCGTCTCTGAAG		4260
Qy	4261	ACTGCTCAGGGCTATCTCTCAGAGTGACATTTTAAACCATCTCAGCAGAGGATACCAATGC		4320
Db	4261	ACTGCTCAGGGCTATCTCTCAGAGTGACATTTTAAACCATCTCAGCAGAGGATACCAATGC		4320
Qy	4321	AACATAACCTGTATAAAGCTCCAGCAGAAATGGCTGAACCTAGAGCTGTGTAGACAGC		4380
Db	4321	AACATAACCTGTATAAAGCTCCAGCAGAAATGGCTGAACCTAGAGCTGTGTAGACAGC		4380
Qy	4381	ATGGAGCCAGCCCTTCTTAAACAGCTTACCCCTTCCATCATAAGTGA	CTCCCTCTGCCCTTTCGAGG	4440
Db	4381	ATGGAGCCAGCCCTTCTTAAACAGCTTACCCCTTCCATCATAAGTGA	CTCCCTCTGCCCTTTCGAGG	4440
Qy	4441	ACTTGCAGAAATTCAGAACAAAGCACA	TCAGAAAAAGCAGTATTAACTTCACAGAAAAAGTA	4500
Db	4441	ACTTGCAGAAATTCAGAAAAAGCACA	TCAGAAAAAGCAGTATTAACTTCACAGAAAAAGTA	4500
Qy	4501	GTGNAATACCTTATAAGCCAGNAATCCAGAGGCCCTTTCTGCTGACAGTTTGTAGGTGCTG		4560
Db	4501	GTGNAATACCTTATAAGCCAGNAATCCAGAGGCCCTTTCTGCTGACAGTTTGTAGGTGCTG		4560
Qy	4561	CAGATAGTCTTACCAAGTAAAAATAAGAAACAGAGGTGGAAGGTCA	TCGCCCTTCTAAAT	4620
Db	4561	CAGATAGTCTTACCAAGTAAAAATAAGAAACAGAGGTGGAAGGTCA	TCGCCCTTCTAAAT	4620
Qy	4621	GCCCATCATTAGATGATAGTGGTACATGACACAGTTGCTCTGGAGTCTTTCAGAAATAGAA		4680
Db	4621	GCCCATCATTAGATGATAGTGGTACATGACACAGTTGCTCTGGAGTCTTTCAGAAATAGAA		4680
Qy	4681	ACTACCCATCTCAGAGAGGCTCATTAAAGTTGTGATGTGGAGGACCAACAGCTGGAAG		4740
Db	4681	ACTACCCATCTCAGAGAGGCTCATTAAAGTTGTGATGTGGAGGACCAACAGCTGGAAG		4740
Qy	4741	AGTCTGGGCCACACGATTGACGGAAACATCTTACTTCCAAAGCAAGATCTCAGAGGAA		4800
Db	4741	AGTCTGGGCCACACGATTGACGGAAACATCTTACTTCCAAAGCAAGATCTCAGAGGAA		4800
Qy	4801	CCCCTTACCTGGAAATCTGGAATCAGCCCTCTTCTCTGATGACCCCTGGAATCTGATCTTCTG		4860
Db	4801	CCCCTTACCTGGAAATCTGGAATCAGCCCTCTTCTCTGATGACCCCTGGAATCTGATCTTCTG		4860
Qy	4861	AAGACAGAGCCGAGATCAGCTCGTGTGGCAACATACCATCTTCAACCTCTGCATTTGA		4920
Db	4861	AAGACAGAGCCGAGATCAGCTCGTGTGGCAACATACCATCTTCAACCTCTGCATTTGA		4920
Qy	4921	AAGTTTCCCCTTCAAAAGTTGCAGAAATCGCCAGGCTCCAGCTGCTGCTCACTACTACTG		4980
Db	4921	AAGTTTCCCCTTCAAAAGTTGCAGAAATCGCCAGGCTCCAGCTGCTGCTCACTACTACTG		4980
Qy	4981	ATACTGCTGGGTATAATGCAATGGAAGAAAGTGTGAGCAGGGAGAACCCAGAAATTTGACAG		5040
Db	4981	ATACTGCTGGGTATAATGCAATGGAAGAAAGTGTGAGCAGGGAGAACCCAGAAATTTGACAG		5040
Qy	5041	CTTCAACAGAAAGGTCACAAAGAAATGTCATGGTGTGTCTGGGCTGACCCAGAAAG		5100
Db	5041	CTTCAACAGAAAGGTCACAAAGAAATGTCATGGTGTGTCTGGGCTGACCCAGAAAG		5100
Qy	5101	AATTTATGCTCGTGTACAGTTTCCAGAAACACCAATCACTTTTAACTTAATCTTAATTA		5160
Db	5101	AATTTATGCTCGTGTACAGTTTCCAGAAACACCAATCACTTTTAACTTAATCTTAATTA		5160
Qy	5161	CTGAAGAGACTACTCATCTGTTGTTATGAAACAGATGCTGAGTTTGTGTGTGAACCGACAC		5220

[illegible]

121 TGGATTTATCTGCTCTTCGCGTTTGAAGAATGACAAAATGTCATTAAATGCTATGAGAAA 180  
121 TGGATTTATCTGCTCTTCGCGTTTGAAGAATGACAAAATGTCATTAAATGCTATGAGAAA 180  
181 TCTTAGAGTGTCCCATCTGCTGAGTGTGATCAAGGAACCTGTCTCCACAAAGTGTGACC 240  
181 TCTTAGAGTGTCCCATCTGCTGAGTGTGATCAAGGAACCTGTCTCCACAAAGTGTGACC 240  
241 ACATATTTGCAAAATTTGCAATCTGCAATCTTCAACCCAGAGAAAGGGGCTTCACAGT 300  
241 ACATATTTGCAAAATTTGCAATCTGCAATCTTCAACCCAGAGAAAGGGGCTTCACAGT 300  
301 GTCCCTTTATGTAAGATGATATAACCAAAAGGAGCCCTACAGAAAGTACGAGATTTAGTC 360  
301 GTCCCTTTATGTAAGATGATATAACCAAAAGGAGCCCTACAGAAAGTACGAGATTTAGTC 360  
361 AACTTGTGTAAGACTATTTGAAAATCATTTGTGCTTTTTCAGCTTGCACACAGTTTGGAGT 420  
361 AACTTGTGTAAGACTATTTGAAAATCATTTGTGCTTTTTCAGCTTGCACACAGTTTGGAGT 420  
421 ATGCACACAGCTATAATTTGCAAAAGGAGAAATTAATCTCTCTGAAACATCTAAAGATG 480  
421 ATGCACACAGCTATAATTTGCAAAAGGAGAAATTAATCTCTCTGAAACATCTAAAGATG 480  
481 AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCAAAAGACTTCTACAGAGTG 540  
481 AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCAAAAGACTTCTACAGAGTG 540  
541 AACCCGAAATTCCTTCTGAGGAAACCAAGTCTCAGTGTCCAACTCTCTAACCTTGGAA 600  
541 AACCCGAAATTCCTTCTGAGGAAACCAAGTCTCAGTGTCCAACTCTCTAACCTTGGAA 600  
601 CTGTGAGAACTCTCAGGACAAAGCAGCGGATACAACTCTCAGGAGCTGTCTACATTTG 660  
601 CTGTGAGAACTCTCAGGACAAAGCAGCGGATACAACTCTCAGGAGCTGTCTACATTTG 660  
661 AATTGGGATCTGATCTTCTGAAATACCGTTAATAGGCAACTTATGTCAGTGTGGAG 720  
661 AATTGGGATCTGATCTTCTGAAATACCGTTAATAGGCAACTTATGTCAGTGTGGAG 720  
721 ATCAAGAAATGTTTACAAATCAACCCCTCAAGGAACCGGATGAAATCAGTTTGGATCTG 780  
721 ATCAAGAAATGTTTACAAATCAACCCCTCAAGGAACCGGATGAAATCAGTTTGGATCTG 780  
781 CAAAGAGGCTGTGTTGAAATTTCTGAGACGGATGTAACAAATCTGAAACATCATCAAC 840  
781 CAAAGAGGCTGTGTTGAAATTTCTGAGACGGATGTAACAAATCTGAAACATCATCAAC 840  
841 CCAGTAATATGATTTGAAACCACTGAGAGCGCTGAGAGCGATCCAGAAAGT 900  
841 CCAGTAATATGATTTGAAACCACTGAGAGCGCTGAGAGCGATCCAGAAAGT 900  
901 ATCAGGATGTTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCAAAATCTCATGCCA 960  
901 ATCAGGATGTTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCAAAATCTCATGCCA 960  
961 GCTCATTTACAGCATGAGAAACAGCAAGTTTATCTACTTAAGACAGAAATGATGAGAAA 1020  
961 GCTCATTTACAGCATGAGAAACAGCAAGTTTATCTACTTAAGACAGAAATGATGAGAAA 1020  
1021 AGGCTGAATTTCTGTAATTAAGCAACAGCTGCTTTAGCAAGGAGCCAAATACAGAT 1080  
1021 AGGCTGAATTTCTGTAATTAAGCAACAGCTGCTTTAGCAAGGAGCCAAATACAGAT 1080  
1081 GGGCTGAAATGAGGAAACATGTAATGATAGGGGACTCCAGACAGAAAGGAGTAG 1140  
1081 GGGCTGAAATGAGGAAACATGTAATGATAGGGGACTCCAGACAGAAAGGAGTAG 1140  
1141 ATCTGAATGCTATCCCTGTGTGAGAGAAAGAAATGGAATAGCAGAAATCTGCCATGCT 1200  
1141 ATCTGAATGCTATCCCTGTGTGAGAGAAAGAAATGGAATAGCAGAAATCTGCCATGCT 1200

1201 CAGAGAAATCCTAGAGATCTGAAGATGTCCTTGGATAAACACTAAATAGCAGCATTCAGA 1260  
1201 CAGAGAAATCCTAGAGATCTGAAGATGTCCTTGGATAAACACTAAATAGCAGCATTCAGA 1260  
1261 AAGTTAATAGTGGTGTTCAGAAAGTGAATGAACTGTGTAGTCTTGATGACTCATCATGATG 1320  
1261 AAGTTAATAGTGGTGTTCAGAAAGTGAATGAACTGTGTAGTCTTGATGACTCATCATGATG 1320  
1321 GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGATTTGGACGTTCTAAATGAGGTAGATG 1380  
1321 GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGATTTGGACGTTCTAAATGAGGTAGATG 1380  
1381 AATATTTCTGCTTCTCAGAGAAATAGACTTACTTGGCCAGTGATCCTCATGAGGCTTTAA 1440  
1381 AATATTTCTGCTTCTCAGAGAAATAGACTTACTTGGCCAGTGATCCTCATGAGGCTTTAA 1440  
1441 TATGTAAGTGAAGAGTTTCACTCCAAATCAGTGTAGAGTAATATTTTGAAGACAAAATAT 1500  
1441 TATGTAAGTGAAGAGTTTCACTCCAAATCAGTGTAGAGTAATATTTTGAAGACAAAATAT 1500  
1501 TTGGGAAACCTATCCGAAGAGCGCAAGCTCCCAACTTAAAGCCATGTAACTGAAAATC 1560  
1501 TTGGGAAACCTATCCGAAGAGCGCAAGCTCCCAACTTAAAGCCATGTAACTGAAAATC 1560  
1561 TAAATATAGGAGCATTTGTTTACTGAGCCACAGATAATACAAGAGCGTCCCTCAACAATA 1620  
1561 TAAATATAGGAGCATTTGTTTACTGAGCCACAGATAATACAAGAGCGTCCCTCAACAATA 1620  
1621 AATTAAGCGTAAAGAGAGACCTACATCAGGCTTCACTCTGAGGATTTTATCAAGAAAG 1680  
1621 AATTAAGCGTAAAGAGAGACCTACATCAGGCTTCACTCTGAGGATTTTATCAAGAAAG 1680  
1681 CAGATTTGGCAGTCTCAAAAGACTCTCTGAATGATAATCAGGGAACCTAAACCAAGCGAGC 1740  
1681 CAGATTTGGCAGTCTCAAAAGACTCTCTGAATGATAATCAGGGAACCTAAACCAAGCGAGC 1740  
1741 AGAATGCTCAAGTGTGAATATTTACTAATAGTGTGATGAGATAAATAAAGAAAGTGTGAT 1800  
1741 AGAATGCTCAAGTGTGAATATTTACTAATAGTGTGATGAGATAAATAAAGAAAGTGTGAT 1800  
1801 CTATTCAGAAATGAGAAATCCTTAAACCAATAGAACTCACTCGAAAGAAATCTGCTTTCA 1860  
1801 CTATTCAGAAATGAGAAATCCTTAAACCAATAGAACTCACTCGAAAGAAATCTGCTTTCA 1860  
1861 AAACGAAAGCTGAACTTAAAGCAGCATATAGCAATATGGAATCGAATTAATATTC 1920  
1861 AAACGAAAGCTGAACTTAAAGCAGCATATAGCAATATGGAATCGAATTAATATTC 1920  
1921 ACAATTCAAAAGCACTTAAAGAAATAGGCTGAGGAGAAAGTCTTCTACAGGCAATATTC 1980  
1921 ACAATTCAAAAGCACTTAAAGAAATAGGCTGAGGAGAAAGTCTTCTACAGGCAATATTC 1980  
1981 ATGCGCTTGAATCTAGTAGTCAAGTGAATACTTAAGCCCACTAATTTGTAATGCAAA 2040  
1981 ATGCGCTTGAATCTAGTAGTCAAGTGAATACTTAAGCCCACTAATTTGTAATGCAAA 2040  
2041 TTGATAGTTGTTTCTAGCAGTGAAGAGATAAAGAAAGAAAGTACAACCAATGCGAGTCA 2100  
2041 TTGATAGTTGTTTCTAGCAGTGAAGAGATAAAGAAAGAAAGTACAACCAATGCGAGTCA 2100  
2101 GGCACAGCAGAAACCTTCAACTCATGGAAGTAAAGAACTGCAACTGGAGCCCAAGAGA 2160  
2101 GGCACAGCAGAAACCTTCAACTCATGGAAGTAAAGAACTGCAACTGGAGCCCAAGAGA 2160  
2161 GTAAACAGCCAAATGAACAGCAAGTAAAGACATGACAGCGGATCTTTCCAGAGCTGA 2220  
2161 GTAAACAGCCAAATGAACAGCAAGTAAAGACATGACAGCGGATCTTTCCAGAGCTGA 2220  
2221 AGTTAACAATGACCTGGTCTTTTACTAAGTGTTCAAATACCAAGTGAATTAAGAAAT 2280  
2221 AGTTAACAATGACCTGGTCTTTTACTAAGTGTTCAAATACCAAGTGAATTAAGAAAT 2280  
2281 TTGTCAATCTAGCTTCCAAAGAGAGAAAGAAAGAGAGAACTAGAAACAGTTAAAGTGT 2340







Db 2701 TCAAGGTTTCAAAGCGCAGTCAATTTGCTCGTTTTCAAATCCAGGAAATCGAGAGAGG 2760  
Qy 2761 AATGTGCAACATCTCTGCCCACCTCTGGGTCCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
Db 2761 AATGTGCAACATCTCTGCCCACCTCTGGGTCCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
Qy 2821 TTGAATGTGAACAAAGAGAAATCAAGAAAGAAATGAGTCTAATATCAAGCCTGTAC 2880  
Db 2821 TTGAATGTGAACAAAGAGAAATCAAGAAAGAAATGAGTCTAATATCAAGCCTGTAC 2880  
Qy 2881 AGACAGTCTAATATCACTGCGAGCTTCTGCTGGTTGCTGAGAAAGATAAGCCAGTTGATA 2940  
Db 2881 AGACAGTCTAATATCACTGCGAGCTTCTGCTGGTTGCTGAGAAAGATAAGCCAGTTGATA 2940  
Qy 2941 ATGCCAAATGTAGTATCAAGAGGAGCTCTAGGTTTGTCTATCATCTCAGTTTCAGAGGCA 3000  
Db 2941 ATGCCAAATGTAGTATCAAGAGGAGCTCTAGGTTTGTCTATCATCTCAGTTTCAGAGGCA 3000  
Qy 3001 ACAGAACTGGACTCAATTAATCAAAATAAAACATGACATTTTACAAAACCCATATCGTATAC 3060  
Db 3001 ACAGAACTGGACTCAATTAATCAAAATAAAACATGACATTTTACAAAACCCATATCGTATAC 3060  
Qy 3061 CACCACATTTTCCCATCAAGTCAATTTGTTAAACTAAATGTAAAGAAATCTGCTAGAGG 3120  
Db 3061 CACCACATTTTCCCATCAAGTCAATTTGTTAAACTAAATGTAAAGAAATCTGCTAGAGG 3120  
Qy 3121 AAAACTTTGAGGAACATTCATGTACCTGAGAGAAATGGGAAATGAGAACATTTCCAA 3180  
Db 3121 AAAACTTTGAGGAACATTCATGTACCTGAGAGAAATGGGAAATGAGAACATTTCCAA 3180  
Qy 3181 GTACAGTGTAGGACAAATTTAGCCGTAATTAACATTAAGAGAAATGTTTTAAAGAGGCCAGCT 3240  
Db 3181 GTACAGTGTAGGACAAATTTAGCCGTAATTAACATTAAGAGAAATGTTTTAAAGAGGCCAGCT 3240  
Qy 3241 CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAA 3300  
Db 3241 CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAA 3300  
Qy 3301 TAGGTTCCAGTGATGAAACATTCAGCAGNACTAGGTAGNAAACAGAGGGCCAAATTTGA 3360  
Db 3301 TAGGTTCCAGTGATGAAACATTCAGCAGNACTAGGTAGNAAACAGAGGGCCAAATTTGA 3360  
Qy 3361 ATGCTATGCTTAGATTTAGGGTTTTGCAACTGAGGCTTAATAACAAAGTCTTCTCGGAA 3420  
Db 3361 ATGCTATGCTTAGATTTAGGGTTTTGCAACTGAGGCTTAATAACAAAGTCTTCTCGGAA 3420  
Qy 3421 GTAATGTGAAGCATCTCGAAATTAATAAGCAAGAAATATGAAGAGTAGTTTCAGACTGTTA 3480  
Db 3421 GTAATGTGAAGCATCTCGAAATTAATAAGCAAGAAATATGAAGAGTAGTTTCAGACTGTTA 3480  
Qy 3481 ATACAGATTTCTCCATATCTGATTTTCAGATACCTTAGAACAGCCCTATGGGAAGTAGTC 3540  
Db 3481 ATACAGATTTCTCCATATCTGATTTTCAGATACCTTAGAACAGCCCTATGGGAAGTAGTC 3540  
Qy 3541 ATGCATCTCAGGTTTGTCTCAGACACTGATGACCTGTTAGATGATGTTGGAATAAAGG 3600  
Db 3541 ATGCATCTCAGGTTTGTCTCAGACACTGATGACCTGTTAGATGATGTTGGAATAAAGG 3600  
Qy 3601 AAGTACTAGTTTGTCTGAAATGACATTAAGGAAAGTTCTGCTGTTTTAGCAAAAGCG 3660  
Db 3601 AAGTACTAGTTTGTCTGAAATGACATTAAGGAAAGTTCTGCTGTTTTAGCAAAAGCG 3660  
Qy 3661 TCCAGAGGAGAGCTTAGCAGGAGTCTGACCTTTTCCACCCATACATTTGGCTCAGG 3720  
Db 3661 TCCAGAGGAGAGCTTAGCAGGAGTCTGACCTTTTCCACCCATACATTTGGCTCAGG 3720  
Qy 3721 GTTACCGAAGAGGGCCAAAGAAATTTAGAGTCTCAGAGAGAACTTATCTAGTGAGGATG 3780  
Db 3721 GTTACCGAAGAGGGCCAAAGAAATTTAGAGTCTCAGAGAGAACTTATCTAGTGAGGATG 3780  
Qy 3781 AAGAGCTTCCCTGTTCCAACTGTTTATTTGTTAAAGTAAACAAATATACCTTCTCAGT 3840  
Db 3781 AAGAGCTTCCCTGTTCCAACTGTTTATTTGTTAAAGTAAACAAATATACCTTCTCAGT 3840

Db 3781 AAGAGCTTCCCTGTTCCAACTGTTTATTTGTTAAAGTAAACAAATATACCTTCTCAGT 3840  
Qy 3841 CTACTAGGCATAGCACCGTTGCTTACCGAGTGTCTGTCTAAGAACACAGAGGAGAAATTTAT 3900  
Db 3841 CTACTAGGCATAGCACCGTTGCTTACCGAGTGTCTGTCTAAGAACACAGAGGAGAAATTTAT 3900  
Qy 3901 TATCATTTGAAGAAATAGCTTAAATGACTCGAGTAAACAGGTAATATTTGGCAAGGCATCTC 3960  
Db 3901 TATCATTTGAAGAAATAGCTTAAATGACTCGAGTAAACAGGTAATATTTGGCAAGGCATCTC 3960  
Qy 3961 AGGAAATCACTTCTAGTGAGGAAACAAATGTTCTGCTAGCTTGTGTTTCTTCACAGTGCA 4020  
Db 3961 AGGAAATCACTTCTAGTGAGGAAACAAATGTTCTGCTAGCTTGTGTTTCTTCACAGTGCA 4020  
Qy 4021 GTCAATTTGGAAGACTTGTGCTGCAAAATACAAACCCAGGATCCTTCTTCTGATTTGTTCTT 4080  
Db 4021 GTCAATTTGGAAGACTTGTGCTGCAAAATACAAACCCAGGATCCTTCTTCTGATTTGTTCTT 4080  
Qy 4081 CCAAAACAAATGAGGCATCACTCTGAAAAGCCAGGAGTTGGTCTGAGTGACAAGGAAATGG 4140  
Db 4081 CCAAAACAAATGAGGCATCACTCTGAAAAGCCAGGAGTTGGTCTGAGTGACAAGGAAATGG 4140  
Qy 4141 TTTTCAGATGATGAAGAAAGAGGAAACGGGCTTTGGAAGAAATAATCAAGAAAGACAAAGCA 4200  
Db 4141 TTTTCAGATGATGAAGAAAGAGGAAACGGGCTTTGGAAGAAATAATCAAGAAAGACAAAGCA 4200  
Qy 4201 TGGATTTCAAACCTTAGGTGAGCAGCATCTGGGTGTGAGAGTGAACAAAGCGTCTCTGAAG 4260  
Db 4201 TGGATTTCAAACCTTAGGTGAGCAGCATCTGGGTGTGAGAGTGAACAAAGCGTCTCTGAAG 4260  
Qy 4261 ACTGCTCAGGCTTATCCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGGATACCATGC 4320  
Db 4261 ACTGCTCAGGCTTATCCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGGATACCATGC 4320  
Qy 4321 AACATAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACCTAGAAAGCTGTGTTAGAACAGC 4380  
Db 4321 AACATAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACCTAGAAAGCTGTGTTAGAACAGC 4380  
Qy 4381 ATGGGAGCCAGCTTCTTAACAGCTACCTTTCATCAATAGTACTCTCTGCCCTTGAGG 4440  
Db 4381 ATGGGAGCCAGCTTCTTAACAGCTACCTTTCATCAATAGTACTCTCTGCCCTTGAGG 4440  
Qy 4441 ACCTGCGAAATCCAGAACAAAGCACATCAGAAAAAGCAGTATTAACCTTCAAGAAAAAGTA 4500  
Db 4441 ACCTGCGAAATCCAGAACAAAGCACATCAGAAAAAGCAGTATTAACCTTCAAGAAAAAGTA 4500  
Qy 4501 GTGAATACCCCTATAGCCAGAAATCCAGAGGCCCTTTCTGCTGACAAAGTTTGAAGTGTCTG 4560  
Db 4501 GTGAATACCCCTATAGCCAGAAATCCAGAGGCCCTTTCTGCTGACAAAGTTTGAAGTGTCTG 4560  
Qy 4561 CAGATAGTTCTACCGATTAATAAAGAACCCAGAGTGGAAAGTCAATCCCTTCTTAAT 4620  
Db 4561 CAGATAGTTCTACCGATTAATAAAGAACCCAGAGTGGAAAGTCAATCCCTTCTTAAT 4620  
Qy 4621 GCCCATCATTTAGATGATAGTGGTATCATGACAGATTTGCTCTGGGAGTCTTTCAGAAATAGAA 4680  
Db 4621 GCCCATCATTTAGATGATAGTGGTATCATGACAGATTTGCTCTGGGAGTCTTTCAGAAATAGAA 4680  
Qy 4681 ACTACCCATCTCAAGAGGAGCTCATTAAGTGTGATGTTGGAGGAGCAACAGCTGGAAG 4740  
Db 4681 ACTACCCATCTCAAGAGGAGCTCATTAAGTGTGATGTTGGAGGAGCAACAGCTGGAAG 4740  
Qy 4741 AGTCTGGGCCACACGATTTTGAACGGAACATCTTACTTTGCCAAGCAGAGATCTAGAGGGAA 4800  
Db 4741 AGTCTGGGCCACACGATTTTGAACGGAACATCTTACTTTGCCAAGCAGAGATCTAGAGGGAA 4800  
Qy 4801 CCCCTTACCTGGAATCTGGAATCAGCCTCTCTCTGATGATGATGATGATGATGATGATGATG 4860  
Db 4801 CCCCTTACCTGGAATCTGGAATCAGCCTCTCTCTGATGATGATGATGATGATGATGATGATG 4860  
Qy 4861 AAGACAGAGCCCCAGAGTCTGCTGTTGGCAACATACCATCTTCAACCTCTGCAATGA 4920  
Db 4861 AAGACAGAGCCCCAGAGTCTGCTGTTGGCAACATACCATCTTCAACCTCTGCAATGA 4920



Qy 4921 AAGTTCCCAATTTGAAAGTTGCAGAACTGCCCCAGGGTCCAGCTGCTGCTCATACTCTG 4980  
Db 4921 AAGTTCCCAATTTGAAAGTTGCAGAACTGCCCCAGAGTCCAGCTGCTGCTCATACTCTG 4980  
Qy 4981 ATACTGCTGGGTATTAATGCAATGGAAGAAAGTGTGACGAGGGAAGCCAGAAATTGACAG 5040  
Db 4981 ATACTGCTGGGTATTAATGCAATGGAAGAAAGTGTGACGAGGGAAGCCAGAAATTGACAG 5040  
Qy 5041 CTTCAACAGAAAGGGTCAACAAAAGAAATGTCATGCTGGTGTCTGCGCTGACCCAGAG 5100  
Db 5041 CTTCAACAGAAAGGGTCAACAAAAGAAATGTCATGCTGGTGTCTGCGCTGACCCAGAG 5100  
Qy 5101 AATTATGCTGCTGTACAAAGTTTGCAGAAACCAACCAATCACTTTAACTAATCTAATTA 5160  
Db 5101 AATTATGCTGCTGTACAAAGTTTGCAGAAACCAACCAATCACTTTAACTAATCTAATTA 5160  
Qy 5161 CTGAAGAGACTACTCATGTTGTTATGAAAACAGATGCTGAGTTGTGTGAAACGGACAC 5220  
Db 5161 CTGAAGAGACTACTCATGTTGTTATGAAAACAGATGCTGAGTTGTGTGAAACGGACAC 5220  
Qy 5221 TGAATAATTTCTAGGAATTCGGGAGGAAATGGGTAGTTAGCTATTTCTGGGTGACCC 5280  
Db 5221 TGAATAATTTCTAGGAATTCGGGAGGAAATGGGTAGTTAGCTATTTCTGGGTGACCC 5280  
Qy 5281 AGTCTATTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAGAGGAGATGTGG 5340  
Db 5281 AGTCTATTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAGAGGAGATGTGG 5340  
Qy 5341 TCAATGGAAGAACCCAGGTCCTGAAGCAGCAAGAGATCCAGGACAGAAAGATCT 5400  
Db 5341 TCAATGGAAGAACCCAGGTCCTGAAGCAGCAAGAGATCCAGGACAGAAAGATCT 5400  
Qy 5401 TCAGGGGCTAGAAATCTGTTGCTATGGGCCCTTCCACCAATGCCACAGATCAACTGG 5460  
Db 5401 TCAGGGGCTAGAAATCTGTTGCTATGGGCCCTTCCACCAATGCCACAGATCAACTGG 5460  
Qy 5461 AATGGATGGTACAGCTGTGTGGTCTTCTGTGGTGAAGGAGCTTTTCATCTACCCCTTG 5520  
Db 5461 AATGGATGGTACAGCTGTGTGGTCTTCTGTGGTGAAGGAGCTTTTCATCTACCCCTTG 5520  
Qy 5521 GCACAGGTGTCACCCCAATTTGTTGTTGTCAGCCAGATGCTTGCAGAGAGCAATGGCT 5580  
Db 5521 GCACAGGTGTCACCCCAATTTGTTGTTGTCAGCCAGATGCTTGCAGAGAGCAATGGCT 5580  
Qy 5581 TCCATGCAATTTGGCAGATGTGAGGCACCTGTGTGACCCGAGAGTGGTGTGGACA 5640  
Db 5581 TCCATGCAATTTGGCAGATGTGAGGCACCTGTGTGACCCGAGAGTGGTGTGGACA 5640  
Qy 5641 GTGTAGCACTTACCAGTCCAGGAGCTGGACACCTACCTGATACCCAGATCCCCCACA 5700  
Db 5641 GTGTAGCACTTACCAGTCCAGGAGCTGGACACCTACCTGATACCCAGATCCCCCACA 5700  
Qy 5701 GCCACTACTGA 5711  
Db 5701 GCCACTACTGA 5711

RESULT 14  
AR184044  
LOCUS AR184044 5712 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 47 from patent US 6342483.  
ACCESSION AR184044  
VERSION AR184044.1 GI:20228013  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 5712)  
AUTHORS Holt, J.T., Jensen, R.A., Page, D.L., Obermiller, P.S.,  
Robinson-Benion, C.L., and Thompson, M.B.  
TITLE Method for detection and treatment of breast cancer  
JOURNAL Patent: US 6342483-A 47 29-JAN-2002;

FEATURES  
source  
BASE COUNT 1956 a 1099 c 1274 g 1383 t  
ORIGIN  
Location/Qualifiers  
1..5712  
/organism="unknown"  
1956 a 1099 c 1274 g 1383 t  
Query Match 99.8%; Score 5699.8; DB 6; Length 5712;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 5704; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
Qy 1 AGCTCGCTGAGACTTCCTGGACCCCGCACAGGCTGTGGGGTTCCTCAGATAACTTGGGCC 60  
Db 1 AGCTCGCTGAGACTTCCTGGACCCCGCACAGGCTGTGGGGTTCCTCAGATAACTTGGGCC 60  
Qy 61 CTTGCGCTCAGGAGGCTTCACCCCTCTGCTCTGGGTAAAGTTTCAATTGGAACAGAAAGAAA 120  
Db 61 CTTGCGCTCAGGAGGCTTCACCCCTCTGCTCTGGGTAAAGTTTCAATTGGAACAGAAAGAAA 120  
Qy 121 TGGATTTATCTGCTCTTTCGGGTGGAAGATGACAAAATGTCATTAATGCTATGAGAAAAA 180  
Db 121 TGGATTTATCTGCTCTTTCGGGTGGAAGATGACAAAATGTCATTAATGCTATGAGAAAAA 180  
Qy 181 TCTTAGAGTGTCCCATCTGCTGGAGTTGATCAAGGAACTGTCTCCACAAGTGTGACC 240  
Db 181 TCTTAGAGTGTCCCATCTGCTGGAGTTGATCAAGGAACTGTCTCCACAAGTGTGACC 240  
Qy 241 ACATATTTTGCATAATTTTGATGCTGAAACTTCTCAACCAAGAAAGGGCTTTCACAGT 300  
Db 241 ACATATTTTGCATAATTTTGATGCTGAAACTTCTCAACCAAGAAAGGGCTTTCACAGT 300  
Qy 301 GTCTTTTATGAAATGATATAACCAAAAGGAGCTTACAGAAAGTACGAGATTTAGTC 360  
Db 301 GTCTTTTATGAAATGATATAACCAAAAGGAGCTTACAGAAAGTACGAGATTTAGTC 360  
Qy 361 AACTTGTGAGAGCTATTGAAATCATTTGTGCTTTTTCAGTTGACACAGTTTGGAGT 420  
Db 361 AACTTGTGAGAGCTATTGAAATCATTTGTGCTTTTTCAGTTGACACAGTTTGGAGT 420  
Qy 421 ATGCAAAACAGCTATAATTTTGCAAAAGGAAATAAATCTCTCTGAAACATCTAAAGATG 480  
Db 421 ATGCAAAACAGCTATAATTTTGCAAAAGGAAATAAATCTCTCTGAAACATCTAAAGATG 480  
Qy 481 AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCAAAAGACTTCTACAGAGTG 540  
Db 481 AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCAAAAGACTTCTACAGAGTG 540  
Qy 541 AACCCGAAATCTTCTTTCGAGGAAACCACTCTCAGTGTCCAACTCTCTAACCTTGGAA 600  
Db 541 AACCCGAAATCTTCTTTCGAGGAAACCACTCTCAGTGTCCAACTCTCTAACCTTGGAA 600  
Qy 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCAAAAGACGCTCTCTACATTG 660  
Db 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCAAAAGACGCTCTCTACATTG 660  
Qy 661 AATTGGGATCTGATTTCTTGAAGATACCGTTAATAAGGCAACTTATTGCAAGTGTGGAG 720  
Db 661 AATTGGGATCTGATTTCTTGAAGATACCGTTAATAAGGCAACTTATTGCAAGTGTGGAG 720  
Qy 721 ATCAAGAAATTTGTAATAATCACCCCTCAGGAAACCGGATGAAATCAGTTTGGATCTG 780  
Db 721 ATCAAGAAATTTGTAATAATCACCCCTCAGGAAACCGGATGAAATCAGTTTGGATCTG 780  
Qy 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGACGGATGTAACAAATCTGAAATCATCAAC 840  
Db 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGACGGATGTAACAAATCTGAAATCATCAAC 840  
Qy 841 CCAGTAATAATGATTTGAACAACCACTGAGAGCGTGCAGCTGAGAGGATCCAGAAAGT 900  
Db 841 CCAGTAATAATGATTTGAACAACCACTGAGAGCGTGCAGCTGAGAGGATCCAGAAAGT 900  
Qy 901 ATCAGGATGATTTCTGTTTCAAACTTGTGATGTGGAGCCATGTGGCACAATACTCATGCCA 960  
Db 901 ATCAGGATGATTTCTGTTTCAAACTTGTGATGTGGAGCCATGTGGCACAATACTCATGCCA 960



Db 3121 AAAAATTGAGGAACATTCATATGTCACCTGAAAGAGAAATGGGAATAGGAACATTCCTCA 3180  
Qy 3181 GTACAGTGAGCAAAATAGCCGTAATAACATTAGAGAAAATGTTTTTAAAGAGGCCAGCT 3240  
Db 3181 GTACAGTGAGCAAAATAGCCGTAATAACATTAGAGAAAATGTTTTTAAAGAGGCCAGCT 3240  
Qy 3241 CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGA 3300  
Db 3241 CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGA 3300  
Qy 3301 TAGGTTCCAGTGATGAAGCAATTCAGCAGCACTAGGTAGAAACAGAGGGGCCAAATTTGA 3360  
Db 3301 TAGGTTCCAGTGATGAAGCAATTCAGCAGCACTAGGTAGAAACAGAGGGGCCAAATTTGA 3360  
Qy 3361 ATGCTATGCTTAGAATTAGGGGTTTTGCAACTGAGGTCTATAAAACAAAGTCTTCCCTGGAA 3420  
Db 3361 ATGCTATGCTTAGAATTAGGGGTTTTGCAACTGAGGTCTATAAAACAAAGTCTTCCCTGGAA 3420  
Qy 3421 GTAAATGTAAGCATCTCTGAATAAATAAGCAAGCAATATGAAGAGTAGTTTCAGACTGTTA 3480  
Db 3421 GTAAATGTAAGCATCTCTGAATAAATAAGCAAGCAATATGAAGAGTAGTTTCAGACTGTTA 3480  
Qy 3481 ATACAGATTTCTCTCCATATCTGATTTTCAGATACTTAGAACAGCCCTATGGGAAGTAGTC 3540  
Db 3481 ATACAGATTTCTCTCCATATCTGATTTTCAGATACTTAGAACAGCCCTATGGGAAGTAGTC 3540  
Qy 3541 ATGCATCTCAGGTTGTTCTCAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGG 3600  
Db 3541 ATGCATCTCAGGTTGTTCTCAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGG 3600  
Qy 3601 AAGTACTAGTTTGTGTAATAAGCAATTAAGGAAAGTTCTGCTGTTTTTACGAAAAGCG 3660  
Db 3601 AAGTACTAGTTTGTGTAATAAGCAATTAAGGAAAGTTCTGCTGTTTTTACGAAAAGCG 3660  
Qy 3661 TCCAGAGGAGAGCTTAGCAGGAGTCTAGCCCTTTTACCCCATACACATTTGGCTCAGG 3720  
Db 3661 TCCAGAGGAGAGCTTAGCAGGAGTCTAGCCCTTTTACCCCATACACATTTGGCTCAGG 3720  
Qy 3721 GTTACCGAAGAGGGGCCAAGAAATAGAGTCTCAGAGAGAACTTATCTAGTCAGGATG 3780  
Db 3721 GTTACCGAAGAGGGGCCAAGAAATAGAGTCTCAGAGAGAACTTATCTAGTCAGGATG 3780  
Qy 3781 AAGAGCTTCCCTGCTTCCAAACACTGTTATTTGGTAAAGTAAACAAATATACCTTCTCAGT 3840  
Db 3781 AAGAGCTTCCCTGCTTCCAAACACTGTTATTTGGTAAAGTAAACAAATATACCTTCTCAGT 3840  
Qy 3841 CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTCTAAGAAACACAGAGAGAAATTTAT 3900  
Db 3841 CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTCTAAGAAACACAGAGAGAAATTTAT 3900  
Qy 3901 TATCATTTGAAGATAGCTTAATGACTGCAGTAACAGGTAATATTGGCAAGGCATCTC 3960  
Db 3901 TATCATTTGAAGATAGCTTAATGACTGCAGTAACAGGTAATATTGGCAAGGCATCTC 3960  
Qy 3961 AGGAACATCACCTTAGTGAGGAAACAAATGTTCTGCTAGCTGTTTTTCTTTCACAGTGCA 4020  
Db 3961 AGGAACATCACCTTAGTGAGGAAACAAATGTTCTGCTAGCTGTTTTTCTTTCACAGTGCA 4020  
Qy 4021 GTGAATTTGGAAGACTTTGCTCAATAACAAACACCCAGGATCCCTTTCTTGAATGGTTCTT 4080  
Db 4021 GTGAATTTGGAAGACTTTGCTCAATAACAAACACCCAGGATCCCTTTCTTGAATGGTTCTT 4080  
Qy 4081 CCAACAAATAGGGCATCAGTCTGAAAGCCAGGGAGTTGGTCTGAGTGACAAAGAAATGG 4140  
Db 4081 CCAACAAATAGGGCATCAGTCTGAAAGCCAGGGAGTTGGTCTGAGTGACAAAGAAATGG 4140  
Qy 4141 TTTTCAGATGATGAAGAGAGCAACGGCTTTGGAGAAATAATCAAGAGAGCAAGCA 4200  
Db 4141 TTTTCAGATGATGAAGAGAGCAACGGCTTTGGAGAAATAATCAAGAGAGCAAGCA 4200  
Qy 4201 TGGATTTCAAACCTTAGGTAAGCAGCATCTGGGTGTGAGAGTGAAACAAAGCGCTCTCTGAAG 4260

Db 4201 TGGATTTCAAACCTTAGGTAAGCAGCATCTGGGTGTGAGAGTGAAACAAAGCGCTCTCTGAAG 4260  
Qy 4261 ACTGCTCAGGGCTATCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGATACCAATGC 4320  
Db 4261 ACTGCTCAGGGCTATCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGATACCAATGC 4320  
Qy 4321 AACATAACCTTGATTAAGCTTCAGCAGGAATGGCTGAAGCTAGAGCTGTGTAGAAACAGC 4380  
Db 4321 AACATAACCTTGATTAAGCTTCAGCAGGAATGGCTGAAGCTAGAGCTGTGTAGAAACAGC 4380  
Qy 4381 ATGGGAGCCAGCCTTTCTAAGCAGCTTCCATCATATAAGTGACTCTCTGCTCCCTTCAGG 4440  
Db 4381 ATGGGAGCCAGCCTTTCTAAGCAGCTTCCATCATATAAGTGACTCTCTGCTCCCTTCAGG 4440  
Qy 4441 ACCTGCGAAATCCAGAACAAAGCAATCAGAAAAAGCAGTATTAACCTTCACAGAAAAAGTA 4500  
Db 4441 ACCTGCGAAATCCAGAACAAAGCAGTATTAACCTTCACAGAAAAAGTA 4500  
Qy 4501 GTGAATACCTTATTAAGCCAGAAATCCAGAAAGCCCTTTCTGCTGACAAAGTTTGAGGTGCTG 4560  
Db 4501 GTGAATACCTTATTAAGCCAGAAATCCAGAAAGCCCTTTCTGCTGACAAAGTTTGAGGTGCTG 4560  
Qy 4561 CAGATAGTCTTACCAGTAAATAAAGCAACAGAGTGGAAAGCTCATCCCTTCTCAAT 4620  
Db 4561 CAGATAGTCTTACCAGTAAATAAAGCAACAGAGTGGAAAGCTCATCCCTTCTCAAT 4620  
Qy 4621 GCCCATCATTAGATGATAGGTGCTACACAGTCTCTGCGAGTCTTTCAGAAATAGAA 4680  
Db 4621 GCCCATCATTAGATGATAGGTGCTACACAGTCTCTGCGAGTCTTTCAGAAATAGAA 4680  
Qy 4681 ACTACCCATCTCAAGAGGAGCTCAATTAAGGTTGTTGATGTGGAGGAGCAACAGCTGGAG 4740  
Db 4681 ACTACCCATCTCAAGAGGAGCTCAATTAAGGTTGTTGATGTGGAGGAGCAACAGCTGGAG 4740  
Qy 4741 AGTCTGGGCCACACGATTTGACGGAACATCTTACTTGGCAAGGCAAGTCTAGAGGGAA 4800  
Db 4741 AGTCTGGGCCACACGATTTGACGGAACATCTTACTTGGCAAGGCAAGTCTAGAGGGAA 4800  
Qy 4801 CCCCTTACCTTGGAAATCTGGAAATCAGCCCTTCTCTGATGACCCCTGAACTCTGATCTCTG 4860  
Db 4801 CCCCTTACCTTGGAAATCTGGAAATCAGCCCTTCTCTGATGACCCCTGAACTCTGATCTCTG 4860  
Qy 4861 AAGCAGAGGCCCAAGAGTCTGCTGTGGCAACATACCAATCTTCAACCTCTGCAATGA 4920  
Db 4861 AAGCAGAGGCCCAAGAGTCTGCTGTGGCAACATACCAATCTTCAACCTCTGCAATGA 4920  
Qy 4921 AAGTTCCCAATTTGAAAGTTGCAGAAATCTGCCAGGGCTCCAGCTGCTGCTCATACTACTG 4980  
Db 4921 AAGTTCCCAATTTGAAAGTTGCAGAAATCTGCCAGAGTCCAGCTGCTGCTCATACTACTG 4980  
Qy 4981 ATACTGCTGGGTATAATGCAATGGAAGAGTGTGAGCAGGAGAGGAGGAGGAGGAGGAGGAG 5040  
Db 4981 ATACTGCTGGGTATAATGCAATGGAAGAGTGTGAGCAGGAGAGGAGGAGGAGGAGGAGGAG 5040  
Qy 5041 CTTCAACAGAAAGGGTCAACAAAAAGATGTCATGGTGGTGTCTGGGCTGACCCAGAGG 5100  
Db 5041 CTTCAACAGAAAGGGTCAACAAAAAGATGTCATGGTGGTGTCTGGGCTGACCCAGAGG 5100  
Qy 5101 AATTATGCTGCTGTAACAAGTTGCCAGAAAAACCAACATCACTTAACTAACTAACTAACTAA 5160  
Db 5101 AATTATGCTGCTGTAACAAGTTGCCAGAAAAACCAACATCACTTAACTAACTAACTAACTAA 5160  
Qy 5161 CTGAAGAGACTACTCATGTTGTTATGAAACAGAGTGTGAGTGTGTGTAACCGACAC 5220  
Db 5161 CTGAAGAGACTACTCATGTTGTTATGAAACAGAGTGTGAGTGTGTGTAACCGACAC 5220  
Qy 5221 TGAATAATTTTCTAGGAAATTTGCGGGAGGAAATGGGTAGTTAGCTATTTCTGGGTGACCC 5280  
Db 5221 TGAATAATTTTCTAGGAAATTTGCGGGAGGAAATGGGTAGTTAGCTATTTCTGGGTGACCC 5280  
Qy 5281 AGTCTATTAAGAAAGAAAAATGCTGAATGAGCATGATTTTGAAGTCTAGAGAGATGTGG 5340  
Db 5281 AGTCTATTAAGAAAGAAAAATGCTGAATGAGCATGATTTTGAAGTCTAGAGAGATGTGG 5340

QY 5341 TCAATGGAAGAAACCAACCAAGGTCCTCAAGCGAGCAAGAGAAATCCAGGACAGAAAGATCT 5400 Db  
|||||  
Db 5341 TCAATGGAAGAAACCAACCAAGGTCCTCAAGCGAGCAAGAGAAATCCAGGACAGAAAGATCT 5400 QY  
|||||  
QY 5401 TCAGGGGCTAGAAATCTGTTGCTATGATGGCCCTTCAACCAATGCGCCACAGATCAACTGG 5460 Db  
|||||  
Db 5401 TCAGGGGCTAGAAATCTGTTGCTATGATGGCCCTTCAACCAATGCGCCACAGATCAACTGG 5460 QY  
|||||  
QY 5461 AATGGATGTTACAGCTGTGGTGTCTGTTGTTGAGGAGCTTTCATCTACCCCTTG 5520 Db  
|||||  
Db 5461 AATGGATGTTACAGCTGTGGTGTCTGTTGTTGAGGAGCTTTCATCTACCCCTTG 5520 QY  
|||||  
QY 5521 GCACAGGTGTCCACCAATTTGTTGTCAGCCAGATGCTTGGACAGAGACAAATGGCT 5580 Db  
|||||  
Db 5521 GCACAGGTGTCCACCAATTTGTTGTCAGCCAGATGCTTGGACAGAGACAAATGGCT 5580 QY  
|||||  
QY 5581 TCCATGCAATTTGGGAGATGTGAGGCACTGTGGTGAACCCGAGAGTGGGTGTTGGACA 5640 Db  
|||||  
Db 5581 TCCATGCAATTTGGGAGATGTGAGGCACTGTGGTGAACCCGAGAGTGGGTGTTGGACA 5640 QY  
|||||  
QY 5641 GTGTAGCACTTACAGTCCAGGAGCTGGACACCTACCTGATACCCAGATCCCCACA 5700 Db  
|||||  
Db 5641 GTGTAGCACTTACAGTCCAGGAGCTGGACACCTACCTGATACCCAGATCCCCACA 5700 QY  
|||||  
QY 5701 GCCACTACTGA 5711 Db  
|||||  
Db 5701 GCCACTACTGA 5711 QY

RESULT 15  
AR004673  
LOCUS AR004673 5914 bp DNA linear PAT 04-DEC-1998  
DEFINITION Sequence 1 from patent US 5747282.  
ACCESSION AR004673  
VERSION AR004673.1 GI:3965552  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 5914)  
AUTHORS Skolnick,M.H., Goldgar,D.E., Miki,Y., Swenson,J., Kamb,A.,  
Harshman,K.D., Shattuck-Eidens,D.M., Tavtigian,S.V., Wiseman,R.W.  
and Futreal,P.Andrew.  
TITLE 170-linked breast and ovarian cancer susceptibility gene  
JOURNAL Patent: US 5747282-A 1 05-MAY-1998;  
FEATURES  
Location/Qualifiers  
source 1..5914  
/organism="unknown"  
BASE COUNT 2006 a 1156 c 1316 g 1436 t  
ORIGIN

Query Match 99.8%; Score 5699.8; DB 6; Length 5914;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 5704; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 AGCTCGCTGAGACTTCCTGGACCCGACAGGCTGTGGGTTTCTCAGATAACTGGGCC 60  
Db 1 AGCTCGCTGAGACTTCCTGGACCCGACAGGCTGTGGGTTTCTCAGATAACTGGGCC 60  
QY 61 CCTCGCTCAGAGGCTTCCACCTCTGCTCTGGGTAAGTTTCATTGGAAACAGAAAGAAA 120  
Db 61 CCTCGCTCAGAGGCTTCCACCTCTGCTCTGGGTAAGTTTCATTGGAAACAGAAAGAAA 120  
QY 121 TGGATTTATCTGCTCTCGGTTGAAGAGTACAAAATGTCATTAATGCTATGAGAAAA 180  
Db 121 TGGATTTATCTGCTCTCGGTTGAAGAGTACAAAATGTCATTAATGCTATGAGAAAA 180  
QY 181 TCTTAGAGTGTCCCATCTGTCTGAGTTGATCAAGGACCTGTCTCCACAAAGTGTGACC 240  
Db 181 TCTTAGAGTGTCCCATCTGTCTGAGTTGATCAAGGACCTGTCTCCACAAAGTGTGACC 240  
QY 241 ACATATTTTGCATATTTTGCATGCTGAAACTTCTCAACAGAGAAAGGGCCTTCACAGT 300

Db 241 ACATATTTTGCATATTTTGCATGCTGAAACTTCTCAACAGAGAAAGGGCCTTCACAGT 300  
QY 301 GTCCCTTTATGAGATGATATTAACCAAAAGAGCCCTACAAGAAAGTACGAGATTTAGTC 360  
Db 301 GTCCCTTTATGAGATGATATTAACCAAAAGAGCCCTACAAGAAAGTACGAGATTTAGTC 360  
QY 361 AACTTTGTTGAGAGCTATTTGAAATCAATTTGTGCTTTTTCAGCTTGAACAGGTTTGAGT 420  
Db 361 AACTTTGTTGAGAGCTATTTGAAATCAATTTGTGCTTTTTCAGCTTGAACAGGTTTGAGT 420  
QY 421 ATGCAAAACAGCTATAATTTTGCAAAAAGGAAATAAATCTCTCTCTGAACATCTAAAAAGATG 480  
Db 421 ATGCAAAACAGCTATAATTTTGCAAAAAGGAAATAAATCTCTCTCTGAACATCTAAAAAGATG 480  
QY 481 AAGTTTCTATCTATCAATCAAGATATGGGCTACAGAAACCGTGCACAAAGATCTTCAAGAGTG 540  
Db 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCACAAAGATCTTCAAGAGTG 540  
QY 541 AACCCGAAATCCCTTCTTCAGGAAACAGTCTCAGTGTCCAACTCTTAACCTTGGAA 600  
Db 541 AACCCGAAATCCCTTCTTCAGGAAACAGTCTCAGTGTCCAACTCTTAACCTTGGAA 600  
QY 601 CTGTGAGAACTCTGAGGACAAAGCAGGAGTACAACTCTCAAGAGCGTCTGTCTACATTTG 660  
Db 601 CTGTGAGAACTCTGAGGACAAAGCAGGAGTACAACTCTCAAGAGCGTCTGTCTACATTTG 660  
QY 661 AATTGGGATCTGATTTCTTGAAGATACCGTTAATAAGGCAACTTATTGAGTGGGAG 720  
Db 661 AATTGGGATCTGATTTCTTGAAGATACCGTTAATAAGGCAACTTATTGAGTGGGAG 720  
QY 721 ATCAAGAAATTTTACAAATCACCCCTCAAGGACAGGATGAATCAGTTTGGATTTCTG 780  
Db 721 ATCAAGAAATTTTACAAATCACCCCTCAAGGACAGGATGAATCAGTTTGGATTTCTG 780  
QY 781 CAAAAAAGGCTGCTTGTGAATTTTCTGAGACGGATGTAAACAAATCTCTGAACATCATCAAC 840  
Db 781 CAAAAAAGGCTGCTTGTGAATTTTCTGAGACGGATGTAAACAAATCTCTGAACATCATCAAC 840  
QY 841 CCAGTAAATATGATTTGAAACCACTGAGAGCGTGTGAGAGGCTCCAGAAAGT 900  
Db 841 CCAGTAAATATGATTTGAAACCACTGAGAGCGTGTGAGAGGCTCCAGAAAGT 900  
QY 901 ATCAGGGTGTCTGTTTCAAACTTGCATGTGGGCGCTTGGCACAATACTCATGCCA 960  
Db 901 ATCAGGGTGTCTGTTTCAAACTTGCATGTGGGCGCTTGGCACAATACTCATGCCA 960  
QY 961 GCTCATTTACAGCATGAGAACAGCAGTTTATTCTCACTAAAGACAGAAATGAATGTAGAAA 1020  
Db 961 GCTCATTTACAGCATGAGAACAGCAGTTTATTCTCACTAAAGACAGAAATGAATGTAGAAA 1020  
QY 1021 AGGCTGAATTTCTGTAATAAGCAACAGCCTGGCTTAGCAAGAGGCAACATAACAGAT 1080  
Db 1021 AGGCTGAATTTCTGTAATAAGCAACAGCCTGGCTTAGCAAGAGGCAACATAACAGAT 1080  
QY 1081 GGCTGGAAGTAAAGAAACATGTAAATCATAGGCGGCTCCAGCACAGAAAGGAGTAG 1140  
Db 1081 GGCTGGAAGTAAAGAAACATGTAAATCATAGGCGGCTCCAGCACAGAAAGGAGTAG 1140  
QY 1141 ATCTGAATGCTGATCCCTCTGTGTGAGAGAAAGAAATGGAATTAAGCAGAAATCTGCATGCT 1200  
Db 1141 ATCTGAATGCTGATCCCTCTGTGTGAGAGAAAGAAATGGAATTAAGCAGAAATCTGCATGCT 1200  
QY 1201 CAGAGAAATCTTAGAGATATCTGAAGATGTTCTCTTGGATTAACATAATAGCAGATTCAGA 1260  
Db 1201 CAGAGAAATCTTAGAGATATCTGAAGATGTTCTCTTGGATTAACATAATAGCAGATTCAGA 1260  
QY 1261 AAGTTAATGAGTGGTTTCCAGAAAGTGAATGAACTGTGTAGGTTCTGATGATCTCATGATG 1320  
Db 1261 AAGTTAATGAGTGGTTTCCAGAAAGTGAATGAACTGTGTAGGTTCTGATGATCTCATGATG 1320  
QY 1321 GGAGGCTGTAATCAAAATGCCCCAGTGTGATTTTGGACGTTCTAAATAGAGGTAGATG 1380

Db 1321 GGGAGTCTGAATCAATGCCAAAGTAGCTGATGATATTGGACGTTCTAAATGAGGTAGATG 1380  
Qy 1381 AATATTCTGGTGTCTTCAGAGAAAATAGACTTTACTGCCCAGTGAATCCTCATGAGGCTTTAA 1440  
Db 1381 AATATTCTGGTGTCTTCAGAGAAAATAGACTTTACTGCCCAGTGAATCCTCATGAGGCTTTAA 1440  
Qy 1441 TATGTAAAAGTGAAGAGTTCCTCCAAATCAGTAGAGAGTAATAATTGGAACAAAATAT 1500  
Db 1441 TATGTAAAAGTGAAGAGTTCCTCCAAATCAGTAGAGAGTAATAATTGGAACAAAATAT 1500  
Qy 1501 TTGGGAAAACTTATCGGAAGAAGGCAAGCCTCCCAACTTAAGCCCATGTAACTGAAAAATC 1560  
Db 1501 TTGGGAAAACTTATCGGAAGAAGGCAAGCCTCCCAACTTAAGCCCATGTAACTGAAAAATC 1560  
Qy 1561 TAAATATAGGAGCAATTTGTACTGAGCCACAGATAATAACAAGAGCGTCCCTCACAATA 1620  
Db 1561 TAAATATAGGAGCAATTTGTACTGAGCCACAGATAATAACAAGAGCGTCCCTCACAATA 1620  
Qy 1621 AATTAAAGGCTAAAGAGACCTACATCAGGCTTCATCCTGAGGATTTTATCAAGAAAG 1680  
Db 1621 AATTAAAGGCTAAAGAGACCTACATCAGGCTTCATCCTGAGGATTTTATCAAGAAAG 1680  
Qy 1681 CAGATTTCGGCAGTTCAAAAGAGCTCCTGAAATGATAAATCAGGAACTAAACCAACGGAGC 1740  
Db 1681 CAGATTTCGGCAGTTCAAAAGAGCTCCTGAAATGATAAATCAGGAACTAAACCAACGGAGC 1740  
Qy 1741 AGAATGGTCAAGTGATGAATATTACTAATAGTGGTTCATGAGAAATAAACAAGAGTGATT 1800  
Db 1741 AGAATGGTCAAGTGATGAATATTACTAATAGTGGTTCATGAGAAATAAACAAGAGTGATT 1800  
Qy 1801 CTATTGAGATGAGAAAAATCTTAACCAATAGAAATCACTCGAAAAAGAAATCTGCTTTCA 1860  
Db 1801 CTATTGAGATGAGAAAAATCTTAACCAATAGAAATCACTCGAAAAAGAAATCTGCTTTCA 1860  
Qy 1861 AAACGAAAGCTGAACCTTAAGCAGCTATAAGCAATATGGAATCTGAAATTAATATCC 1920  
Db 1861 AAACGAAAGCTGAACCTTAAGCAGCTATAAGCAATATGGAATCTGAAATTAATATCC 1920  
Qy 1921 ACAATTTCAAAAGCACCTAAAAGAAATAGGCTGAGGAGGAAGTCTTTACACGAGGATATTC 1980  
Db 1921 ACAATTTCAAAAGCACCTAAAAGAAATAGGCTGAGGAGGAAGTCTTTACACGAGGATATTC 1980  
Qy 1981 ATGGCTTTGAATAGTAGTAGTGAATAATCTAAGCCCACTTAATGTACTGAAATGCAAA 2040  
Db 1981 ATGGCTTTGAATAGTAGTAGTGAATAATCTAAGCCCACTTAATGTACTGAAATGCAAA 2040  
Qy 2041 TTGATAGTTGTTCTAGCAGTGAAGATAAAGAAAAAAGTACAAACAAATGCCAGTCA 2100  
Db 2041 TTGATAGTTGTTCTAGCAGTGAAGATAAAGAAAAAAGTACAAACAAATGCCAGTCA 2100  
Qy 2101 GGCACAGCAAGAAACCTACAACTCATGGGAAGGTAAAGAACTGGCACTGGAGCCCAAGAGA 2160  
Db 2101 GGCACAGCAAGAAACCTACAACTCATGGGAAGGTAAAGAACTGGCACTGGAGCCCAAGAGA 2160  
Qy 2161 GTAAACAGCCAAATGAACAGACAAGTAAAGACATGACAGTGATATTTTCCAGAGCTGA 2220  
Db 2161 GTAAACAGCCAAATGAACAGACAAGTAAAGACATGACAGCGATACTTTTCCAGAGCTGA 2220  
Qy 2221 AGTTAAACAATGCACTGCTGTTCTTTTACTAGTGTTCAAATACCAAGTGAACCTTAAAGAT 2280  
Db 2221 AGTTAAACAATGCACTGCTGTTCTTTTACTAGTGTTCAAATACCAAGTGAACCTTAAAGAT 2280  
Qy 2281 TTGTCAATCTTAGCCTTCCAGAGAGAAAAAGAGAGAACTAGAAACAGTTTAAAGTGT 2340  
Db 2281 TTGTCAATCTTAGCCTTCCAGAGAGAAAAAGAGAGAACTAGAAACAGTTTAAAGTGT 2340  
Qy 2341 CTAATAATGCTCAAGACCCCAAGATCTCATGTTTAAGTGGAGAAAGGGTTTTCGAAACTG 2400  
Db 2341 CTAATAATGCTCAAGACCCCAAGATCTCATGTTTAAGTGGAGAAAGGGTTTTCGAAACTG 2400  
Qy 2401 AAAGATCTGTAGAGAGTAGAGTATTTTCACTGGTATCTGGTATCTGATATGCGCATCAGG 2460  
Db 2401 AAAGATCTGTAGAGAGTAGAGTATTTTCACTGGTATCTGGTATCTGATATGCGCATCAGG 2460

Qy 2461 AAAGTATCTCGTTACTGGAAGTTAGCACTCTTAGGGAAGGCAAAAAACAGAACCAATAAAT 2520  
Db 2461 AAAGTATCTCGTTACTGGAAGTTAGCACTCTTAGGGAAGGCAAAAAACAGAACCAATAAAT 2520  
Qy 2521 GTGTGAGTCAGTGTGCAGCATTTGAAAACCCCAAGGGACTAATTCATCGTTGTTTCCAAAG 2580  
Db 2521 GTGTGAGTCAGTGTGCAGCATTTGAAAACCCCAAGGGACTAATTCATCGTTGTTTCCAAAG 2580  
Qy 2581 AATAATAGAAATGACACAGAAAGGCTTTAAGTATCAATTTGGGACATGAAGTTAAACACAGTC 2640  
Db 2581 AATAATAGAAATGACACAGAAAGGCTTTAAGTATCAATTTGGGACATGAAGTTAAACACAGTC 2640  
Qy 2641 GGGAAAAACAAGCATAGAAATGGAAGAAAGTGAATCTTGATGCTCAGTATTTTGCAGAATACAT 2700  
Db 2641 GGGAAAAACAAGCATAGAAATGGAAGAAAGTGAATCTTGATGCTCAGTATTTTGCAGAATACAT 2700  
Qy 2701 TCAAGGTTTCAAGGCGCCAGTCATTTGCTCTGTTTCAAAATCCAGGAATGCAAGAGAGG 2760  
Db 2701 TCAAGGTTTCAAGGCGCCAGTCATTTGCTCTGTTTCAAAATCCAGGAATGCAAGAGAGG 2760  
Qy 2761 AATGTGCAACATTTCTGCCCCACTCTGGGCTCTTAAAGAAAAAAGTCCAAAAGTCACTT 2820  
Db 2761 AATGTGCAACATTTCTGCCCCACTCTGGGCTCTTAAAGAAAAAAGTCCAAAAGTCACTT 2820  
Qy 2821 TTGAATGTGAACAAAAAGGAAGAAAAATCAAGGAAAAAGAAATGAGTCTAATAATCAAGCCTGTAC 2880  
Db 2821 TTGAATGTGAACAAAAAGGAAGAAAAATCAAGGAAAAAGAAATGAGTCTAATAATCAAGCCTGTAC 2880  
Qy 2881 AGACAGTTAATATACATGTCAGGCTTTCTGTTGGTGGTTCAGAAAAAGATGAAGCAGTTGATA 2940  
Db 2881 AGACAGTTAATATACATGTCAGGCTTTCTGTTGGTGGTTCAGAAAAAGATGAAGCAGTTGATA 2940  
Qy 2941 ATGCCAAATGATGATCAAGAGGAGCTCTAGGTTTGTCTATCATCTCAGTTTCAGAGGCA 3000  
Db 2941 ATGCCAAATGATGATCAAGAGGAGCTCTAGGTTTGTCTATCATCTCAGTTTCAGAGGCA 3000  
Qy 3001 ACGAAACTGGACTCATTTACTCCAAATAAATGAGGCTTTTACAAAACCCATATCGTATAC 3060  
Db 3001 ACGAAACTGGACTCATTTACTCCAAATAAATGAGGCTTTTACAAAACCCATATCGTATAC 3060  
Qy 3061 CACCACATTTTCCCATCAAGTCATTTGTTTAAACTTAAATGTAAGAAAAATCTGCTAGAGG 3120  
Db 3061 CACCACATTTTCCCATCAAGTCATTTGTTTAAACTTAAATGTAAGAAAAATCTGCTAGAGG 3120  
Qy 3121 AAAACTTTGAGGACATTTCAATGTCACTGAAAGAGAAATGCGGAAATGAGAACTTCCAA 3180  
Db 3121 AAAACTTTGAGGACATTTCAATGTCACTGAAAGAGAAATGCGGAAATGAGAACTTCCAA 3180  
Qy 3181 GTACAGTGAGCACAAATTAGCCGTAAATACATTTAGAGAAAAATGTTTTTAAAGGAGCCAGCT 3240  
Db 3181 GTACAGTGAGCACAAATTAGCCGTAAATACATTTAGAGAAAAATGTTTTTAAAGGAGCCAGCT 3240  
Qy 3241 CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA 3300  
Db 3241 CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA 3300  
Qy 3301 TAGGTTCCAGTGATGAAAACATTTCAACAGAGAACTAGGTAGAAACAGAGGGCCAAAATGA 3360  
Db 3301 TAGGTTCCAGTGATGAAAACATTTCAACAGAGAACTAGGTAGAAACAGAGGGCCAAAATGA 3360  
Qy 3361 ATGCTATGCTTAGAATTAGGGGTTTTGCAACTGAGGTCTATAAAACAAAGTCTTCTCTGAA 3420  
Db 3361 ATGCTATGCTTAGAATTAGGGGTTTTGCAACTGAGGTCTATAAAACAAAGTCTTCTCTGAA 3420  
Qy 3421 GTAAATGTAAGCAGCTCTGAAAATAAAAAAGCAAGAAATATGAAGAAAGTAGTTCAGACTGTTA 3480  
Db 3421 GTAAATGTAAGCAGCTCTGAAAATAAAAAAGCAAGAAATATGAAGAAAGTAGTTCAGACTGTTA 3480  
Qy 3481 ATACAGATTTCTCTCCATATCTGATTTTTCAGATACTTAGAACAGCCTATGGAAGTAGTC 3540  
Db 3481 ATACAGATTTCTCTCCATATCTGATTTTTCAGATACTTAGAACAGCCTATGGAAGTAGTC 3540

Qy 3541 ATGCATCTCAGGTTGTTCTGAGACACCTGATGACCTGTTAGATGATGTTGAAATAAAGG 3600  
Db |||||  
Qy 3541 ATGCATCTCAGGTTGTTCTGAGACACCTGATGACCTGTTAGATGATGTTGAAATAAAGG 3600  
Db |||||  
Qy 3601 AAGATACATGTTGCTGGAATAATGACATTAAGGAAAGTTCTGCTGTTTATAGCAAAAGCG 3660  
Db |||||  
Qy 3601 AAGATACATGTTGCTGGAATAATGACATTAAGGAAAGTTCTGCTGTTTATAGCAAAAGCG 3660  
Db |||||  
Qy 3661 TCCAGAGGAGAGCTTAGCAGGAGTCTTAGCCCTTCCACCATACACATTTGCTCAGG 3720  
Db |||||  
Qy 3661 TCCAGAGGAGAGCTTAGCAGGAGTCTTAGCCCTTCCACCATACACATTTGCTCAGG 3720  
Db |||||  
Qy 3721 GTTACCGAAGAGGGCCCAAGAAATAGAGTCTCAGAGAGAACTTATCTAGTCAGGATG 3780  
Db |||||  
Qy 3721 GTTACCGAAGAGGGCCCAAGAAATAGAGTCTCAGAGAGAACTTATCTAGTCAGGATG 3780  
Db |||||  
Qy 3781 AAGAGCTTCCCTGTTCCAAACACTTGTGTTTATGTTGTAAGTAAACAAATATACCTTCTCAGT 3840  
Db |||||  
Qy 3781 AAGAGCTTCCCTGTTCCAAACACTTGTGTTTATGTTGTAAGTAAACAAATATACCTTCTCAGT 3840  
Db |||||  
Qy 3841 CTACTAGGCATGACCGTTGCTACCGAGTCTGCTCTAGAAACACAGAGGAGAAATTTAT 3900  
Db |||||  
Qy 3841 CTACTAGGCATGACCGTTGCTACCGAGTCTGCTCTAGAAACACAGAGGAGAAATTTAT 3900  
Db |||||  
Qy 3901 TATCATTTGAAGATAGCTTAAATGACTGACGTAAACACAGGTAAATATTTGCAAGGCATCTC 3960  
Db |||||  
Qy 3901 TATCATTTGAAGATAGCTTAAATGACTGACGTAAACACAGGTAAATATTTGCAAGGCATCTC 3960  
Db |||||  
Qy 3961 AGGAACATCACCTTAGTGAGGAAACAAATGTTCTGCTAGTCTGTTTCTTCAAGTGCA 4020  
Db |||||  
Qy 3961 AGGAACATCACCTTAGTGAGGAAACAAATGTTCTGCTAGTCTGTTTCTTCAAGTGCA 4020  
Db |||||  
Qy 4021 GTGAAATTTGGAGACTTGACTGCAATACAAACACCCAGGATCCTTCTTGATTTGGTTCTT 4080  
Db |||||  
Qy 4021 GTGAAATTTGGAGACTTGACTGCAATACAAACACCCAGGATCCTTCTTGATTTGGTTCTT 4080  
Db |||||  
Qy 4081 CCAACAAATCAGGCATCAGTCTGAAACCCAGGAGTTGGTCTGAGTGACAAAGAAATGG 4140  
Db |||||  
Qy 4081 CCAACAAATCAGGCATCAGTCTGAAACCCAGGAGTTGGTCTGAGTGACAAAGAAATGG 4140  
Db |||||  
Qy 4141 TTTCCAGATGATGAAGAAAGAGAAACGGGCTTTGGAAGAAATAATCAAGAGAGCAAAAGCA 4200  
Db |||||  
Qy 4141 TTTCCAGATGATGAAGAAAGAGAAACGGGCTTTGGAAGAAATAATCAAGAGAGCAAAAGCA 4200  
Db |||||  
Qy 4201 TGGATTCGAACCTTAGGTGAACGACATCTGGTGTGAGGTGAACAGGCTCTCTGAAG 4260  
Db |||||  
Qy 4201 TGGATTCGAACCTTAGGTGAACGACATCTGGTGTGAGGTGAACAGGCTCTCTGAAG 4260  
Db |||||  
Qy 4261 ACTGCTCAGGGCTATCCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGGATACCATGC 4320  
Db |||||  
Qy 4261 ACTGCTCAGGGCTATCCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGGATACCATGC 4320  
Db |||||  
Qy 4321 AACATAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACCTAGAAAGCTGTGTTAGAACAGC 4380  
Db |||||  
Qy 4321 AACATAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACCTAGAAAGCTGTGTTAGAACAGC 4380  
Db |||||  
Qy 4381 ATGGAGCCAGCCTTCTTAACGACTACCTTCCATCATTAAGTACTCTCTGCCCTTGAGG 4440  
Db |||||  
Qy 4381 ATGGAGCCAGCCTTCTTAACGACTACCTTCCATCATTAAGTACTCTCTGCCCTTGAGG 4440  
Db |||||  
Qy 4441 ACCTGCGAAATCCAGAACAAAGCAGATCAGAAAAAGCAGTAACTTCAAGAAAAAGTA 4500  
Db |||||  
Qy 4441 ACCTGCGAAATCCAGAACAAAGCAGATCAGAAAAAGCAGTAACTTCAAGAAAAAGTA 4500  
Db |||||  
Qy 4501 GTGAATACCTTATTAAGCCAGAAATCCAGAAAGCCCTTCTGCTGCAAGATTTGAGTGTCTG 4560  
Db |||||  
Qy 4501 GTGAATACCTTATTAAGCCAGAAATCCAGAAAGCCCTTCTGCTGCAAGATTTGAGTGTCTG 4560  
Db |||||  
Qy 4561 CAGATGTTCTACCAAGTAAATTAAGAACACAGAGTGGAAAGCTCATCCCTTCTTAAT 4620  
Db |||||  
Qy 4561 CAGATGTTCTACCAAGTAAATTAAGAACACAGAGTGGAAAGCTCATCCCTTCTTAAT 4620  
Db |||||  
Qy 4621 GCCCATCATTAGATGATAGGTGGTACATGCACAGTTGCTCTGGGAGTCTTTCAGAAATAGAA 4680  
Db |||||

Db 4621 GCCCATCATTAGATGATAGGTGGTACATGCACAGTTGCTCTGGAGTCTTTCAGAAATAGAA 4680  
Qy |||||  
Qy 4681 ACTACCCATCTCAAGAGGAGCTCATTAAGGTTGTTGATGTTGGAGGAGCAACAGCTGAAG 4740  
Db |||||  
Qy 4681 ACTACCCATCTCAAGAGGAGCTCATTAAGGTTGTTGATGTTGGAGGAGCAACAGCTGAAG 4740  
Db |||||  
Qy 4741 AGTCTGGGCCACACGATTTTCACCGAAACATCTTACTTTGCCAAGCAGAGATCTAGAGGAA 4800  
Db |||||  
Qy 4741 AGTCTGGGCCACACGATTTTCACCGAAACATCTTACTTTGCCAAGCAGAGATCTAGAGGAA 4800  
Db |||||  
Qy 4801 CCCCTTACCTGGAATCTGGAATCAGCCTCTTCTCTGATGACCCCTGAAATCTGATCTCTG 4860  
Db |||||  
Qy 4801 CCCCTTACCTGGAATCTGGAATCAGCCTCTTCTCTGATGACCCCTGAAATCTGATCTCTG 4860  
Db |||||  
Qy 4861 AAGACAGAGCCACAGAGTCTGCTGTTGGCAACATACCATCTTCAACCTCTGCAATGA 4920  
Db |||||  
Qy 4861 AAGACAGAGCCACAGAGTCTGCTGTTGGCAACATACCATCTTCAACCTCTGCAATGA 4920  
Db |||||  
Qy 4921 AAGTTCCCCCAATTTGAAAGTTGCAAGATCTGCCAGGCTCCAGCTGCTCATACTACTG 4980  
Db |||||  
Qy 4921 AAGTTCCCCCAATTTGAAAGTTGCAAGATCTGCCAGGCTCCAGCTGCTCATACTACTG 4980  
Db |||||  
Qy 4981 ATACTGCTGGGTATTAATGCAATGGAAGAAAGTGTGAGCAGGAGAGCCAGAAATGACAG 5040  
Db |||||  
Qy 4981 ATACTGCTGGGTATTAATGCAATGGAAGAAAGTGTGAGCAGGAGAGCCAGAAATGACAG 5040  
Db |||||  
Qy 5041 CTTTCAACAGAAAGGCTCAACAAAGAAATGTCATGTTGGTGTCTGGCTCAACCCAGAG 5100  
Db |||||  
Qy 5041 CTTTCAACAGAAAGGCTCAACAAAGAAATGTCATGTTGGTGTCTGGCTCAACCCAGAG 5100  
Db |||||  
Qy 5101 AATTTATGCTCGTGTCAAGTTTCCAGAAACACCAACATCCTTTAACTTAATCTAATTA 5160  
Db |||||  
Qy 5101 AATTTATGCTCGTGTCAAGTTTCCAGAAACACCAACATCCTTTAACTTAATCTAATTA 5160  
Db |||||  
Qy 5161 CTGAAGAGACTACTCATGTTGTTATGAAAAACAGATGCTGAGTTGTTGTGTAACGGACAC 5220  
Db |||||  
Qy 5161 CTGAAGAGACTACTCATGTTGTTATGAAAAACAGATGCTGAGTTGTTGTGTAACGGACAC 5220  
Db |||||  
Qy 5221 TGAATAATTTTCTAGGAATTTCCGGAGGAAATGGGTAGTTAGCTATTTCTGGGTGACCC 5280  
Db |||||  
Qy 5221 TGAATAATTTTCTAGGAATTTCCGGAGGAAATGGGTAGTTAGCTATTTCTGGGTGACCC 5280  
Db |||||  
Qy 5281 AGTCTATTTAAAGAAAGAAAAATGCTGAATCAGCATGATTTTGAAGTCAGAGGAGATGTGG 5340  
Db |||||  
Qy 5281 AGTCTATTTAAAGAAAGAAAAATGCTGAATCAGCATGATTTTGAAGTCAGAGGAGATGTGG 5340  
Db |||||  
Qy 5341 TCAATGGAAGAAACCAAGGTTCCAAAGCGAGCAAGAGAAATCCAGGACAGAAAGATCT 5400  
Db |||||  
Qy 5341 TCAATGGAAGAAACCAAGGTTCCAAAGCGAGCAAGAGAAATCCAGGACAGAAAGATCT 5400  
Db |||||  
Qy 5401 TCAGGGGGCTAGAAAATCTGTTGCTATGGGCCCTTTCACCAACATGCCACAGATCAACTGG 5460  
Db |||||  
Qy 5401 TCAGGGGGCTAGAAAATCTGTTGCTATGGGCCCTTTCACCAACATGCCACAGATCAACTGG 5460  
Db |||||  
Qy 5461 AATGATGTTGACAGCTGTGTGTGCTTCTGTTGTTGAAGGAGCTTTTCACTTACCCCTTG 5520  
Db |||||  
Qy 5461 AATGATGTTGACAGCTGTGTGTGCTTCTGTTGTTGAAGGAGCTTTTCACTTACCCCTTG 5520  
Db |||||  
Qy 5521 GCACAGGTGTCACCCCAATTTGTTGTTGTGAGCCAGATGCTTGGACAGAGGACAAATGGCT 5580  
Db |||||  
Qy 5521 GCACAGGTGTCACCCCAATTTGTTGTTGTGAGCCAGATGCTTGGACAGAGGACAAATGGCT 5580  
Db |||||  
Qy 5581 TCCATGCAATTTGGGCAGATGTGAGGCACCTGTGTGTGACCCCGAGAGTGGGTGTGACACA 5640  
Db |||||  
Qy 5581 TCCATGCAATTTGGGCAGATGTGAGGCACCTGTGTGTGACCCCGAGAGTGGGTGTGACACA 5640  
Db |||||  
Qy 5641 GTGTAGCACTCTACCAAGTCCAGAGCTGGACACCTTACCTGTATACCCCAAGATCCCCACA 5700  
Db |||||  
Qy 5641 GTGTAGCACTCTACCAAGTCCAGAGCTGGACACCTTACCTGTATACCCCAAGATCCCCACA 5700  
Db |||||  
Qy 5701 GCCACTACTGA 5711  
Db |||||



Db 5701 GCCACTACTGA 5711

Search completed: December 14, 2003, 17:37:48  
Job time : 19970 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 02:03:55 ; Search time 1329 Seconds  
(without alignments)  
11600.068 Million cell updates/sec

Title: US-09-923-327a-263

Perfect score: 5711

Sequence: 1 agctcgtgagattctcttg.....tccccacagccactactga 5711

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq 19Jun03;\*

```

1: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1980.DAT:*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1982.DAT:*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1983.DAT:*
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1984.DAT:*
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1985.DAT:*
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1986.DAT:*
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1987.DAT:*
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1988.DAT:*
10: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1989.DAT:*
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1990.DAT:*
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1991.DAT:*
13: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1992.DAT:*
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1993.DAT:*
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1994.DAT:*
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1995.DAT:*
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1996.DAT:*
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1997.DAT:*
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1998.DAT:*
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:*
25: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2003.DAT:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5711	100.0	5711	18	Human BRCA1 gene c
2	5711	100.0	5711	19	BRCA1 (omi1) codin
3	5711	100.0	5711	19	Human BRCA1 omi1 c
4	5711	100.0	5711	21	Human BRCA1 (omi1)
5	5710.6	100.0	5711	19	Human BRCA1 omi3 p
6	5710.6	100.0	5711	19	Human BRCA1 omi1 p
7	5710.6	100.0	5711	19	Human BRCA1 omi1 p
8	5710.6	100.0	5711	19	Human BRCA1 omi1 p

9	5710.6	100.0	5711	19	AAV46454	Human BRCA1 omi1 p
10	5710.6	100.0	5711	19	AAV46455	Human BRCA1 omi1 p
11	5710.6	100.0	5711	19	AAV46456	Human BRCA1 omi1 p
12	5710.6	100.0	5711	19	AAV46457	Human BRCA1 omi1 p
13	5709.4	100.0	5711	19	AAV46450	Human BRCA1 omi3 c
14	5709.4	100.0	5711	21	AAC60794	Human BRCA1 (omi2)
15	5709	100.0	5711	19	AAV46455	Human BRCA1 omi3 p
16	5709	100.0	5711	19	AAV46456	Human BRCA1 omi3 p
17	5709	100.0	5711	19	AAV46457	Human BRCA1 omi3 p
18	5709	100.0	5711	19	AAV46468	Human BRCA1 omi3 p
19	5709	100.0	5711	19	AAV46469	Human BRCA1 omi3 p
20	5709	100.0	5711	19	AAV46471	Human BRCA1 omi3 p
21	5702.6	99.9	5711	19	AAV46463	Human BRCA1 omi2 p
22	5702.6	99.9	5711	19	AAV46464	Human BRCA1 omi2 p
23	5702.6	99.9	5711	19	AAV46459	Human BRCA1 omi2 p
24	5702.6	99.9	5711	19	AAV46461	Human BRCA1 omi2 p
25	5702.6	99.9	5711	19	AAV46462	Human BRCA1 omi2 p
26	5701.4	99.8	5711	19	AAV46449	Human BRCA1 omi2 c
27	5701.4	99.8	5711	21	AAC60795	Human BRCA1 (omi3)
28	5701.4	99.8	5711	17	AAT17491	Mutated BRCA1 codi
29	5701.4	99.8	5711	17	AAT17492	Mutated BRCA1 codi
30	5701.4	99.8	5711	17	AAT17493	Mutated BRCA1 codi
31	5701.4	99.8	5711	17	AAT17494	Mutated BRCA1 codi
32	5701.4	99.8	5711	17	AAT17495	Mutated BRCA1 codi
33	5701.4	99.8	5711	17	AAT17496	Mutated BRCA1 codi
34	5701	99.8	5711	19	AAV46458	Human BRCA1 omi2 p
35	5701	99.8	5711	25	AB223502	Nucleotide sequenc
36	5699.8	99.8	5711	19	AAV46460	Human BRCA1 omi2 p
37	5699.8	99.8	5712	18	ATG84840	Human breast and o
38	5699.8	99.8	5712	21	AA287995	BRCA1 gene sequenc
39	5699.8	99.8	5712	17	AAT32601	BRCA1, breast and
40	5699.8	99.8	5712	17	AAT17438	BRCA1 coding seque
41	5699.8	99.8	5712	17	AAT18310	BRCA1, breast and
42	5698.2	99.8	5711	17	AAT42024	BRCA1 allele #8403
43	5698.2	99.8	5711	17	AAT42030	BRCA1 allele #7408
44	5698.2	99.8	5711	18	AAT70067	Mutant BRCA1 allele
45	5698.2	99.8	5711	18	AAT70073	Mutant BRCA1 allele

#### ALIGNMENTS

##### RESULT 1

AAT87085

ID AAT87085 standard; cDNA; 5711 BP.

XX AAT87085;

AC AAT87085;

DT 06-JAN-1998 (first entry)

XX Human BRCA1 gene consensus.

DB BRCA1 gene; BRCA1(omi1); breast cancer; ovary cancer; polymorphism;

KW genetic testing; diagnosis; gene therapy; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 120..5711

FT variation /\*tag= a

FT variation /\*tag= b

FT variation /\*tag= c

FT variation /\*tag= d

FT variation /\*tag= e

FT variation /\*tag= f

FT variation /\*tag= g

FT variation /\*tag= h

FT variation /\*tag= i

FT variation /\*tag= j

FT variation /\*tag= k

FT variation /\*tag= l

FT variation /\*tag= m

FT variation /\*tag= n

FT variation /\*tag= o

FT variation /\*tag= p

FT variation /\*tag= q

FT variation /\*tag= r

FT variation /\*tag= s

FT variation /\*tag= t

FT variation /\*tag= u

FT variation /\*tag= v

```

FT FT /*tag= e
FT FT /note= "35-45% GAA (Glu) and 55-65% GGA (Gly)
FT FT variation 3667 polymorphism at position 3232"
FT FT /*tag= f
FT FT /note= "35-45% AAA (Lys) and 55-65% AGA (Arg)
FT FT variation 4427 polymorphism at position 3667"
FT FT /*tag= g
FT FT /note= "45-55% TCT (Ser) and 45-55% TCC (Ser)
FT FT variation 4956 polymorphism at position 4427"
FT FT /*tag= h
FT FT /note= "35-45% AGT (Ser) and 55-65% GGT (Gly)
FT FT polymorphism at position 4956"
XX US5654155-A.
XX
XX 05-AUG-1997.
XX
XX 12-FEB-1996; 96US-0598591.
XX
XX 12-FEB-1996; 96US-0598591.
XX (ONCO-) ONCORMED INC.
XX
XX Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ;
XX Scheiter DB, Zeng B;
XX
XX WPI; 1997-401843/37.
XX P-PSDB; AAW26522.
XX
XX Human BRCA1 gene coding sequence with common normal polymorphisms -
XX for assessing susceptibility to breast or ovarian cancer
XX
XX Claim 1; Column 19-24; 35pp; English.
XX
XX This nucleotide sequence comprises a consensus DNA sequence,
XX designated BRCA1(oni), for the normal human BRCA1 gene. It was
XX found by end-to-end sequencing of the BRCA1 gene from 5 individuals
XX randomly drawn from the population and found to have no family
XX history of breast or ovarian cancer. The BRCA1(oni) gene and the
XX seven polymorphic sites (which are not associated with breast or
XX ovarian cancer) will provide greater accuracy and reliability for
XX genetic testing. A claimed method for detecting an increased
XX genetic susceptibility to breast and ovarian cancer resulting from
XX the presence of a mutation in the BRCA1 coding sequence involves
XX amplifying and sequencing the BRCA1 coding sequence from an
XX individual and comparing the sequence with BRCA1(oni). The
XX consensus normal BRCA1 sequence can also be used in gene therapy,
XX to make diagnostic probes and to express normal BRCA1 polypeptide
XX (see AAW26522).
XX
SQ Sequence 5711 BP; 1953 A; 1099 C; 1277 G; 1382 T; 0 other;

Query Match 100.0%; Score 5711; DB 18; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTCGCTGAGACTTCTGACCCCGCACAGGCTGTGGGGTTTCTCAGATAACTGGGCC 60
DB 1 AGTCGCTGAGACTTCTGACCCCGCACAGGCTGTGGGGTTTCTCAGATAACTGGGCC 60

QY 61 CCTCGCCTCAGAGGCTTACCCCTCTGCTCTGGTAAAGTTATTGGGAACAGAGAAA 120
DB 61 CCTCGCCTCAGAGGCTTACCCCTCTGCTCTGGTAAAGTTATTGGGAACAGAGAAA 120

QY 121 TGGATTATCTGCTCTTCGGGTTGAAGAAGTACAAAATGTCATTATGCTATCAGAAA 180
DB 121 TGGATTATCTGCTCTTCGGGTTGAAGAAGTACAAAATGTCATTATGCTATCAGAAA 180

QY 181 TCTTAGAGTCTCCATCTGTCTGGAGTTGATCAAGGAACCTGTCTCCACAAAGTGTGACC 240
DB 181 TCTTAGAGTCTCCATCTGTCTGGAGTTGATCAAGGAACCTGTCTCCACAAAGTGTGACC 240

```

```

DB 181 TCTTAGAGTCTCCATCTGTCTGGAGTTGATCAAGGAACCTGTCTCCACAAAGTGTGACC 240
QY 241 ACATATTTTGCBAATTTTGCATCTGAACTTCTCAACACAGAGAAAGGCGCTTCACAGT 300
DB 241 ACATATTTTGCBAATTTTGCATCTGAACTTCTCAACACAGAGAAAGGCGCTTCACAGT 300
QY 301 GTCTTTTATGTAAGATGATATAACCAAAAAGGAGCCCTACAAAGAAAGTACGAGATTTAGTC 360
DB 301 GTCTTTTATGTAAGATGATATAACCAAAAAGGAGCCCTACAAAGAAAGTACGAGATTTAGTC 360
QY 361 AACTTGTGAAAGACTATTGAAATCATTTTGTCTTTTACAGTTGACACAGGTTTGAGT 420
DB 361 AACTTGTGAAAGACTATTGAAATCATTTTGTCTTTTACAGTTGACACAGGTTTGAGT 420
QY 421 ATGCAACAGCTATAATTTTGCAAAAGGAGAAATTAACCTCTGACATCTAAAGATG 480
DB 421 ATGCAACAGCTATAATTTTGCAAAAGGAGAAATTAACCTCTGACATCTAAAGATG 480
QY 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCACAAAGACTTCTACAGAGTG 540
DB 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCACAAAGACTTCTACAGAGTG 540
QY 541 AACCCGAAATCCTTCTTCGAGGAAACCAAGTCTCAGTGTCCAACCTCTAAACCTTGAA 600
DB 541 AACCCGAAATCCTTCTTCGAGGAAACCAAGTCTCAGTGTCCAACCTCTAAACCTTGAA 600
QY 601 CTGTGAGACTCTGAGGACAAAGCAGCGGATACAACTCAAAAGAGCTGTGTCTACATTG 660
DB 601 CTGTGAGACTCTGAGGACAAAGCAGCGGATACAACTCAAAAGAGCTGTGTCTACATTG 660
QY 661 AATTGGGATCTGATTCTTCTGAAGATACCGCTTAATAAGGCAACTTATTGCAGTGTGGAG 720
DB 661 AATTGGGATCTGATTCTTCTGAAGATACCGCTTAATAAGGCAACTTATTGCAGTGTGGAG 720
QY 721 ATCAAGAATTTTACAAATCACCCCTCAAGGAACCGGATGAAATCAGTTTGGATCTG 780
DB 721 ATCAAGAATTTTACAAATCACCCCTCAAGGAACCGGATGAAATCAGTTTGGATCTG 780
QY 781 CAAAAGGCTGCTGTGAAATTTTCTGAGACGATGTACAAATCTGACATCTCAAC 840
DB 781 CAAAAGGCTGCTGTGAAATTTTCTGAGACGATGTACAAATCTGACATCTCAAC 840
QY 841 CCAGTAAATGATTTTGAACACCACTGAGAAAGGCTGAGAGGCTCCAGAAAGT 900
DB 841 CCAGTAAATGATTTTGAACACCACTGAGAAAGGCTGAGAGGCTCCAGAAAGT 900
QY 901 ATCAGGCTAGTTCTGTTTCAAACTTGCAATGTGGAGCCATGTGGCAAAATCTATGCCA 960
DB 901 ATCAGGCTAGTTCTGTTTCAAACTTGCAATGTGGAGCCATGTGGCAAAATCTATGCCA 960
QY 961 GCTCATTTACAGCATGAGAACAGCAGTTTATTCTCACTAAGACAGAAATGAATGTAGAA 1020
DB 961 GCTCATTTACAGCATGAGAACAGCAGTTTATTCTCACTAAGACAGAAATGAATGTAGAA 1020
QY 1021 AGGCTGAATTTCTGTAATAAAGCAACAGCCTGGCTTTAGCAAGGAGCCAAACATACAGAT 1080
DB 1021 AGGCTGAATTTCTGTAATAAAGCAACAGCCTGGCTTTAGCAAGGAGCCAAACATACAGAT 1080
QY 1081 GGCTCGGAAGTAAAGAAACATGTAATGATAGCGGACTCCACAGACAGAAAAAAGGTAG 1140
DB 1081 GGCTCGGAAGTAAAGAAACATGTAATGATAGCGGACTCCACAGACAGAAAAAAGGTAG 1140
QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGGAAATAGCAGAAATCGCATGCT 1200
DB 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGGAAATAGCAGAAATCGCATGCT 1200
QY 1201 CAGAGAAATCTCAGAGATCTGAAAGATGTTCTTGGATTAACACTAAATAGCAGATTTGAGA 1260
DB 1201 CAGAGAAATCTCAGAGATCTGAAAGATGTTCTTGGATTAACACTAAATAGCAGATTTGAGA 1260
QY 1261 AAGTTAATGAGTGGTTTTTCCAGAAAGTGAACCTGTGTAGGTTCTGATGATCAATGATG 1320
DB 1261 AAGTTAATGAGTGGTTTTTCCAGAAAGTGAACCTGTGTAGGTTCTGATGATCAATGATG 1320

```

Qy	1321	GGGAGTCTGAAATCAAATGCCAAAGTAGCTGATGATATTGGACGTTCTAAATGAGGTAGATG	1380
Dd	1321		
Qy	1381	GGGAGTCTGAAATCAAATGCCAAAGTAGCTGATGATATTGGACGTTCTAAATGAGGTAGATG	1380
Dd	1381		
Qy	1381	AATATTCTGGTTCTTTCAGAGAAATAGACTTACTTGGCCAGTGCATCTCATGAGGCTTTAA	1440
Dd	1381		
Qy	1441	AATATTCTGGTTCTTTCAGAGAAATAGACTTACTTGGCCAGTGCATCTCATGAGGCTTTAA	1440
Dd	1441		
Qy	1441	TATGTAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGAGTAATATTGAAAGACAAATAT	1500
Dd	1441		
Qy	1501	TTGGGAAAACCTTATCGGAAGAGGCAAGCCCTCCCAACTTAAGCCATGTAACTGAAATC	1560
Dd	1501		
Qy	1561	TAATTTATGAGGCAATTTGTTACTGAGCCACAGATAATACAGAGCGTCCCTCCACAATA	1620
Dd	1561		
Qy	1621	AATTTAAAGCGTAAAGGAGACCTACATCAGGCGTTTCACTCTGAGGATTTTATCAAGAAAG	1680
Dd	1621		
Qy	1681	CAGATTTGGCAGTTCAAAGAGCTCCTGAAATGATAAATCAGGGAATTAACCAACGGAGC	1740
Dd	1681		
Qy	1741	AGATGTCAGTGAATGATTAATTAATTAATGATGATGATGATGATGATGATGATGATGATG	1800
Dd	1741		
Qy	1801	CTATTCAAGATGAGAAATCTTAACCAATAGAAATCACTCGAAAGAAATCTGCTTTCA	1860
Dd	1801		
Qy	1861	AAACGAAAGCTGAACCTTAAAGCAGCAGTATAAGCAATATGGAATCGAATTAATATCC	1920
Dd	1861		
Qy	1921	ACAAATCAAAGCACTTAAAGAAATAGGCTGAGGAGGAAGTCTTACACAGGCATATTC	1980
Dd	1921		
Qy	1981	ATCGCTTGAACCTTAAAGAAATAGGCTGAGGAGGAAGTCTTACACAGGCATATTC	2040
Dd	1981		
Qy	2041	TTGATAGTTGTTCTAGCAGTGAAGAGATAAGAAAAAAGTACAACCAATGCCAGTCA	2100
Dd	2041		
Qy	2101	GGCAGCAGAAACCTTCAACTATGGAAGTAAAGAACTGCACTGAGGAGGAGGAGGAGGAGG	2160
Dd	2101		
Qy	2161	GTCACAGCAGAAACCTTCAACTATGGAAGTAAAGAACTGCACTGAGGAGGAGGAGGAGGAGG	2220
Dd	2161		
Qy	2221	AGTTAAACAAATGCAACCTTCTTTTACTAAGTGTCCAAATACCAGTGAACCTTAAAGAAAT	2280
Dd	2221		
Qy	2281	TTGTCAAATCTAGCCTTCCAAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2340
Dd	2281		
Qy	2341	CTAATAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGGAGGAGGAGGAGGAGGAGGAGG	2400
Dd	2341		
Qy	2401	AAAGATCTGTAGAGAGTAGCAGTATTTTCACTGGTACTGGTACTGATTTATGGCACTCAGG	2460
Dd	2401		
Qy	2461	AAAGATCTGTAGAGAGTAGCAGTATTTTCACTGGTACTGGTACTGATTTATGGCACTCAGG	2460
Dd	2461		
Qy	2521	GTGTAGTCACTGTGAGCAATTTGAAAAACCCCAAGGACCTAATTCATGGTGTGTTCCAAAG	2580
Dd	2521		
Qy	2581	ATATAGAAATGACACAGAAAGGCTTTAAAGTATCCATTTGGGACATGAAAGTTAAACACAGTC	2640
Dd	2581		
Qy	2641	GGGAAACCAAGCATAGAAATGGAAGAAAGTCAATTTGATGCTCAGTATTTGCGAAGTACAT	2700
Dd	2641		
Qy	2701	TCAAGGTTTCAAAGCGCCAGTCAATTTGCTCTGTTTTCAAAATCCAGGAAATGCAGAGAGG	2760
Dd	2701		
Qy	2761	AATGTGCAACATTTCTGTGCCCCACTCTGGGCTCTTAAAGAAACAAAGTCCAAAAGTCACTT	2820
Dd	2761		
Qy	2821	TTGAAATGTGAACAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2880
Dd	2821		
Qy	2881	AGACAGTAAATATACATCGCAGGCTTTCTGCTGGTGTGCTCAGAAAGATAAGCCAGTGTATA	2940
Dd	2881		
Qy	2941	ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTCTATCATCTCAGTTCAGAGGCA	3000
Dd	2941		
Qy	3001	ACGAAATGCACTTACTTCCAAATTAACATGAGCTTTTACAAAACCCATATCGTATAC	3060
Dd	3001		
Qy	3061	CACCACTTTTCCCATCAAGTCAATTTGTTTAAACTAAATGTAAAGAAATCTGCTAGAGG	3120
Dd	3061		
Qy	3121	AAAACCTTTGAGGAACTTCAATGTCACTGAAAGAGAGAAATGGGAAATGAGAACTTCCAA	3180
Dd	3121		
Qy	3181	GTACAGTGACCAATTTAGCCGTAAATACATTAAGAGAAATGTTTTTAAAGGAGCCAGCT	3240
Dd	3181		
Qy	3241	CAAGCAATTAATTAAGTAGGTTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA	3300
Dd	3241		
Qy	3301	TAGGTTCCAGTGATGAAAACATTCAGCAGACATAGGTAGAAACAGAGGGCCAAAATTGA	3360
Dd	3301		
Qy	3361	ATGCTATGCTTAGATTAGGGTTTTGCAACTGAGGCTTATAAACAAGTCTTCTCTGAA	3420
Dd	3361		
Qy	3421	GTAAATGCTAGCACTCTGAAATTAAGAAAGCAAGATATGAAGAGTGTAGTTCAGACTGTTA	3480
Dd	3421		
Qy	3481	ATACAGATTTTCTCTCCATATCTGATTTTCAAGTAACTTAGAAGAGCCTATGGGAAGTAGTC	3540
Dd	3481		

Qy	2401	AAAGATCTGTAGAGAGTAGCAGTATTTTCACTGGTACTGGTACTGATTTATGGCACTCAGG	2460
Dd	2401		
Qy	2461	AAAGATCTGTAGAGAGTAGCAGTATTTTCACTGGTACTGGTACTGATTTATGGCACTCAGG	2460
Dd	2461		
Qy	2521	GTGTAGTCACTGTGAGCAATTTGAAAAACCCCAAGGACCTAATTCATGGTGTGTTCCAAAG	2580
Dd	2521		
Qy	2581	ATATAGAAATGACACAGAAAGGCTTTAAAGTATCCATTTGGGACATGAAAGTTAAACACAGTC	2640
Dd	2581		
Qy	2641	GGGAAACCAAGCATAGAAATGGAAGAAAGTCAATTTGATGCTCAGTATTTGCGAAGTACAT	2700
Dd	2641		
Qy	2701	TCAAGGTTTCAAAGCGCCAGTCAATTTGCTCTGTTTTCAAAATCCAGGAAATGCAGAGAGG	2760
Dd	2701		
Qy	2761	AATGTGCAACATTTCTGTGCCCCACTCTGGGCTCTTAAAGAAACAAAGTCCAAAAGTCACTT	2820
Dd	2761		
Qy	2821	TTGAAATGTGAACAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2880
Dd	2821		
Qy	2881	AGACAGTAAATATACATCGCAGGCTTTCTGCTGGTGTGCTCAGAAAGATAAGCCAGTGTATA	2940
Dd	2881		
Qy	2941	ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTCTATCATCTCAGTTCAGAGGCA	3000
Dd	2941		
Qy	3001	ACGAAATGCACTTACTTCCAAATTAACATGAGCTTTTACAAAACCCATATCGTATAC	3060
Dd	3001		
Qy	3061	CACCACTTTTCCCATCAAGTCAATTTGTTTAAACTAAATGTAAAGAAATCTGCTAGAGG	3120
Dd	3061		
Qy	3121	AAAACCTTTGAGGAACTTCAATGTCACTGAAAGAGAGAAATGGGAAATGAGAACTTCCAA	3180
Dd	3121		
Qy	3181	GTACAGTGACCAATTTAGCCGTAAATACATTAAGAGAAATGTTTTTAAAGGAGCCAGCT	3240
Dd	3181		
Qy	3241	CAAGCAATTAATTAAGTAGGTTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA	3300
Dd	3241		
Qy	3301	TAGGTTCCAGTGATGAAAACATTCAGCAGACATAGGTAGAAACAGAGGGCCAAAATTGA	3360
Dd	3301		
Qy	3361	ATGCTATGCTTAGATTAGGGTTTTGCAACTGAGGCTTATAAACAAGTCTTCTCTGAA	3420
Dd	3361		
Qy	3421	GTAAATGCTAGCACTCTGAAATTAAGAAAGCAAGATATGAAGAGTGTAGTTCAGACTGTTA	3480
Dd	3421		
Qy	3481	ATACAGATTTTCTCTCCATATCTGATTTTCAAGTAACTTAGAAGAGCCTATGGGAAGTAGTC	3540
Dd	3481		

|||||  
Db 3481 ATACAGATTTCTCTCCATATCTGATTTTCAGATATCTTTAGAACAGCCTATGGGAGTAGTC 3540  
|||||  
Qy 3541 ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGG 3600  
|||||  
Db 3541 ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGG 3600  
|||||  
Qy 3601 AAGTACTAGTTTTGCTGAAAAATGACATTAAGGAAAGTTCTGCTGTTTTAGCAAAAGCG 3660  
|||||  
Db 3601 AAGTACTAGTTTTGCTGAAAAATGACATTAAGGAAAGTTCTGCTGTTTTAGCAAAAGCG 3660  
|||||  
Qy 3661 TCCAGAGAGAGAGCTTAGCAGGAGTCTTAGCCCTTTCCACCATAACATTTGGCTCAGG 3720  
|||||  
Db 3661 TCCAGAGAGAGAGCTTAGCAGGAGTCTTAGCCCTTTCCACCATAACATTTGGCTCAGG 3720  
|||||  
Qy 3721 GTTACCCAAGAGGGGCCAAGAAATAGAGTCTCAGAGAGAACTTATCTAGTGAGGATG 3780  
|||||  
Db 3721 GTTACCCAAGAGGGGCCAAGAAATAGAGTCTCAGAGAGAACTTATCTAGTGAGGATG 3780  
|||||  
Qy 3781 AAGAGCTTCCCTGCTCCACACACTTGTATTTGGTAAAGTAAACAATATACCTTCTCAGT 3840  
|||||  
Db 3781 AAGAGCTTCCCTGCTCCACACACTTGTATTTGGTAAAGTAAACAATATACCTTCTCAGT 3840  
|||||  
Qy 3841 CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGTCTAAAGACACAGAGAGAAATTTAT 3900  
|||||  
Db 3841 CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGTCTAAAGACACAGAGAGAAATTTAT 3900  
|||||  
Qy 3901 TATCATTTGAAGATAGCTTAAATGACTGCAGTAAACAGGTAATTTGGCAAGGCATCTC 3960  
|||||  
Db 3901 TATCATTTGAAGATAGCTTAAATGACTGCAGTAAACAGGTAATTTGGCAAGGCATCTC 3960  
|||||  
Qy 3961 AGGAACATCACCTTAGTGAGGAAACAAAATGTTCTGCTAGCTTGTGTTTTCTTCACAGTGCA 4020  
|||||  
Db 3961 AGGAACATCACCTTAGTGAGGAAACAAAATGTTCTGCTAGCTTGTGTTTTCTTCACAGTGCA 4020  
|||||  
Qy 4021 GTGAATTTGGAAGACTTGACTGCAATAACAAACCCAGGATCCTTTCTTGATTTGGTTCTT 4080  
|||||  
Db 4021 GTGAATTTGGAAGACTTGACTGCAATAACAAACCCAGGATCCTTTCTTGATTTGGTTCTT 4080  
|||||  
Qy 4081 CCAACAAATGAGGCATCAGTCTGAAGCCAGGAGTGGTCTGAGTGACAAGGAATGG 4140  
|||||  
Db 4081 CCAACAAATGAGGCATCAGTCTGAAGCCAGGAGTGGTCTGAGTGACAAGGAATGG 4140  
|||||  
Qy 4141 TTTTCAGATGATGAAGAAAGGAAACGGGCTTGAAGAAATAATCAAGAAAGACAAAGCA 4200  
|||||  
Db 4141 TTTTCAGATGATGAAGAAAGGAAACGGGCTTGAAGAAATAATCAAGAAAGACAAAGCA 4200  
|||||  
Qy 4201 TGGATTCAAACTTAGTGGAAGCAGCATCTGGGTGTGAGGTGAAGAAACAAAGCTCTCTGAAG 4260  
|||||  
Db 4201 TGGATTCAAACTTAGTGGAAGCAGCATCTGGGTGTGAGGTGAAGAAACAAAGCTCTCTGAAG 4260  
|||||  
Qy 4261 ACTGCTCAGGCTATCCTCTCAGAGTGACATTTTAAACCTCAGCAGGAGGATACCATGC 4320  
|||||  
Db 4261 ACTGCTCAGGCTATCCTCTCAGAGTGACATTTTAAACCTCAGCAGGAGGATACCATGC 4320  
|||||  
Qy 4321 AACATAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACCTAGAAAGCTGTGTAGAACAGC 4380  
|||||  
Db 4321 AACATAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACCTAGAAAGCTGTGTAGAACAGC 4380  
|||||  
Qy 4381 ATGGAGCCAGCCTTTCTAAACAGTACCCCTTTCCATCATAGTGAATCTCTGCCCTTGAGG 4440  
|||||  
Db 4381 ATGGAGCCAGCCTTTCTAAACAGTACCCCTTTCCATCATAGTGAATCTCTGCCCTTGAGG 4440  
|||||  
Qy 4441 ACCTGCGAATCCAGAACAGACATCAGAAAAGCAGTATTAATCTTCAGAAAAGTA 4500  
|||||  
Db 4441 ACCTGCGAATCCAGAACAGACATCAGAAAAGCAGTATTAATCTTCAGAAAAGTA 4500  
|||||  
Qy 4501 GTGAATACCTTATAAGCCAGAAATCCAGAAAGCCCTTTCTGCTGACAAAGTTTGGGTGCTG 4560  
|||||  
Db 4501 GTGAATACCTTATAAGCCAGAAATCCAGAAAGCCCTTTCTGCTGACAAAGTTTGGGTGCTG 4560  
|||||  
Qy 4561 CAGATAGTTCTACAGTTAAAAATAAGAACACAGAGTGGAAAGGTCTATCCCTTCTAAAT 4620  
|||||

Db 4561 CAGATAGTTCTACAGGTAAAAATAAGAACACAGAGTGGAAAGGTCTATCCCTTCTAAAT 4620  
Qy 4621 GCCCATCATTTAGATGATAGTGTGTACATGACACAGTTGCTCTGGGAGTCTTTTCAGAAATAGAA 4680  
|||||  
Db 4621 GCCCATCATTTAGATGATAGTGTGTACATGACACAGTTGCTCTGGGAGTCTTTTCAGAAATAGAA 4680  
|||||  
Qy 4681 ACTACCCATCTCAAGAGGAGCTCATTTAAGGTTGTGATGTGGAGGAGCAACAGCTGGAAG 4740  
|||||  
Db 4681 ACTACCCATCTCAAGAGGAGCTCATTTAAGGTTGTGATGTGGAGGAGCAACAGCTGGAAG 4740  
|||||  
Qy 4741 AGTCTGGGCCACACAGATTTGACCGAAACATCTTTACTTTGCCAAGCAGATCTAGAGGGAA 4800  
|||||  
Db 4741 AGTCTGGGCCACACAGATTTGACCGAAACATCTTTACTTTGCCAAGCAGATCTAGAGGGAA 4800  
|||||  
Qy 4801 CCCCTTACCTGGAAATCTGGAATCAGCCTCTTCTGATGACCCCTGAAATCTGATCCTTCTG 4860  
|||||  
Db 4801 CCCCTTACCTGGAAATCTGGAATCAGCCTCTTCTGATGACCCCTGAAATCTGATCCTTCTG 4860  
|||||  
Qy 4861 AAGACAGAGCCCGCAGAGTCAAGTCTGTTGGCAACATACCATCTTCAACCTCTGCATTGA 4920  
|||||  
Db 4861 AAGACAGAGCCCGCAGAGTCAAGTCTGTTGGCAACATACCATCTTCAACCTCTGCATTGA 4920  
|||||  
Qy 4921 AAGTCCCAATTTGAAAGTTGCAAGATCTGCCAGGGTCCAGCTGTCTCATCTACTG 4980  
|||||  
Db 4921 AAGTCCCAATTTGAAAGTTGCAAGATCTGCCAGGGTCCAGCTGTCTCATCTACTG 4980  
|||||  
Qy 4981 ATACTCTGGGTATTAATGCAATGGAAGAAAGTGTGAGCAGGGAGAGCCAGAAATTGACAG 5040  
|||||  
Db 4981 ATACTCTGGGTATTAATGCAATGGAAGAAAGTGTGAGCAGGGAGAGCCAGAAATTGACAG 5040  
|||||  
Qy 5041 CTTTCAACAGAAAGGGTCAACAAAGAAATGTCCATGGTGGTGTCTGGCTCAGCCCCAGAG 5100  
|||||  
Db 5041 CTTTCAACAGAAAGGGTCAACAAAGAAATGTCCATGGTGGTGTCTGGCTCAGCCCCAGAG 5100  
|||||  
Qy 5101 AATTTATGCTCGTGTAACAAGTTTGCAGAAAAACACACATCACTTTAACTTAATTA 5160  
|||||  
Db 5101 AATTTATGCTCGTGTAACAAGTTTGCAGAAAAACACACATCACTTTAACTTAATTA 5160  
|||||  
Qy 5161 CTCAGAGAGCTACTCATGTTGTTATGAAGACAGATGCTGAGTTTGTGTGAGACGGACAC 5220  
|||||  
Db 5161 CTCAGAGAGCTACTCATGTTGTTATGAAGAAACAGATGCTGAGTTTGTGTGAGACGGACAC 5220  
|||||  
Qy 5221 TGAATAATTTTCTAGGAAATTCGCGGAGGAAAAATGGGTAGTTAGCTATTTCTGGGTGACCC 5280  
|||||  
Db 5221 TGAATAATTTTCTAGGAAATTCGCGGAGGAAAAATGGGTAGTTAGCTATTTCTGGGTGACCC 5280  
|||||  
Qy 5281 AGTCTATTAAGAAAGAAAAATCTGAAATGAGCATGATTTTGAAGTCAGAGGAGATGCG 5340  
|||||  
Db 5281 AGTCTATTAAGAAAGAAAAATCTGAAATGAGCATGATTTTGAAGTCAGAGGAGATGCG 5340  
|||||  
Qy 5341 TCAATGGAAGAAACCCAGAGTCCAAAGCGAGCAAGAGAAATCCAGGACAGAAAGATCT 5400  
|||||  
Db 5341 TCAATGGAAGAAACCCAGAGTCCAAAGCGAGCAAGAGAAATCCAGGACAGAAAGATCT 5400  
|||||  
Qy 5401 TCAGGGGCTTAGAAAAATCTGTTGCTATGGGCCCTTCCACCAATGCCCCACAGATCAACTGG 5460  
|||||  
Db 5401 TCAGGGGCTTAGAAAAATCTGTTGCTATGGGCCCTTCCACCAATGCCCCACAGATCAACTGG 5460  
|||||  
Qy 5461 AATGGATGTAAGCTGTGTGTGTCTGTGTGTGAGGAGCTTTTCAATCATTCACCCCTTG 5520  
|||||  
Db 5461 AATGGATGTAAGCTGTGTGTGTCTGTGTGTGAGGAGCTTTTCAATCATTCACCCCTTG 5520  
|||||  
Qy 5521 GCACAGTGTCCACCAATTTGTTGTCAGCAGCATGCTGAGCAGAGGAGCAATGGCT 5580  
|||||  
Db 5521 GCACAGTGTCCACCAATTTGTTGTCAGCAGCATGCTGAGCAGAGGAGCAATGGCT 5580  
|||||  
Qy 5581 TCCATGCAATTTGGGCGAGATGTGTGAGGCACCTGTGTGTGACCCCGAGAGTGGGTGTGACA 5640  
|||||  
Db 5581 TCCATGCAATTTGGGCGAGATGTGTGAGGCACCTGTGTGTGACCCCGAGAGTGGGTGTGACA 5640  
|||||  
Qy 5641 GTGTAGCACTTACAGAGTGCAGAGGCTTGACACTTACCTGTATACCCAGATCCCCCACA 5700  
|||||  
Db 5641 GTGTAGCACTTACAGAGTGCAGAGGCTTGACACTTACCTGTATACCCAGATCCCCCACA 5700  
|||||



```

Qy 5701 GCCACTACTGA 5711
Db 5701 GCCACTACTGA 5711

RESULT 2
AAV62180
ID AAV62180 standard; DNA; 5711 BP.
XX
XX AC AAV62180;
XX
XX 11-FEB-1999 (first entry)
XX
XX BRCA1 (om1) coding sequence.
XX
XX BRCA1; mutation detection; disease screening; multiple allele variation;
XX breast cancer; ovarian cancer; cystic fibrosis; Li-Fraumeni syndrome;
XX Duchenne muscular dystrophy; Becker muscular dystrophy; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 120..5711
XX /*tag= a
XX
XX WO9844157-A2.
XX
XX 08-OCT-1998.
XX
XX 26-MAR-1998; 98WO-US06002.
XX
XX 28-MAR-1997; 97US-0825487.
XX
XX (ONCO-) ONCORMED INC.
XX
XX Murphy PD, White MB;
XX
XX WPI; 1998-542713/46.
XX
XX P-PSDB; AAW79665.
XX
XX Identifying variations in polynucleotide sequences - using allele
XX specific hybridisation assay, sequence variation locating assay, and
XX direct sequencing, in a stepwise procedure
XX
XX Disclosure; Fig 1a-j; 62pp; English.
XX
XX This sequence encodes the human BRCA (om1) protein, and was used to test
XX the method of the invention. The method is for determining the presence
XX or absence of a sequence variation in a gene sample, and comprises:
XX (a) performing an allele specific hybridisation assay for one or more
XX pre-determined sequence variations; (b) if no pre-determined sequence
XX variation found in step (a) then performing a sequence variation location
XX assay; (ci) if no sequence variation found in step (b) then sequencing
XX the gene sample; (cii) if sequence variation is found in step (b) then
XX targeted confirmatory sequencing is performed; and (d) determining the
XX presence of a sequence variation by analysing the sequence(s) obtained in
XX step (ci) or step (cii) against a reference sample. Alternatively, step
XX (a) or step (b) is omitted from the method. The invention provides a
XX stepwise and integrated method for the efficient and accurate detection
XX of variations in polynucleotide sequences, being directed towards
XX screening for diseases associated with multiple allele variations,
XX including breast and ovarian cancer, cystic fibrosis, Duchenne and Becker
XX muscular dystrophy, and Li-Fraumeni syndrome.
XX
XX Sequence 5711 BP; 1953 A; 1099 C; 1277 G; 1382 T; 0 other;
XX
XX Query Match 100.0%; Score 5711; DB 19; Length 5711;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 AGCTCGCTGAGACTTCTCGGACCCCGCACAGGCTGTGGGGTTTCTCAGATAACTGGGCC 60
Db 1 AGCTCGCTGAGACTTCTCGGACCCCGCACAGGCTGTGGGGTTTCTCAGATAACTGGGCC 60
Qy 61 CCTCGCTCAGGAGGCTTCAACCTCTGCTCTGGTAAAGTTTATTGGAAACAGAAAGAAA 120
Db 61 CCTCGCTCAGGAGGCTTCAACCTCTGCTCTGGTAAAGTTTATTGGAAACAGAAAGAAA 120
Qy 121 TGGATTATCTGCTCTTCGGGTTGAGAGAGTACAAATGTCATTAATGCTATGCGAGAAA 180
Db 121 TGGATTATCTGCTCTTCGGGTTGAGAGAGTACAAATGTCATTAATGCTATGCGAGAAA 180
Qy 181 TCTTAGAGTGTCCATCTGCTCTGAGTGTGATCAAGGAACCTGTCTCCACAAGTGTGACC 240
Db 181 TCTTAGAGTGTCCATCTGCTCTGAGTGTGATCAAGGAACCTGTCTCCACAAGTGTGACC 240
Qy 241 ACATATTTTGCATAATTTTGCATGCTGAAACTTCTCAACAGAGAAAGGGCTTTCACAGT 300
Db 241 ACATATTTTGCATAATTTTGCATGCTGAAACTTCTCAACAGAGAAAGGGCTTTCACAGT 300
Qy 301 GTCTTTTATGTAAGATGATATTAACCAAAAGGAGCCCTACAAAGAAAGTACGAGATTAGTC 360
Db 301 GTCTTTTATGTAAGATGATATTAACCAAAAGGAGCCCTACAAAGAAAGTACGAGATTAGTC 360
Qy 361 AACTTGTGAGAGACTTATTCGAAATCATTTTGTGCTTTTTCAGTTTGACACAGGTTTGAGT 420
Db 361 AACTTGTGAGAGACTTATTCGAAATCATTTTGTGCTTTTTCAGTTTGACACAGGTTTGAGT 420
Qy 421 ATGCAACAGCTATATTTTGCATAAAAGGAAATAACTCTCTGGAACATCTAAAGATG 480
Db 421 ATGCAACAGCTATATTTTGCATAAAAGGAAATAACTCTCTGGAACATCTAAAGATG 480
Qy 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCACAAAGACTTCTACAGAGTG 540
Db 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCACAAAGACTTCTACAGAGTG 540
Qy 541 AACCCGAAATCTCTCTCGAGGAAACCAAGTCTCAGTGTCCAACTCTTAACCTTGGAA 600
Db 541 AACCCGAAATCTCTCTCGAGGAAACCAAGTCTCAGTGTCCAACTCTTAACCTTGGAA 600
Qy 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCAAAAGACGCTCTCTACATTG 660
Db 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCAAAAGACGCTCTCTACATTG 660
Qy 661 AATTGGGATCTGATTTCTTCAAGATACCGTTAATAAGGCAACTTATTGCGAGTGTGGAG 720
Db 661 AATTGGGATCTGATTTCTTCAAGATACCGTTAATAAGGCAACTTATTGCGAGTGTGGAG 720
Qy 721 ATCAAGAAATTTTACAATCACCCCTCAGGAACCGGATGAAATCAATCAGTTTGGATTCTG 780
Db 721 ATCAAGAAATTTTACAATCACCCCTCAGGAACCGGATGAAATCAATCAGTTTGGATTCTG 780
Qy 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGACGGATGTAACAAATACTGAAACATCATCAAC 840
Db 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGACGGATGTAACAAATACTGAAACATCATCAAC 840
Qy 841 CCAGTAATAATGATTTTCAACACCACTGAGAAGCGTGCAGCTGAGAGGCATCCAGAAAAGT 900
Db 841 CCAGTAATAATGATTTTCAACACCACTGAGAAGCGTGCAGCTGAGAGGCATCCAGAAAAGT 900
Qy 901 ATCAGGAGTAGTTCTGTTTCAAACTTGCATGTGAGAGCCATGTGGCACAATACTCATGCCA 960
Db 901 ATCAGGAGTAGTTCTGTTTCAAACTTGCATGTGAGAGCCATGTGGCACAATACTCATGCCA 960
Qy 961 GCTCATTTACAGCATGAGAACAGCAGTTTATTACTCACTTAAGACAGATGAATGTAGAAA 1020
Db 961 GCTCATTTACAGCATGAGAACAGCAGTTTATTACTCACTTAAGACAGATGAATGTAGAAA 1020
Qy 1021 AGGCTGAATTTCTGTAATAAAAGCAACAGCTGCTGCTTAGCAAGGAGCCAAACATACAGAT 1080
Db 1021 AGGCTGAATTTCTGTAATAAAAGCAACAGCTGCTGCTTAGCAAGGAGCCAAACATACAGAT 1080
Qy 1081 GGGCTGGAAGTAAGAAACATGTAAATGATAGCGGACTCCACAGCACAGAAAAAAGGTAG 1140
Db 1081 GGGCTGGAAGTAAGAAACATGTAAATGATAGCGGACTCCACAGCACAGAAAAAAGGTAG 1140

```

Qy	1141	ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGSAATTAAGCAGAAACTGCCATGCT	1200
Db	1141	ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGSAATTAAGCAGAAACTGCCATGCT	1200
Qy	1201	CAGAAATCCTTAGAGATACTGAAGATGTTCTTGGATAACAATAAATAGCAGCATTCAGA	1260
Db	1201	CAGAAATCCTTAGAGATACTGAAGATGTTCTTGGATAACAATAAATAGCAGCATTCAGA	1260
Qy	1261	AAGTTAATGATGTTTTCAGAAAGTGAATGAACTGTTAGGTTCTGATGACTCAGATGATG	1320
Db	1261	AAGTTAATGATGTTTTCAGAAAGTGAATGAACTGTTAGGTTCTGATGACTCAGATGATG	1320
Qy	1321	GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGATTAATGGAGCTTCTAAATGAGGTAGATG	1380
Db	1321	GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGATTAATGGAGCTTCTAAATGAGGTAGATG	1380
Qy	1381	AATATTCCTGTTCTCAGAGAAATATAGACTTACTGGCCAGTGATCCTCATGAGGCTTTAA	1440
Db	1381	AATATTCCTGTTCTCAGAGAAATATAGACTTACTGGCCAGTGATCCTCATGAGGCTTTAA	1440
Qy	1441	TATGTAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGATTAATTTGAAGACAAATAT	1500
Db	1441	TATGTAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGATTAATTTGAAGACAAATAT	1500
Qy	1501	TTGGGAAAACCTATCGGAAGAGGCAAGCCTCCCAACTTAAGCCATGTAACGTGAAAATC	1560
Db	1501	TTGGGAAAACCTATCGGAAGAGGCAAGCCTCCCAACTTAAGCCATGTAACGTGAAAATC	1560
Qy	1561	TAATTTATGAGGACATTTGTTTACTGAGCCACAGATAATACAAAGAGCGTCCCTCACAAATA	1620
Db	1561	TAATTTATGAGGACATTTGTTTACTGAGCCACAGATAATACAAAGAGCGTCCCTCACAAATA	1620
Qy	1621	AATTAAGCGTAAAGAGACCTACATCAGGCCCTTCACTCTGAGGATTTTATCAGAAAG	1680
Db	1621	AATTAAGCGTAAAGAGACCTACATCAGGCCCTTCACTCTGAGGATTTTATCAGAAAG	1680
Qy	1681	CAGATTTGGCAGTTTCAAAAGACTCCTGAAATGATTAATCAGGAACTAACCAACGGAGC	1740
Db	1681	CAGATTTGGCAGTTTCAAAAGACTCCTGAAATGATTAATCAGGAACTAACCAACGGAGC	1740
Qy	1741	AGAAATGCTAAGTGATGAATATTAATAATAGTGTGATGAGAAATAAACAACAAAGGTGATT	1800
Db	1741	AGAAATGCTAAGTGATGAATATTAATAATAGTGTGATGAGAAATAAACAACAAAGGTGATT	1800
Qy	1801	CTATTCAAGATGAGAAATCCTTAACCAATAGATCAGTAAAGAAAGATCTGCTTTCA	1860
Db	1801	CTATTCAAGATGAGAAATCCTTAACCAATAGATCAGTAAAGAAAGATCTGCTTTCA	1860
Qy	1861	AAACGAAAGCTGAACCTATTAAGCAGCAGTATTAAGCAATATGGAATCGAATTAATATCC	1920
Db	1861	AAACGAAAGCTGAACCTATTAAGCAGCAGTATTAAGCAATATGGAATCGAATTAATATCC	1920
Qy	1921	ACAAATCAAAAGCACCTAAAGAAATAGGTGAGGAGAAAGTCTTTACCAAGGCATATTC	1980
Db	1921	ACAAATCAAAAGCACCTAAAGAAATAGGTGAGGAGAAAGTCTTTACCAAGGCATATTC	1980
Qy	1981	ATGGCTTGAATCTAGTAGTCAAGTAATCTTAAGCCCACTAATTTGTAAGTAATGCAAA	2040
Db	1981	ATGGCTTGAATCTAGTAGTCAAGTAATCTTAAGCCCACTAATTTGTAAGTAATGCAAA	2040
Qy	2041	TTGATAGTGTCTTAGCAGTGAAGAGATAAAGAAAAAAGTACAAACCAATGCCAGTCA	2100
Db	2041	TTGATAGTGTCTTAGCAGTGAAGAGATAAAGAAAAAAGTACAAACCAATGCCAGTCA	2100
Qy	2101	GGCAGCAGAAACCTTCAACTCATGGAAGGTAAAGAACTGCAACTGGAGCCCAAGAGA	2160
Db	2101	GGCAGCAGAAACCTTCAACTCATGGAAGGTAAAGAACTGCAACTGGAGCCCAAGAGA	2160
Qy	2161	GTAACAGCCAAATGACACAGTAAGTAAGACATGACAGTGATCTTTCCAGAGCTGA	2220
Db	2161	GTAACAGCCAAATGACACAGTAAGTAAGACATGACAGTGATCTTTCCAGAGCTGA	2220

Qy	2221	AGTTAAACAAATGACCTGGTTCTTTTACTAAGTGTTCAAATACCAGTGAACCTTAAAGAAT	2280
Db	2221	AGTTAAACAAATGACCTGGTTCTTTTACTAAGTGTTCAAATACCAGTGAACCTTAAAGAAT	2280
Qy	2281	TTGTCAATCCTAGCTTCCAAAGAGAGAAAAAGAGAGAACTAGAAAAACAGTTTAAAGTGT	2340
Db	2281	TTGTCAATCCTAGCTTCCAAAGAGAGAAAAAGAGAGAACTAGAAAAACAGTTTAAAGTGT	2340
Qy	2341	CTAATAATGCTGAAGACCCCAAGATCTCATGTAAAGTGAGAGAAAGGTTTTCGAAACTG	2400
Db	2341	CTAATAATGCTGAAGACCCCAAGATCTCATGTAAAGTGAGAGAAAGGTTTTCGAAACTG	2400
Qy	2401	AAAGATCTGTAGAGAGTAGCAGTATTTCACTGGTACCTGCTACTGATTTATGGCACTCAGG	2460
Db	2401	AAAGATCTGTAGAGAGTAGCAGTATTTCACTGGTACCTGCTACTGATTTATGGCACTCAGG	2460
Qy	2461	AAAAGTATCTCGTTACTGGAAAGTTAGCACTCTAGGGAAGGCAAAAACAGAAACCAATTAAT	2520
Db	2461	AAAAGTATCTCGTTACTGGAAAGTTAGCACTCTAGGGAAGGCAAAAACAGAAACCAATTAAT	2520
Qy	2521	GTGTGAGTCACTGTGAGCAATTTGAAAACCCCAAGGCACTAATTCATGGTTGTTCCAAAG	2580
Db	2521	GTGTGAGTCACTGTGAGCAATTTGAAAACCCCAAGGCACTAATTCATGGTTGTTCCAAAG	2580
Qy	2581	ATAATAGAAATGACACAGAAAGGCTTTAAGTATCCATTGGGACATGAAGTTAAACACAGTC	2640
Db	2581	ATAATAGAAATGACACAGAAAGGCTTTAAGTATCCATTGGGACATGAAGTTAAACACAGTC	2640
Qy	2641	GGGAAACAAAGCATAGAAAATGGAAGAAAGTGAATCTGCTCAGTATTTTCAGAAATACAT	2700
Db	2641	GGGAAACAAAGCATAGAAAATGGAAGAAAGTGAATCTGCTCAGTATTTTCAGAAATACAT	2700
Qy	2701	TCAGGTTTCAAAGCGCAGTCAATTTGCTCTGTTTCAAATCAGGAAATGCAGAAAGG	2760
Db	2701	TCAGGTTTCAAAGCGCAGTCAATTTGCTCTGTTTCAAATCAGGAAATGCAGAAAGG	2760
Qy	2761	AATGTGCAACATTTCTCTGCCCACTCTGGGCTCTTAAAGAAACAAAGTCCAAAAGTCACTT	2820
Db	2761	AATGTGCAACATTTCTCTGCCCACTCTGGGCTCTTAAAGAAACAAAGTCCAAAAGTCACTT	2820
Qy	2821	TTGAAATGTGAACAAAAAGGAAAGAAATCAAGGAAAGAAATGAGTCTAATATCAAGCCTGTAC	2880
Db	2821	TTGAAATGTGAACAAAAAGGAAAGAAATCAAGGAAAGAAATGAGTCTAATATCAAGCCTGTAC	2880
Qy	2881	AGACAGTTAATATACATGCAAGGCTTCTCTGCTGCTGAGAAAGATAAGCCAGTTCATA	2940
Db	2881	AGACAGTTAATATACATGCAAGGCTTCTCTGCTGCTGAGAAAGATAAGCCAGTTCATA	2940
Qy	2941	ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTGTCTCTATCATCTCAGTTCAGAGGCA	3000
Db	2941	ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTGTCTCTATCATCTCAGTTCAGAGGCA	3000
Qy	3001	ACGAAACTGGAATCTTATCTCCAAATAAACAATGAGCTTTTACAAAACCCATATCGTATAC	3060
Db	3001	ACGAAACTGGAATCTTATCTCCAAATAAACAATGAGCTTTTACAAAACCCATATCGTATAC	3060
Qy	3061	CACCACTTTTCCCATCAAGTCAATTTGTTAAACTAAATGTAAGAAATCTGCTAGAGG	3120
Db	3061	CACCACTTTTCCCATCAAGTCAATTTGTTAAACTAAATGTAAGAAATCTGCTAGAGG	3120
Qy	3121	AAAACCTTTGAGGAAACATTCATGTCACCTGAAAGAGAAATGGGAAATGAGAACTTCCAA	3180
Db	3121	AAAACCTTTGAGGAAACATTCATGTCACCTGAAAGAGAAATGGGAAATGAGAACTTCCAA	3180
Qy	3181	GTAACAGTGAACAATAGCCGTAATAACAATTAAGAAAAATGTTTTAAAGGAGCCAGCT	3240
Db	3181	GTAACAGTGAACAATAGCCGTAATAACAATTAAGAAAAATGTTTTAAAGGAGCCAGCT	3240
Qy	3241	CAAGCAATATTAATGAGTAGGTTCCAGTACTAATGAGTGGCTCCAGTATTAATGAAA	3300
Db	3241	CAAGCAATATTAATGAGTAGGTTCCAGTACTAATGAGTGGCTCCAGTATTAATGAAA	3300
Qy	3301	TAGGTTCCAGTATGAAAAACATTTCAAGCAGAACTAGGTGAAAAACAGAGGGGCCAAATTGA	3360

Db ||||| TAGGTTCCAGTGATGAAACAACTTCAAGCAGAACTAGGTAGAAACAGAGGGGCCAAAATTGA 3360  
Qy ||||| ATGCTATGCTTAGAATTAGGGGTTTTGCAACTGAGGCTATATAACAAAGTCTTCTCTGGAA 3420  
Db ||||| ATGCTATGCTTAGAATTAGGGGTTTTGCAACTGAGGCTATATAACAAAGTCTTCTCTGGAA 3420  
Qy ||||| GTAAATTGAAGCTCTGAAATAAATAAAGCAAGCAAGATATGAAGAGTAGTTCAGACTGTTA 3480  
Db ||||| GTAAATTGAAGCTCTGAAATAAATAAAGCAAGCAAGATATGAAGAGTAGTTCAGACTGTTA 3480  
Qy ||||| ATACAGATTTCTCCATATCTGATTTTCAGATTAATCTAGACAGCCTATGGGAGTAGTC 3540  
Db ||||| ATACAGATTTCTCCATATCTGATTTTCAGATTAATCTAGACAGCCTATGGGAGTAGTC 3540  
Qy ||||| ATGCAATCTCAGGTTGTTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGG 3600  
Db ||||| ATGCAATCTCAGGTTGTTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGG 3600  
Qy ||||| AAGATACTAGTTTGTCTGAAATGACATTAAGGAAAGTCTGCTGTTTTAGCAAAAGCG 3660  
Db ||||| AAGATACTAGTTTGTCTGAAATGACATTAAGGAAAGTCTGCTGTTTTAGCAAAAGCG 3660  
Qy ||||| TCCAGAGGAGAGCTTAGCAGGAGTCTAGCCCTTTACCCATACACATTTGCGCTCAGG 3720  
Db ||||| TCCAGAGGAGAGCTTAGCAGGAGTCTAGCCCTTTACCCATACACATTTGCGCTCAGG 3720  
Qy ||||| GTTACCGAAGAGGGCCCAAGAAATTAGAGTCTCAGAAAGCACTTATCTAGTCAGGATG 3780  
Db ||||| GTTACCGAAGAGGGCCCAAGAAATTAGAGTCTCAGAAAGCACTTATCTAGTCAGGATG 3780  
Qy ||||| AAGAGCTTCCCTGCTCCAACTGTTTATTTGGTAAAGTAAACAATATACCTTCTCAGT 3840  
Db ||||| AAGAGCTTCCCTGCTCCAACTGTTTATTTGGTAAAGTAAACAATATACCTTCTCAGT 3840  
Qy ||||| CTACTAGGATAGACACCGTTGCTACCGAGTGTCTGCTAGAGTGTCTTAAGAAACAGAGAGAGATTTAT 3900  
Db ||||| CTACTAGGATAGACACCGTTGCTACCGAGTGTCTGCTAGAGTGTCTTAAGAAACAGAGAGAGATTTAT 3900  
Qy ||||| TATCATTGAAAGATAGCTTAAATGACTGCAATACAGTAAACAGGATTAATTTGGCAAGGATCTC 3960  
Db ||||| TATCATTGAAAGATAGCTTAAATGACTGCAATACAGTAAACAGGATTAATTTGGCAAGGATCTC 3960  
Qy ||||| AGGAACATCACCTTAGTGAGGAAACAAATGTTCTGCTAGCTGTTTTCTTTCACAGTGCA 4020  
Db ||||| AGGAACATCACCTTAGTGAGGAAACAAATGTTCTGCTAGCTGTTTTCTTTCACAGTGCA 4020  
Qy ||||| GTGAATTGGAAGACTTGACTGCAATAAACAACCCAGGATCCTTTCTTGATTTGGTCTTT 4080  
Db ||||| GTGAATTGGAAGACTTGACTGCAATAAACAACCCAGGATCCTTTCTTGATTTGGTCTTT 4080  
Qy ||||| CCAACAAATGAGGCATCAGTCTGAAAGCCAGGAGTGTGCTGAGTGCACAGGAATTGG 4140  
Db ||||| CCAACAAATGAGGCATCAGTCTGAAAGCCAGGAGTGTGCTGAGTGCACAGGAATTGG 4140  
Qy ||||| TTTGAGATGATGAAGAAAGAGCAAGGCTTGGAGAAATAAATCAAGAAAGCAAAAGCA 4200  
Db ||||| TTTGAGATGATGAAGAAAGAGCAAGGCTTGGAGAAATAAATCAAGAAAGCAAAAGCA 4200  
Qy ||||| TGGATTCAACTTAGTGGAAGCAGCATCTGGGTGTGAGAGTGAAACAAAGCGTCTCTGAAG 4260  
Db ||||| TGGATTCAACTTAGTGGAAGCAGCATCTGGGTGTGAGAGTGAAACAAAGCGTCTCTGAAG 4260  
Qy ||||| ACTGCTAGGCGTATCTCTCAGAGTGACATTTTAAACACTCAGGAGGATACCATGC 4320  
Db ||||| ACTGCTAGGCGTATCTCTCAGAGTGACATTTTAAACACTCAGGAGGATACCATGC 4320  
Qy ||||| AACATACTGATAAGCTCCAGCAGGAAATGGCTGAACTAGAGAGCTGTGTAGAACAGC 4380  
Db ||||| AACATACTGATAAGCTCCAGCAGGAAATGGCTGAACTAGAGAGCTGTGTAGAACAGC 4380  
Qy ||||| ATGGAGCCAGCTTCTTAACAGTACCTTCCATCATTAAGTGACTCTCTCTGCCCTTGAGG 4440  
Db ||||| ATGGAGCCAGCTTCTTAACAGTACCTTCCATCATTAAGTGACTCTCTCTGCCCTTGAGG 4440

Db 4381 ATGGAGCCAGCCTTCTTAACAGTACCTTCCATCATTAAGTGACTCTCTCTGCCCTTGAGG 4440  
Qy 4441 ACCTGCGAAATCCAGAAACAAAGCACAATCAGAAAAAGCAGATTAACTTTCACAGAAAAAGTA 4500  
Db 4441 ACCTGCGAAATCCAGAAACAAAGCACAATCAGAAAAAGCAGATTAACTTTCACAGAAAAAGTA 4500  
Qy 4501 GTGAATACCTTATTAAGCCAGAAATCCAGAAAGCCCTTCTGCTGACAAAGTTTGAGGTGCTG 4560  
Db 4501 GTGAATACCTTATTAAGCCAGAAATCCAGAAAGCCCTTCTGCTGACAAAGTTTGAGGTGCTG 4560  
Qy 4561 CAGATAGTCTTACCAAGTAAATAAAGAAACACAGAGTGGAAAGTCTATCCCTTCTTAAT 4620  
Db 4561 CAGATAGTCTTACCAAGTAAATAAAGAAACACAGAGTGGAAAGTCTATCCCTTCTTAAT 4620  
Qy 4621 GCCCATCATTTAGATGATAGGTGTGCTGACAGTGTCTCTGGAGTCTTTCAGAAATAGAA 4680  
Db 4621 GCCCATCATTTAGATGATAGGTGTGCTGACAGTGTCTCTGGAGTCTTTCAGAAATAGAA 4680  
Qy 4681 ACTACCATCTCAAGAGGAGCTCATTTAAGGTTGTTGATGTGGAGGAGCAACAGCTGGAG 4740  
Db 4681 ACTACCATCTCAAGAGGAGCTCATTTAAGGTTGTTGATGTGGAGGAGCAACAGCTGGAG 4740  
Qy 4741 AGTCTGGGCCACACGATTTTGCAGGAAACATCTTACTTGGCAAGGCAAGATCTAGAGGAA 4800  
Db 4741 AGTCTGGGCCACACGATTTTGCAGGAAACATCTTACTTGGCAAGGCAAGATCTAGAGGAA 4800  
Qy 4801 CCCCTTACCTTGGATCTGGAAATCAGCCCTTCTCTGATGACCCCTGAAATCTGATCCTTCTG 4860  
Db 4801 CCCCTTACCTTGGATCTGGAAATCAGCCCTTCTCTGATGACCCCTGAAATCTGATCCTTCTG 4860  
Qy 4861 AAGCAGAGCCCCAGAGTCTGCTGTTGGCAACATACCATCTTCAACCTCTGCAATTGA 4920  
Db 4861 AAGCAGAGCCCCAGAGTCTGCTGTTGGCAACATACCATCTTCAACCTCTGCAATTGA 4920  
Qy 4921 AAGTCTCCCAATTTGAAAGTTGCAAGATCTGCCAGGGTCCAGCTGCTCATACTACTG 4980  
Db 4921 AAGTCTCCCAATTTGAAAGTTGCAAGATCTGCCAGGGTCCAGCTGCTCATACTACTG 4980  
Qy 4981 ATACTGCTGGTATAATGCAATGGAAGAAAGTGTGAGCAGGAGAAAGCCAGAAATTGACAG 5040  
Db 4981 ATACTGCTGGTATAATGCAATGGAAGAAAGTGTGAGCAGGAGAAAGCCAGAAATTGACAG 5040  
Qy 5041 CTTCAACAGAAAGGCTCAACAAAGAAATGCTGTTGGTGTGCTGGCTGACCCAGAAAG 5100  
Db 5041 CTTCAACAGAAAGGCTCAACAAAGAAATGCTGTTGGTGTGCTGGCTGACCCAGAAAG 5100  
Qy 5101 AATTATGCTGCTGACAGTTTCCAGAAACACCAATCACTTTAACTTAATCTAATTA 5160  
Db 5101 AATTATGCTGCTGACAGTTTCCAGAAACACCAATCACTTTAACTTAATCTAATTA 5160  
Qy 5161 CTGAAGAGACTACTCATGTTGTTATGAAACAGAGTGTGAGTGTGTTGTGTAACGACAC 5220  
Db 5161 CTGAAGAGACTACTCATGTTGTTATGAAACAGAGTGTGAGTGTGTTGTGTAACGACAC 5220  
Qy 5221 TGAATATTTTCTAGGAATTTGCGGAGGAAATGGGTAGTTAGCTATTTCTGGGTGACCC 5280  
Db 5221 TGAATATTTTCTAGGAATTTGCGGAGGAAATGGGTAGTTAGCTATTTCTGGGTGACCC 5280  
Qy 5281 AGTCTATTAAGAAAGAAATGCTGTAAGCAATGATTTTGAAGTGCAGAGAGATGTTGG 5340  
Db 5281 AGTCTATTAAGAAAGAAATGCTGTAAGCAATGATTTTGAAGTGCAGAGAGATGTTGG 5340  
Qy 5341 TCAATGGAAGAAACCAAGGTTCCAAAGGCAAGAGATCCAGGACAGAAAGATCT 5400  
Db 5341 TCAATGGAAGAAACCAAGGTTCCAAAGGCAAGAGATCCAGGACAGAAAGATCT 5400  
Qy 5401 TCAGGGGCTAGAAATCTGTTGCTATGGGCCCTTCAACCAATGCCCCACAGATCAACTGG 5460  
Db 5401 TCAGGGGCTAGAAATCTGTTGCTATGGGCCCTTCAACCAATGCCCCACAGATCAACTGG 5460  
Qy 5461 AATGGATGGTACAGCTGTGTTGCTCTCTGTTGGTGAAGGAGCTTTCATCTACCTTGG 5520  
Db 5461 AATGGATGGTACAGCTGTGTTGCTCTCTGTTGGTGAAGGAGCTTTCATCTACCTTGG 5520

Qy 5521 GCACAGGTGTCCACCAATTGTTGTTGTCAGCCAGATGCTTGACAGAGACAAATGGCT 5580  
Db 5521 GCACAGGTGTCCACCAATTGTTGTTGTCAGCCAGATGCTTGACAGAGACAAATGGCT 5580  
Qy 5581 TCCATGCATATGGGAGAGTGTGAGGACCTGTGGTGACCCGAGAGTGGGTGTGGACA 5640  
Db 5581 TCCATGCATATGGGAGAGTGTGAGGACCTGTGGTGACCCGAGAGTGGGTGTGGACA 5640  
Qy 5641 GTGTAGCACTTACCAGTGCCAGAGCTGGACACCTACCTGATACCCAGATCCGCCACA 5700  
Db 5641 GTGTAGCACTTACCAGTGCCAGAGCTGGACACCTACCTGATACCCAGATCCGCCACA 5700  
Qy 5701 GCCACTACTGA 5711  
Db 5701 GCCACTACTGA 5711

RESULT 3  
AAV46448  
ID AAV46448 standard; cDNA; 5711 BP.  
AC AAV46448;

XX 18-NOV-1998 (first entry)

XX Human BRCA1 omil cDNA.

XX BRCA1; omil; human; breast and ovarian cancer predisposing gene;  
KW polymorphism; susceptibility; anti-oncogene; tumour suppressor;  
KW chromosome 17q; ss.

XX Homo sapiens.

EH Key Location/Qualifiers  
FT CDS 120..5711  
FT /\*tag= a  
FT /product= "BRCA1 omil protein"

XX US5750400-A.

XX 12-MAY-1998.

XX 12-FEB-1997; 97US-0798691.

XX 12-FEB-1996; 96US-0598591.

XX 12-FEB-1997; 97US-0798691.

XX (ONCO-) ONCORMED INC.

XX Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ;  
PI Schelter DB, Zeng B;

XX WPI; 1998-296774/26.

XX P-PSDB; AAV76098.

XX BRCA1 omi gene coding sequences - useful for distinguishing between  
PT polymorphisms and mutation(s) in the screening for disposition to  
PT breast or ovarian cancer

XX Claim 2d; Column 27-32; 54pp; English.

XX This sequence encodes the human BRCA1 (breast and ovarian cancer  
CC predisposing gene) omil gene. This sequence and polymorphic variations of  
CC this sequence are useful for the identification of an individual who may  
CC or may not have an increased susceptibility to breast or ovarian cancer.  
CC The sequences used identify gene changes which are due to polymorphisms,  
CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour  
CC suppressor) which is involved in genetic inheritance of cancers,  
CC especially breast and ovarian cancer. It is found at human chromosome 17q  
CC which is known to be linked to cancer susceptibility, especially breast  
CC cancer. Cells containing a mutation in this gene lose the wild-type  
CC function of BRCA1 and are more susceptible to cancers.

XX SQ Sequence 5711 BP; 1953 A; 1099 C; 1277 G; 1382 T; 0 other;  
Query Match 100.0%; Score 5711; DB 19; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AGCTCGCTGAGACTTCCCTGACACCCCGACAGGCTGTGGGTTTCTCAGATAACTGGGCC 60  
Db 1 AGCTCGCTGAGACTTCCCTGACACCCCGACAGGCTGTGGGTTTCTCAGATAACTGGGCC 60  
Qy 61 CTTGCGCTCAGGAGGCTTCAACCTCTGCTCTGGGTAAAGTTTCAATTGGAACAGAAAGAAA 120  
Db 61 CTTGCGCTCAGGAGGCTTCAACCTCTGCTCTGGGTAAAGTTTCAATTGGAACAGAAAGAAA 120  
Qy 121 TGGATTTATCTGCTCTTCGGGTTGAAGAAGTACAAAATGCTAATGCTATGAGAAAAA 180  
Db 121 TGGATTTATCTGCTCTTCGGGTTGAAGAAGTACAAAATGCTAATGCTATGAGAAAAA 180  
Qy 181 TCTTAGAGTGTCCCATCTGCTGAGTTGATCAAGGAACCTGTCTCCACAAGTGTGACC 240  
Db 181 TCTTAGAGTGTCCCATCTGCTGAGTTGATCAAGGAACCTGTCTCCACAAGTGTGACC 240  
Qy 241 ACATATTTTGCATAATTTTGCATGCTGAACTTCTCAACAGAGAAAGGSCCTTCACAGT 300  
Db 241 ACATATTTTGCATAATTTTGCATGCTGAACTTCTCAACAGAGAAAGGSCCTTCACAGT 300  
Qy 301 GTCTTTTATGTAAGATGATATAACAAAGAGGCTTACAAAGAAAGTACAGATTTAGTC 360  
Db 301 GTCTTTTATGTAAGATGATATAACAAAGAGGCTTACAAAGAAAGTACAGATTTAGTC 360  
Qy 361 AACTTGTGAAGAGTATTGAAATCATTTGTGCTTTTCAAGTTTGACACAGGTTTGAGT 420  
Db 361 AACTTGTGAAGAGTATTGAAATCATTTGTGCTTTTCAAGTTTGACACAGGTTTGAGT 420  
Qy 421 ATGCAACACGCTATTAATTTTGCATAAAGGAAATAACTCTCTCTGAACATCTAAAAGATG 480  
Db 421 ATGCAACACGCTATTAATTTTGCATAAAGGAAATAACTCTCTCTGAACATCTAAAAGATG 480  
Qy 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAAGACTTCTACAGAGTG 540  
Db 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAAGACTTCTACAGAGTG 540  
Qy 541 AACCCGAAATCTCTCTTCAGGAAACCACTCTCAGTGCCAACTCTCTAAACCTTGAA 600  
Db 541 AACCCGAAATCTCTCTTCAGGAAACCACTCTCAGTGCCAACTCTCTAAACCTTGAA 600  
Qy 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGTATACAACTCAAAAGACGCTCTGTCTACATTG 660  
Db 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGTATACAACTCAAAAGACGCTCTGTCTACATTG 660  
Qy 661 AATTGGGATCTGATTTCTTCTGAAGATACCGTTAATAGGCAACTTATGAGTGTGGAG 720  
Db 661 AATTGGGATCTGATTTCTTCTGAAGATACCGTTAATAGGCAACTTATGAGTGTGGAG 720  
Qy 721 ATCAAGAAATGTTTACAAATCACCCCTCAAGGAACCGGATGAATCAGTTTGGATTCTG 780  
Db 721 ATCAAGAAATGTTTACAAATCACCCCTCAAGGAACCGGATGAATCAGTTTGGATTCTG 780  
Qy 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGACGGATGTAAACAAATCTGAACATCATCAAC 840  
Db 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGACGGATGTAAACAAATCTGAACATCATCAAC 840  
Qy 841 CAGTAAATATGATTTGAACACCACTGAGAGCGTGCAGCTGAGAGGCTCCAGAAAGT 900  
Db 841 CAGTAAATATGATTTGAACACCACTGAGAGCGTGCAGCTGAGAGGCTCCAGAAAGT 900  
Qy 901 ATCAGGCTAGTCTGTGTTCAAACTTGCATGTCAGGCACTGTGCACAAATCTCATGCCA 960  
Db 901 ATCAGGCTAGTCTGTGTTCAAACTTGCATGTCAGGCACTGTGCACAAATCTCATGCCA 960  
Qy 961 GCTCATTACAGCATGAGAAACAGCAGTATTATTCTCACTAAAGACAGAAATGAGAAA 1020  
Db 961 GCTCATTACAGCATGAGAAACAGCAGTATTATTCTCACTAAAGACAGAAATGAGAAA 1020

Db 961 GCTCATTACAGCATGAGAACAGCAGGTTTATTACTCTCACTAAAGACAGAAATGTAGAAA 1020  
Qy 1021 AGGCTGAATTTCTGTAATAAAGCAAAACAGCCTGGCTTTAGCAAGGAGCCAAACATAACAGAT 1080  
Db 1021 AGGCTGAATTTCTGTAATAAAGCAAAACAGCCTGGCTTTAGCAAGGAGCCAAACATAACAGAT 1080  
Qy 1081 GGCTGGAAGTAAGGAACATGTAATGATAGGGGGACTCCAGCACAGAAAAAGGTAG 1140  
Db 1081 GGCTGGAAGTAAGGAACATGTAATGATAGGGGGACTCCAGCACAGAAAAAGGTAG 1140  
Qy 1141 ATCTGAATGCTGATCCCTCTGTGTAGAGAAAAAGAAATGGAATAAGCAGAAAACTGCCATGCT 1200  
Db 1141 ATCTGAATGCTGATCCCTCTGTGTAGAGAAAAAGAAATGGAATAAGCAGAAAACTGCCATGCT 1200  
Qy 1201 CAGAGAACTCTAGAGATPACTGAAGATGTTCTCTGGATAACACATAAATPAGCAGATTCAGA 1260  
Db 1201 CAGAGAACTCTAGAGATPACTGAAGATGTTCTCTGGATAACACATAAATPAGCAGATTCAGA 1260  
Qy 1261 AAGTTAATGAGTGGTTTTCCAGAAAGTGATGAACTGTTAGGTTCTGATGACTCAATGATG 1320  
Db 1261 AAGTTAATGAGTGGTTTTCCAGAAAGTGATGAACTGTTAGGTTCTGATGACTCAATGATG 1320  
Qy 1321 GGAGTCTGTAATCAAAATGCCAAAGTAGCTGATGTAATGGACGTTCTAAATGAGGTAGATG 1380  
Db 1321 GGAGTCTGTAATCAAAATGCCAAAGTAGCTGATGTAATGGACGTTCTAAATGAGGTAGATG 1380  
Qy 1381 AATAATCTGGTTCTTCAGAGAAAAATAGACTTACTTGGCCAGTGATCTTCATGAGGCTTTAA 1440  
Db 1381 AATAATCTGGTTCTTCAGAGAAAAATAGACTTACTTGGCCAGTGATCTTCATGAGGCTTTAA 1440  
Qy 1441 TATGTAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGAGTAATATTTGAAGACAAAATAT 1500  
Db 1441 TATGTAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGAGTAATATTTGAAGACAAAATAT 1500  
Qy 1501 TTGGGAAAACCTATCGGAAGAGGCAAGCCCTCCCAACTTAAGCCATGTAACCTGAAAATC 1560  
Db 1501 TTGGGAAAACCTATCGGAAGAGGCAAGCCCTCCCAACTTAAGCCATGTAACCTGAAAATC 1560  
Qy 1561 TAATTTATAGGAGCATTTGTTTACTGAGCCACACAGATAATACAGAGCGTCCCTCCACAATA 1620  
Db 1561 TAATTTATAGGAGCATTTGTTTACTGAGCCACACAGATAATACAGAGCGTCCCTCCACAATA 1620  
Qy 1621 AATTAAAGCGTAAAGGAGACCTACATCAGCCCTTCATCTGAGGATTTTATCAAGAAAG 1680  
Db 1621 AATTAAAGCGTAAAGGAGACCTACATCAGCCCTTCATCTGAGGATTTTATCAAGAAAG 1680  
Qy 1681 CAGATTTGGCAGTTCAAAAGACTCTGAAATGATAAATCAGGGAACCTAACCAACGGAGC 1740  
Db 1681 CAGATTTGGCAGTTCAAAAGACTCTGAAATGATAAATCAGGGAACCTAACCAACGGAGC 1740  
Qy 1741 AGAATGTTCAAGTCATGAATATTACTAATAGTGGTCAATGAGAAATAAAACAAAGGTGATT 1800  
Db 1741 AGAATGTTCAAGTCATGAATATTACTAATAGTGGTCAATGAGAAATAAAACAAAGGTGATT 1800  
Qy 1801 CTATTTCAAGATGAGAAAAATCCTAACCCTAAGAGTATCACTCGAAAAAGAAATCTGCTTTCA 1860  
Db 1801 CTATTTCAAGATGAGAAAAATCCTAACCCTAAGAGTATCACTCGAAAAAGAAATCTGCTTTCA 1860  
Qy 1861 AAACGAAAGCTGAACCTTATAGAGAGCAGTATAAGCAATATGGAATCTGAAATTAATATCC 1920  
Db 1861 AAACGAAAGCTGAACCTTATAGAGAGCAGTATAAGCAATATGGAATCTGAAATTAATATCC 1920  
Qy 1921 ACAATTCAAAGACACCTTAAAGAAATAGGCTGAGGAGGAAGTCTTCTACAGGCGATATTC 1980  
Db 1921 ACAATTCAAAGACACCTTAAAGAAATAGGCTGAGGAGGAAGTCTTCTACAGGCGATATTC 1980  
Qy 1981 ATGGCTTTGAATCTAGTAGTACAGTAAATCTAAGCCCACTTAATTTGACTGAAATTCGAAA 2040  
Db 1981 ATGGCTTTGAATCTAGTAGTACAGTAAATCTAAGCCCACTTAATTTGACTGAAATTCGAAA 2040  
Qy 2041 TTGATAGTTGTTTCTAGCAGTGAAGAGATAAAGAAAAAAGTACAAACCAATGCCAGTCA 2100  
Db 2041 TTGATAGTTGTTTCTAGCAGTGAAGAGATAAAGAAAAAAGTACAAACCAATGCCAGTCA 2100

Qy 2101 GGCAACGACGAAACCTTACAACTCATGGAAGGTAAAGAACTCTGCAACTGGAGCCAGNAGA 2160  
Db 2101 GGCAACGACGAAACCTTACAACTCATGGAAGGTAAAGAACTCTGCAACTGGAGCCAGNAGA 2160  
Qy 2161 GTAAACAGCCAAATGAACAGACAGCAAGTAAAGACATGACAGCTGATCTTTCCAGAGCTGA 2220  
Db 2161 GTAAACAGCCAAATGAACAGACAGCAAGTAAAGACATGACAGCTGATCTTTCCAGAGCTGA 2220  
Qy 2221 AGTTAAACAAATGACACCTGGTCTTTTACTAAGTGTTCAAATACCAAGTGAATTTAAAGAAAT 2280  
Db 2221 AGTTAAACAAATGACACCTGGTCTTTTACTAAGTGTTCAAATACCAAGTGAATTTAAAGAAAT 2280  
Qy 2281 TTGTCAATCTAGCCTTCCAAAGAGAGAAAAAGAGAAAACTAGAAAAAGTTHAAAGTGT 2340  
Db 2281 TTGTCAATCTAGCCTTCCAAAGAGAGAAAAAGAGAAAACTAGAAAAAGTTHAAAGTGT 2340  
Qy 2341 CTAAATATGCTGAAGACCCCAAGATCTCAATGTTTAAAGTGAGAAAAAGGTTTTGCNAACTG 2400  
Db 2341 CTAAATATGCTGAAGACCCCAAGATCTCAATGTTTAAAGTGAGAAAAAGGTTTTGCNAACTG 2400  
Qy 2401 AAAGATCTGTAGAGAGTAGCAGTATTTCTCTGGTACCTGGTACTGATTTATGGCACTCAGG 2460  
Db 2401 AAAGATCTGTAGAGAGTAGCAGTATTTCTCTGGTACCTGGTACTGATTTATGGCACTCAGG 2460  
Qy 2461 AAAGTATCTCGTTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAAACAGAACCAATTAAT 2520  
Db 2461 AAAGTATCTCGTTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAAACAGAACCAATTAAT 2520  
Qy 2521 GTCTGAGTCACTGTCAGCAGCATTTGAAACCCCAAGGACCTAAATTCATGTTGTTCCAAAG 2580  
Db 2521 GTCTGAGTCACTGTCAGCAGCATTTGAAACCCCAAGGACCTAAATTCATGTTGTTCCAAAG 2580  
Qy 2581 ATAATAGAAATGACACAGAAGGCTTTAAAGTATCCATTGGGACATGAAGTTAAACACAGTC 2640  
Db 2581 ATAATAGAAATGACACAGAAGGCTTTAAAGTATCCATTGGGACATGAAGTTAAACACAGTC 2640  
Qy 2641 GGGAACACAGCATAGAAAAAGAAAGTGAATGAACTTGATGCTCAGTATTTGCGAATACAT 2700  
Db 2641 GGGAACACAGCATAGAAAAAGAAAGTGAATGAACTTGATGCTCAGTATTTGCGAATACAT 2700  
Qy 2701 TCAAGGTTTCAAGCGCCAGTCATTTGCTCTGTTTCCAAATCCAGGAATTCGCAAGAGG 2760  
Db 2701 TCAAGGTTTCAAGCGCCAGTCATTTGCTCTGTTTCCAAATCCAGGAATTCGCAAGAGG 2760  
Qy 2761 AATGTGCAACATTTCTGCCCCACTCTGGGCTCTTAAAGAAACAAAGTCCAAAAGTCACTT 2820  
Db 2761 AATGTGCAACATTTCTGCCCCACTCTGGGCTCTTAAAGAAACAAAGTCCAAAAGTCACTT 2820  
Qy 2821 TTGAATGTGAACAAAAGGAAGAAAAATCAAGGAAAGAAATGAGTCTTAATATCAAGCCTGTAC 2880  
Db 2821 TTGAATGTGAACAAAAGGAAGAAAAATCAAGGAAAGAAATGAGTCTTAATATCAAGCCTGTAC 2880  
Qy 2881 AGACAGTTAATATACATGCGAGGCTTTCTCTGGTGGTTCAGAAAGATAAGCCAGTTGATA 2940  
Db 2881 AGACAGTTAATATACATGCGAGGCTTTCTCTGGTGGTTCAGAAAGATAAGCCAGTTGATA 2940  
Qy 2941 ATGCCAAATCTAGTATCAAAAGGAGGCTTAGGTTTCTCTATCATCTCAGTTCCAGAGGCA 3000  
Db 2941 ATGCCAAATCTAGTATCAAAAGGAGGCTTAGGTTTCTCTATCATCTCAGTTCCAGAGGCA 3000  
Qy 3001 ACGAAACTGGACCTCATTTACTCCAAATAAACATGAGCTTTTACAAAACCCATATCGTATAC 3060  
Db 3001 ACGAAACTGGACCTCATTTACTCCAAATAAACATGAGCTTTTACAAAACCCATATCGTATAC 3060  
Qy 3061 CACCACATTTTCCCATCAAGTCAATTTGTTTAAACTAAATGTAAGAAAAATCTGCTAGAGG 3120  
Db 3061 CACCACATTTTCCCATCAAGTCAATTTGTTTAAACTAAATGTAAGAAAAATCTGCTAGAGG 3120  
Qy 3121 AAACCTTTGAGGACATTTCAATGTCCACTGAAAGAGAAATGGGAAATGAGAACATTTCCAA 3180  
Db 3121 AAACCTTTGAGGACATTTCAATGTCCACTGAAAGAGAAATGGGAAATGAGAACATTTCCAA 3180

QY 3181 GTACAGTACGACAAATAGCCGTAAATAACATTAGAGAAAATGTTTTAAAGGAGCCAGCT 3240  
DB GTACAGTACGACAAATAGCCGTAAATAACATTAGAGAAAATGTTTTAAAGGAGCCAGCT 3240  
QY 3241 CAAGCAATATTAATGAAGTAGGTTCCAGTAGTAATAAGAGTGGGCTCCAGTATTAATGAAA 3300  
DB CAAGCAATATTAATGAAGTAGGTTCCAGTAGTAATAAGAGTGGGCTCCAGTATTAATGAAA 3300  
QY 3301 TAGGTTCCAGTGATGAAGAAACATTCAGCAGAACCTAGGTAGAGAAACAGAGGGGCCAAATTTGA 3360  
DB TAGGTTCCAGTGATGAAGAAACATTCAGCAGAACCTAGGTAGAGAAACAGAGGGGCCAAATTTGA 3360  
QY 3361 ATGCTATGCTTAGATAGGAGTTTGGCAACCTGAGGCTATATAACAAAGTCTTCCCTGGAA 3420  
DB ATGCTATGCTTAGATAGGAGTTTGGCAACCTGAGGCTATATAACAAAGTCTTCCCTGGAA 3420  
QY 3421 GTAATTTGAGCATCTCGAAATATAAAGCAAGCAAGTATGAAGAGTAGTTAGACTGTTA 3480  
DB GTAATTTGAGCATCTCGAAATATAAAGCAAGCAAGTATGAAGAGTAGTTAGACTGTTA 3480  
QY 3481 ATACAGATTTCTCTCCATATCTGATTTTCAGATACCTTAGACAGCCCTATGGGAGTAGTC 3540  
DB ATACAGATTTCTCTCCATATCTGATTTTCAGATACCTTAGACAGCCCTATGGGAGTAGTC 3540  
QY 3541 ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATATAAGG 3600  
DB ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATATAAGG 3600  
QY 3601 AAGTACTAGTTTGTCTGAAATGACATTAAGGAAAGTCTGCTGTTTTAGCAAAAGCG 3660  
DB AAGTACTAGTTTGTCTGAAATGACATTAAGGAAAGTCTGCTGTTTTAGCAAAAGCG 3660  
QY 3661 TCCAGAGAGGAGCTTAGCAGGAGTCTAGCCCTTTCCCCATACACATTTGGCTCAGG 3720  
DB TCCAGAGAGGAGCTTAGCAGGAGTCTAGCCCTTTCCCCATACACATTTGGCTCAGG 3720  
QY 3721 GTTACCGAAGAGGGCCCAAGAAATTAGAGTCTCAGAGAGAACTTATCTAGTGAGGATG 3780  
DB GTTACCGAAGAGGGCCCAAGAAATTAGAGTCTCAGAGAGAACTTATCTAGTGAGGATG 3780  
QY 3781 AAGAGCTTCCGTGTTCCACACATTTGTTTGGTAAAGTAAACATATACCTTCTCAGT 3840  
DB AAGAGCTTCCGTGTTCCACACATTTGTTTGGTAAAGTAAACATATACCTTCTCAGT 3840  
QY 3841 CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGCTTAAGAACACAGAGGAGAAATTTAT 3900  
DB CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGCTTAAGAACACAGAGGAGAAATTTAT 3900  
QY 3901 TATCATTGAAGAATAGCTTAAATGACTGCAGTAACCAAGGTAATATTGGCAAAAGGCATCTC 3960  
DB TATCATTGAAGAATAGCTTAAATGACTGCAGTAACCAAGGTAATATTGGCAAAAGGCATCTC 3960  
QY 3961 AGGAACATACCTTAGTGAGGAAACAAATGTTCTGCTAGCTTGTGTTTTCTTCAGTGCA 4020  
DB AGGAACATACCTTAGTGAGGAAACAAATGTTCTGCTAGCTTGTGTTTTCTTCAGTGCA 4020  
QY 4021 GTGAATTTGGAAGACTTGCAGTGCAGTAACAAACCCAGGATCCTTCTGATTTGGTTCTT 4080  
DB GTGAATTTGGAAGACTTGCAGTGCAGTAACAAACCCAGGATCCTTCTGATTTGGTTCTT 4080  
QY 4081 CCAAAACAAATGAGGCATCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGACAAGGAATGG 4140  
DB CCAAAACAAATGAGGCATCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGACAAGGAATGG 4140  
QY 4141 TTTCAGATGATGAAGAAAGGAAACCGGCTTGGAAAGAAATATCAAGAAAGCAAGCA 4200  
DB TTTCAGATGATGAAGAAAGGAAACCGGCTTGGAAAGAAATATCAAGAAAGCAAGCA 4200  
QY 4201 TGGATTCAAACTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAAACAAAGCGTCTCTGAAG 4260  
DB TGGATTCAAACTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAAACAAAGCGTCTCTGAAG 4260  
QY 4261 ACTGCTCAGGGCTATCCTCTCAGAGTGACATTTTAAACCCTCAGCAGAGGGGATACCATGC 4320

DB 4261 ACTGCTCAGGGCTATCCTCTCAGAGTGACATTTTAAACCATCTCAGCAGAGGGATACCATGC 4320  
QY 4321 AACATAACCTGATAAAGCTCCAGCAGGAAATGCGTGAAGCTGTGTTAGAACAGC 4380  
DB AACATAACCTGATAAAGCTCCAGCAGGAAATGCGTGAAGCTGTGTTAGAACAGC 4380  
QY 4381 ATGGGAGCCAGCCTTCTAAACAGCTACCTTCCATCATTAAGTACTCTCTGCCCTTGAGG 4440  
DB ATGGGAGCCAGCCTTCTAAACAGCTACCTTCCATCATTAAGTACTCTCTGCCCTTGAGG 4440  
QY 4441 ACCTTGGAAAATCCAGAAACAAAGCACATCAGAAAAAGCAGTATTAACTTTCACAGAAAAAGTA 4500  
DB ACCTTGGAAAATCCAGAAACAAAGCACATCAGAAAAAGCAGTATTAACTTTCACAGAAAAAGTA 4500  
QY 4501 GTGAATAACCTTATAAGCCAGAAATCCAGAAAGCCCTTCTGCTGACAAAGTTTGAAGTGTCTG 4560  
DB GTGAATAACCTTATAAGCCAGAAATCCAGAAAGCCCTTCTGCTGACAAAGTTTGAAGTGTCTG 4560  
QY 4561 CAGATAGTTCTACACGTTAAANAATAAGAACACAGAGTGGAAAGGTCAATCCCTTCTTAAT 4620  
DB CAGATAGTTCTACACGTTAAANAATAAGAACACAGAGTGGAAAGGTCAATCCCTTCTTAAT 4620  
QY 4621 GCCCATCATTTAGATGATAGTGGTGTACATGACACAGTTGCTCTGGAGTCTTTCAGAAATAGAA 4680  
DB GCCCATCATTTAGATGATAGTGGTGTACATGACACAGTTGCTCTGGAGTCTTTCAGAAATAGAA 4680  
QY 4681 ACTACCCATCTCAAGAGGAGCTCATTAAGGTTGTTGATGTGGAGGAGCAACAGCTGGAAG 4740  
DB ACTACCCATCTCAAGAGGAGCTCATTAAGGTTGTTGATGTGGAGGAGCAACAGCTGGAAG 4740  
QY 4741 AGTCTGGGCCACACAGATTTTACCGGAACATCTTACTTTCGCAAGGCAAGATCTAGAGGGAA 4800  
DB AGTCTGGGCCACACAGATTTTACCGGAACATCTTACTTTCGCAAGGCAAGATCTAGAGGGAA 4800  
QY 4801 CCCCTTACCTTGAATCTGGAATCAGGCTCTTCTCTGATGACCCCTGGAATCTGATCTTCTG 4860  
DB CCCCTTACCTTGAATCTGGAATCAGGCTCTTCTCTGATGACCCCTGGAATCTGATCTTCTG 4860  
QY 4861 AAGACAGAGCCCAGAGTCTGCTGTTGGCAACATACATCTTCAACCTCTGCATCTGA 4920  
DB AAGACAGAGCCCAGAGTCTGCTGTTGGCAACATACATCTTCAACCTCTGCATCTGA 4920  
QY 4921 AAGTCTCCCAATTTGAAGTTGACAGATCTGCCAGAGGTGACGCTGCTGCTCATCTACTG 4980  
DB AAGTCTCCCAATTTGAAGTTGACAGATCTGCCAGAGGTGACGCTGCTGCTCATCTACTG 4980  
QY 4981 ATACTGCTGGGTATAATGCAATGGAAGAAAGTGTGAGCAGGGAGAGCCAGAAATTCACAG 5040  
DB ATACTGCTGGGTATAATGCAATGGAAGAAAGTGTGAGCAGGGAGAGCCAGAAATTCACAG 5040  
QY 5041 CTTTCAACAGAAAGGGTCAACAAAGAAATGTCCATGTTGTTGCTGGCTGACCCCAAG 5100  
DB CTTTCAACAGAAAGGGTCAACAAAGAAATGTCCATGTTGTTGCTGGCTGACCCCAAG 5100  
QY 5101 AATTTATGCTCGTGTAACAGTTTGGCAGAAAAACACACATCACTTTAACTTAATTA 5160  
DB AATTTATGCTCGTGTAACAGTTTGGCAGAAAAACACACATCACTTTAACTTAATTA 5160  
QY 5161 CTGAAGAGACTACTCATGTTGTTTATGAAAACAGATGCTGAGTTTGTGTGTAACGGACAC 5220  
DB CTGAAGAGACTACTCATGTTGTTTATGAAAACAGATGCTGAGTTTGTGTGTAACGGACAC 5220  
QY 5221 TGAATATTTTCTAGGAAATGCGGAGGAAATGGGTAGTTAGCTATTTCTGGGTGACCC 5280  
DB TGAATATTTTCTAGGAAATGCGGAGGAAATGGGTAGTTAGCTATTTCTGGGTGACCC 5280  
QY 5281 AGTCTATTTAAAGAAAGAAATGCTCAATGACGATGATTTGAGTTCAGAGGAGATGTTGG 5340  
DB AGTCTATTTAAAGAAAGAAATGCTCAATGACGATGATTTGAGTTCAGAGGAGATGTTGG 5340  
QY 5341 TCAATGGAAGAAACCAAGGCTCAAGCGAGAGAAATCCAGGACAGAAAGATCT 5400



Db 5341 TCAATGGAAGAACCAAGGTCCTCAAGGAGCAAGAGAAATCCAGGACAGAAAGATCT 5400  
 Qy TCAGGGGGCTAGAAATCTGTGCTATGAGGCGCTTCCACCAACATGCCACAGATCAACTGG 5460  
 Db TCAGGGGGCTAGAAATCTGTGCTATGAGGCGCTTCCACCAACATGCCACAGATCAACTGG 5460  
 Qy AATGGATGGTACAGCTGTGGTCTTCTGTGGTGAAGGAGCTTTCATCATCACCCTTG 5520  
 Db AATGGATGGTACAGCTGTGGTCTTCTGTGGTGAAGGAGCTTTCATCATCACCCTTG 5520  
 Qy GCACAGGTGTCCACCCCAATGTGGTGTGCGAGCCAGATGCTGACAGAGGACAAATGGCT 5580  
 Db GCACAGGTGTCCACCCCAATGTGGTGTGCGAGCCAGATGCTGACAGAGGACAAATGGCT 5580  
 Qy TCCATGCAATTTGGGCGAGATGTGAGGACACCTGTGGTGACCCGAGAGTGGGTGTTGGACA 5640  
 Db TCCATGCAATTTGGGCGAGATGTGAGGACACCTGTGGTGACCCGAGAGTGGGTGTTGGACA 5640  
 Qy GTGTAGCACTTACAGTGCAGGAGCTGGACACCTTACCTGATACCCGAGATCCCCCACA 5700  
 Db GTGTAGCACTTACAGTGCAGGAGCTGGACACCTTACCTGATACCCGAGATCCCCCACA 5700  
 Qy GCCACTACTGA 5711  
 Db GCCACTACTGA 5711

## RESULT 4

AAC60793  
 ID AAC60793 standard; cDNA; 5711 BP.  
 XX  
 AC AAC60793;  
 DT 07-FEB-2001 (first entry)  
 XX Human BRCA1 (om1) nucleotide sequence SEQ ID NO:1.  
 DE Human; BRCA1; chromosome 17; 17q21; breast cancer; ovarian cancer;  
 KW gene therapy; diagnosis; cytostatic; genetic susceptibility; mutation;  
 KW polymorphism; identification; ss.  
 XX Homo sapiens.

XX US6130322-A.  
 XX 10-OCT-2000.  
 XX 06-MAY-1998; 98US-0074476.  
 XX 12-FEB-1996; 96US-0598591.  
 XX 12-DEC-1997; 97US-0798691.  
 XX (GENE-) GENE LOGIC INC.  
 XX Zeng B, Thurber D, Olson SJ, Alvares CP, Allen ACP, Murphy PD;  
 PI Critz BS;  
 XX WPI; 2000-646756/62.  
 XX P-PSDB; AAB24217.

XX New coding sequence of the human BRCA1 gene, i.e. BRCA1 (om12), useful  
 in gene therapy, especially for preventing or treating breast or  
 PT ovarian cancer, as well as for diagnosing or monitoring breast or  
 PT ovarian cancer.

XX Example 2; Column 29-36; 56pp; English.

XX AAC60793 to AAC60795 encode the human BRCA1 (om1-3) proteins given in  
 CC AAB24217 to AAB24219 respectively. BRCA1 is found on chromosome 17  
 CC mapping to position 17q21. The BRCA1 (om12) coding sequence is  
 CC specifically claimed in the present invention. The BRCA1 (om12) coding  
 CC sequence is useful in gene therapy, especially for preventing or treating  
 CC breast or ovarian cancer. It is also useful for diagnosing or monitoring

CC breast or ovarian cancer. Furthermore, the BRCA1 (om12) coding sequence  
 CC is useful for: (a) identifying individuals having BRCA1 gene mutations  
 CC and having an increased genetic susceptibility to breast or ovarian  
 CC cancer, or identifying a mutation that increases the genetic  
 CC susceptibility to breast or ovarian cancer; (b) avoiding  
 CC misinterpretation of polymorphisms found in the BRCA1 gene; (c)  
 CC determining the presence of a previously unknown mutation in the BRCA1  
 CC gene; (d) probing a human sample of the BRCA1 gene by allele to determine  
 CC the presence of either polymorphic alleles or mutations; and (e)  
 CC performing diagnosis with a reagent derived from the BRCA1 (om1) cDNA  
 CC sequence. AAC60796 to AAC60861 represent PCR primers for the BRCA1 gene,  
 CC which are used in an example from the present invention.  
 XX  
 SQ Sequence 5711 BP; 1953 A; 1099 C; 1277 G; 1382 T; 0 other;  
 Query Match 100.0%; Score 5711; DB 21; Length 5711;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 AGTTCGTGAGACTTCTGGACCCCGCACAGGCTGTGGGGTTTCTCAGATAACTGGGCC 60  
 Db 1 AGTTCGTGAGACTTCTGGACCCCGCACAGGCTGTGGGGTTTCTCAGATAACTGGGCC 60  
 Qy 61 CCTGCGCTCAGGAGGCGCTTCAACCTCTGCTTGGTAAAGTTTCAATGGAACAGAAAGAA 120  
 Db 61 CCTGCGCTCAGGAGGCGCTTCAACCTCTGCTTGGTAAAGTTTCAATGGAACAGAAAGAA 120  
 Qy 121 TGGATTTATCTGCTCTTCGGGTTGAAGAAGTACAAAATGTCAATTAATGCTATGAGAAA 180  
 Db 121 TGGATTTATCTGCTCTTCGGGTTGAAGAAGTACAAAATGTCAATTAATGCTATGAGAAA 180  
 Qy 181 TCTTAGAGTGTCCCATCTGTCTGGAGTTGATCAAGGAACCTGTCTCCACAAAGTGTGACC 240  
 Db 181 TCTTAGAGTGTCCCATCTGTCTGGAGTTGATCAAGGAACCTGTCTCCACAAAGTGTGACC 240  
 Qy 241 ACATATTTTGCATTTTGTGATGCTGAACTTCTCAACACAGAAAGGGGCTTTCACAGT 300  
 Db 241 ACATATTTTGCATTTTGTGATGCTGAACTTCTCAACACAGAAAGGGGCTTTCACAGT 300  
 Qy 301 GTCTTTTATGTAAGAATGATATAACCAAAAGGAGCCTACAAAGAAAGTACGAGATTTAGTC 360  
 Db 301 GTCTTTTATGTAAGAATGATATAACCAAAAGGAGCCTACAAAGAAAGTACGAGATTTAGTC 360  
 Qy 361 AACTTTGTTGAAGAGCTATTGAAATCATTTGTGCTTTTTCAGCTTTGACACAGTTGGAGT 420  
 Db 361 AACTTTGTTGAAGAGCTATTGAAATCATTTGTGCTTTTTCAGCTTTGACACAGTTGGAGT 420  
 Qy 421 ATGCAAAACAGCTATAATTTTGCACAAAAGGAAATAACTCTCTCTGAAACATCTAAAGATG 480  
 Db 421 ATGCAAAACAGCTATAATTTTGCACAAAAGGAAATAACTCTCTCTGAAACATCTAAAGATG 480  
 Qy 481 AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTCCCAAAAGACTTCTACAGAGTG 540  
 Db 481 AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTCCCAAAAGACTTCTACAGAGTG 540  
 Qy 541 AACCCGAAAATCCCTTCTGAGGAAAACAGTCTCAGTGTCCAACTCTCTAACCTTGGAA 600  
 Db 541 AACCCGAAAATCCCTTCTGAGGAAAACAGTCTCAGTGTCCAACTCTCTAACCTTGGAA 600  
 Qy 601 CTGTGAGAACTCTGAGGACAAAAGCAGGGATACAACTCTCAAAAGACGCTCTGTACATTTG 660  
 Db 601 CTGTGAGAACTCTGAGGACAAAAGCAGGGATACAACTCTCAAAAGACGCTCTGTACATTTG 660  
 Qy 661 AATTGGGATCTGATTCTTCAAGATACCGTTAATAGGCAACTTATTGACAGTGGGAG 720  
 Db 661 AATTGGGATCTGATTCTTCAAGATACCGTTAATAGGCAACTTATTGACAGTGGGAG 720  
 Qy 721 ATCAAGAAATTTTACAAATCACCCCTCAAGGAACAGGGATCAAAATCAGTTTGAATCTG 780  
 Db 721 ATCAAGAAATTTTACAAATCACCCCTCAAGGAACAGGGATCAAAATCAGTTTGAATCTG 780  
 Qy 781 CAAAAAGGCTGTGTGAATTTTCTGAGACGGATGTAAACAAATCTGAAACATCATCAAC 840  
 Db 781 CAAAAAGGCTGTGTGAATTTTCTGAGACGGATGTAAACAAATCTGAAACATCATCAAC 840

Db	781	CAAAAAGGCTGCTGTGGAATTTTCTTGAGACGGATGTAA	CAAAATCTGAAACATCATCAAC	840
Qy	841	CCAGTAAATAATGATTTGAAACCACTAGAGAACGCTG	CAGCTGAGAGGCATCCAGAAAAGT	900
Db	841	CCAGTAAATAATGATTTGAAACCACTAGAGAACGCTG	CAGCTGAGAGGCATCCAGAAAAGT	900
Qy	901	ATCAGGGTAGTTCGTGTTTCAAACCTTGATGTGGAGCC	ATGTGGCACAAAATACTCATGCCA	960
Db	901	ATCAGGGTAGTTCGTGTTTCAAACCTTGATGTGGAGCC	ATGTGGCACAAAATACTCATGCCA	960
Qy	961	GCTCATTTACGACATGAGAACGACGAGTTTATTACT	CACTTAAAGACAGATGAATGTAGAA	1020
Db	961	GCTCATTTACGACATGAGAACGACGAGTTTATTACT	CACTTAAAGACAGATGAATGTAGAA	1020
Qy	1021	AGGCTGAAATTCGTAAATAAAAGCAACAGCCTGCTT	AGCAAGGAGCCAAACATAACAGAT	1080
Db	1021	AGGCTGAAATTCGTAAATAAAAGCAACAGCCTGCTT	AGCAAGGAGCCAAACATAACAGAT	1080
Qy	1081	GGGCTGGAAGTAAAGAAACATGTAAATGATAGCGGAT	CTCCAGCACAGAAAAAAGGTAG	1140
Db	1081	GGGCTGGAAGTAAAGAAACATGTAAATGATAGCGGAT	CTCCAGCACAGAAAAAAGGTAG	1140
Qy	1141	ATCTGAATGCTGATCCCTGTGTCAGAGAAAAGAAAT	CGAATAAGCAGAAATGCCATGCT	1200
Db	1141	ATCTGAATGCTGATCCCTGTGTCAGAGAAAAGAAAT	CGAATAAGCAGAAATGCCATGCT	1200
Qy	1201	CAGAGAACTCTAGAGATACCTCAACATGTTCTCTGG	ATAACACTAAATAGCAGCAATTCAGA	1260
Db	1201	CAGAGAACTCTAGAGATACCTCAACATGTTCTCTGG	ATAACACTAAATAGCAGCAATTCAGA	1260
Qy	1261	AAGTTAATGATGGTGTTCACAGAAATGATGAACCT	GTGTAGGTTCTGTGATGACTCACATGATG	1320
Db	1261	AAGTTAATGATGGTGTTCACAGAAATGATGAACCT	GTGTAGGTTCTGTGATGACTCACATGATG	1320
Qy	1321	GGGAGTCTGAAATCAAAATGCCAAAGTACTGATGT	ATTGAGAGCTTTAAATGAGGTAGATG	1380
Db	1321	GGGAGTCTGAAATCAAAATGCCAAAGTACTGATGT	ATTGAGAGCTTTAAATGAGGTAGATG	1380
Qy	1381	AATATCTGGTCTTTCAGAGAAAATAGACTTTACT	GGCCAGTGTCTTCATGAGGCTTTAA	1440
Db	1381	AATATCTGGTCTTTCAGAGAAAATAGACTTTACT	GGCCAGTGTCTTCATGAGGCTTTAA	1440
Qy	1441	TATGTAAGAAGTGAAAGAGTTTCACTCCAAATCAG	TAGAGAGTAAATATTGAAAGACAAATAT	1500
Db	1441	TATGTAAGAAGTGAAAGAGTTTCACTCCAAATCAG	TAGAGAGTAAATATTGAAAGACAAATAT	1500
Qy	1501	TTGGGAAAACTATCGGAAGAGGCAAGCCTCCCAA	CTTAAGCCATGTAACTGAAAATC	1560
Db	1501	TTGGGAAAACTATCGGAAGAGGCAAGCCTCCCAA	CTTAAGCCATGTAACTGAAAATC	1560
Qy	1561	TAATTTATAGAGCAATTTGTTACTGAGCCACAGAT	AAATACAGAGCGTCCCTCCACAAATA	1620
Db	1561	TAATTTATAGAGCAATTTGTTACTGAGCCACAGAT	AAATACAGAGCGTCCCTCCACAAATA	1620
Qy	1621	AAATTAAGCGTAAAAAGGAGACCTACATCAGGCC	CTTCATCTGAGGATTTTATCAAGAAAG	1680
Db	1621	AAATTAAGCGTAAAAAGGAGACCTACATCAGGCC	CTTCATCTGAGGATTTTATCAAGAAAG	1680
Qy	1681	CAGATTTGGCAGTTCAAAGACTCTCTGAAATGAT	AAATACAGGGAATTAACCAAACGGAGC	1740
Db	1681	CAGATTTGGCAGTTCAAAGACTCTCTGAAATGAT	AAATACAGGGAATTAACCAAACGGAGC	1740
Qy	1741	AGAAATGCTCAAGTGATGAATATTACTTAATAGT	GGTCAATGAGATAAACAAGGTGATTT	1800
Db	1741	AGAAATGCTCAAGTGATGAATATTACTTAATAGT	GGTCAATGAGATAAACAAGGTGATTT	1800
Qy	1801	CTATTTCAGAATGAGAAAAATCCTTAACCAAT	TAGAAATCACTCGAAAAAGAAATCTGCTTTCA	1860
Db	1801	CTATTTCAGAATGAGAAAAATCCTTAACCAAT	TAGAAATCACTCGAAAAAGAAATCTGCTTTCA	1860
Qy	1861	AAACGAAAGCTGAACCTTATAGCAGCAGTATAAG	CAATATTGGAACCTCGAAATATAATATCC	1920
Db	1861	AAACGAAAGCTGAACCTTATAGCAGCAGTATAAG	CAATATTGGAACCTCGAAATATAATATCC	1920

Qy	1921	ACAATTCAAAAGCACCTTA	AAAAGAAATAGGCTG	GGAGGAAGTCTTCTTAC	CAGGCATATTC	1988
Db	1921	ACAATTCAAAAGCACCTTA	AAAAGAAATAGGCTG	GGAGGAAGTCTTCTTAC	CAGGCATATTC	1988
Qy	1981	ATGCGCTTTGAATCTAGT	AGTACAGTAAAGCTCTA	AGCCCACTAATTCGTACT	GAATTTGCAAA	2040
Db	1981	ATGCGCTTTGAATCTAGT	AGTACAGTAAAGCTCTA	AGCCCACTAATTCGTACT	GAATTTGCAAA	2040
Qy	2041	TTGATAGTTGTTCTAGC	AGTGAAGATAAAGAAAAA	AGTACAAACCAATG	CCCAATGCCAGTCA	2100
Db	2041	TTGATAGTTGTTCTAGC	AGTGAAGATAAAGAAAAA	AGTACAAACCAATG	CCCAATGCCAGTCA	2100
Qy	2101	GGCACAGCAAAACCTTCA	CTCACTCATGGAGGTAAGA	CACTGCAACTG	GAGCCGAAGA	2160
Db	2101	GGCACAGCAAAACCTTCA	CTCACTCATGGAGGTAAGA	CACTGCAACTG	GAGCCGAAGA	2160
Qy	2161	GTAAACAGCCAAATGAAC	AGACAAGTAAAGACATG	ACACAGTATCTTTCC	CAGAGCTGA	2220
Db	2161	GTAAACAGCCAAATGAAC	AGACAAGTAAAGACATG	ACACAGTATCTTTCC	CAGAGCTGA	2220
Qy	2221	AGTTAACAAATGACCTG	GTCTTTTCTAAGTGTTC	AAATACCGAGTGAAC	CTTAAAGAAT	2280
Db	2221	AGTTAACAAATGACCTG	GTCTTTTCTAAGTGTTC	AAATACCGAGTGAAC	CTTAAAGAAT	2280
Qy	2281	TTGTCAATCTGACCTTCC	AAAGAGAAAGAAAGAG	AGAACTAGAGAACAG	TTAAAGTGT	2340
Db	2281	TTGTCAATCTGACCTTCC	AAAGAGAAAGAAAGAG	AGAACTAGAGAACAG	TTAAAGTGT	2340
Qy	2341	CTAATAATGCTGAAGAC	CCCCAAAGATCTCATG	TAAAGTGGAGAAAGG	TTTTGCAAACTG	2400
Db	2341	CTAATAATGCTGAAGAC	CCCCAAAGATCTCATG	TAAAGTGGAGAAAGG	TTTTGCAAACTG	2400
Qy	2401	AAAGATCTGTAGAGAGT	AGCAGTATTTTCACTGG	TACTGGTACTGATATG	GCACCTCAGG	2460
Db	2401	AAAGATCTGTAGAGAGT	AGCAGTATTTTCACTGG	TACTGGTACTGATATG	GCACCTCAGG	2460
Qy	2461	AAAGTATCTCGTTTAC	TGGAAGTTAGCACTCT	AGGGAAGGCAAAAA	CAGAACCAATTAAT	2520
Db	2461	AAAGTATCTCGTTTAC	TGGAAGTTAGCACTCT	AGGGAAGGCAAAAA	CAGAACCAATTAAT	2520
Qy	2521	GTGTGAGTCAAGTGTG	CAGCATTTTGA	AAACCCCAAGGCACTA	ATTCATGTTGTTCC	2580
Db	2521	GTGTGAGTCAAGTGTG	CAGCATTTTGA	AAACCCCAAGGCACTA	ATTCATGTTGTTCC	2580
Qy	2581	ATAATAGAAATGACAC	AGAGGCTTTTAAAGTAT	TCCATTGGGACATGA	AGTTTAAACCAAGT	2640
Db	2581	ATAATAGAAATGACAC	AGAGGCTTTTAAAGTAT	TCCATTGGGACATGA	AGTTTAAACCAAGT	2640
Qy	2641	GGGAAACAAGCATAG	AAATGGGAAGTGAAC	CTTGATCTCAGTAT	TTTGCAGAAATACAT	2700
Db	2641	GGGAAACAAGCATAG	AAATGGGAAGTGAAC	CTTGATCTCAGTAT	TTTGCAGAAATACAT	2700
Qy	2701	TCAAGGTTTTCAAGCC	CACTCATTTGCTCTG	TTTCAAACTCAGG	AAATGCAAGAGG	2760
Db	2701	TCAAGGTTTTCAAGCC	CACTCATTTGCTCTG	TTTCAAACTCAGG	AAATGCAAGAGG	2760
Qy	2761	AATGTGCAACATTTCT	CTGCCACTCTGGGCT	CTTAAAGAAA	CAAAAGTCCAAAGT	2820
Db	2761	AATGTGCAACATTTCT	CTGCCACTCTGGGCT	CTTAAAGAAA	CAAAAGTCCAAAGT	2820
Qy	2821	TTGAATGTGAA	CAAAAGGAAGAAAT	CAAGGAAGAAATG	AGTCTAATATCAAG	2880
Db	2821	TTGAATGTGAA	CAAAAGGAAGAAAT	CAAGGAAGAAATG	AGTCTAATATCAAG	2880
Qy	2881	AGACAGTTAATATCA	CTGCAGGCTTTCC	TGTTGTTGTCAG	AAAGATAGCCAGT	2940
Db	2881	AGACAGTTAATATCA	CTGCAGGCTTTCC	TGTTGTTGTCAG	AAAGATAGCCAGT	2940
Qy	2941	ATGCCAAATGTAGTAT	CAAGAGGCTCTAGG	TTTTTGTCTATCAT	CTCATGTTT	3000
Db	2941	ATGCCAAATGTAGTAT	CAAGAGGCTCTAGG	TTTTTGTCTATCAT	CTCATGTTT	3000



```
Db 5161 CTGAAGAGACTACTGCTGTTGTAATGAAGAAACAGATGCTGAGTTGTGTGTGAACGGACAC 5220
Qy 5221 TGAATATTTTCTAGGAATTCGGGAGGAGAAATGGGTAGTTAGCTATTTCTTGGGTGACCC 5280
Db 5221 TGAATATTTTCTAGGAATTCGGGAGGAGAAATGGGTAGTTAGCTATTTCTTGGGTGACCC 5280
Qy 5281 AGTCTATTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAGAGGATGCG 5340
Db 5281 AGTCTATTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAGAGGATGCG 5340
Qy 5341 TCAATGAGAAACCCACCAAGGTCCTCAAGCGAGCAAGAGATCCAGGACAGAAAGATCT 5400
Db 5341 TCAATGAGAAACCCACCAAGGTCCTCAAGCGAGCAAGAGATCCAGGACAGAAAGATCT 5400
Qy 5401 TCAGGGGCTAGAAATCTGTTGCTATGCGCCCTTCACCAACATGCCACAGATCAACTGG 5460
Db 5401 TCAGGGGCTAGAAATCTGTTGCTATGCGCCCTTCACCAACATGCCACAGATCAACTGG 5460
Qy 5461 AATGGATGGTACAGCTGTGTGCTCTTCTGTGTGAAGGAGCTTTTCATCATTCACCCCTTG 5520
Db 5461 AATGGATGGTACAGCTGTGTGCTCTTCTGTGTGAAGGAGCTTTTCATCATTCACCCCTTG 5520
Qy 5521 GCACAGTGTCCACCAATGTTGTTGTGTCAGCCAGATGCTGACAGAGACAAATGGCT 5580
Db 5521 GCACAGTGTCCACCAATGTTGTTGTGTCAGCCAGATGCTGACAGAGACAAATGGCT 5580
Qy 5581 TCCATGCAATTTGGGCAGATGTGTGAGGCACCTGTGTGTGACCCGAGTGGGTGTTGGACA 5640
Db 5581 TCCATGCAATTTGGGCAGATGTGTGAGGCACCTGTGTGTGACCCGAGTGGGTGTTGGACA 5640
Qy 5641 GTGTAGCACTCTACAGTGCAGGAGCTGGACACCTACCTGATACCCAGATCCCCCACA 5700
Db 5641 GTGTAGCACTCTACAGTGCAGGAGCTGGACACCTACCTGATACCCAGATCCCCCACA 5700
Qy 5701 GCCACTACTGA 5711
Db 5701 GCCACTACTGA 5711

RESULT 5
ID AAV46470 standard; cDNA; 5711 BP.
XX
AC AAV46470;
XX
DT 18-NOV-1998 (first entry)
XX
DE Human BRCA1 omi3 polymorphism #6 cDNA.
XX
KW BRCA1; omi3; human; breast and ovarian cancer predisposing gene;
KW polymorphism; susceptibility; anti-oncogene; tumour suppressor;
KW Chromosome 17q; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 120..5711
FT /*tag= a
FT /product= "BRCA1 omi3 protein"
FT variation 4427
FT /*tag= b
FT /note= "This polymorphic variation can be a T or C
nucleotide"
XX
FN US5750400-A.
XX
PD 12-MAY-1998.
XX
PF 12-FEB-1997; 97US-0798691.
XX
PR 12-FEB-1996; 96US-0598591.
PR 12-FEB-1997; 97US-0798691.
XX
```

PA (ONCO-) ONCORMED INC.

XX Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ;

PI Schelter DB, Zeng B;

XX WPI; 1998-296774/26.

DR BRCA1 omi gene coding sequences - useful for distinguishing between

XX polymorphisms and mutation(s) in the screening for disposition to

PT Breast or ovarian cancer

XX Claim 2e; Page -; 54pp; English.

PS This sequence encodes a human BRCA1 (breast and ovarian cancer

XX predisposing gene) omi3 gene in which a polymorphic variation occurs at

CC nucleotide 427. This sequence and other polymorphic variations of this

CC sequence are useful for the identification of an individual who may or

CC may not have an increased susceptibility to breast or ovarian cancer.

CC The sequences used identify gene changes which are due to polymorphisms,

CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour

CC suppressor) which is involved in genetic inheritance of cancers,

CC especially breast and ovarian cancer. It is found at human chromosome

CC 17q which is known to be linked to cancer susceptibility, especially

CC breast cancer. Cells containing a mutation in this gene lose the

CC wild-type function of BRCA1 and are more susceptible to cancers.

CC NOTE: This sequence does not appear in the specification but has been

CC created from the wild type BRCA1 omi3 gene represented in AAV46450.

XX Sequence 5711 BP; 1953 A; 1098 C; 1277 G; 1382 T; 1 other;

SQ Query Match 100.0%; Score 5710.6; DB 19; Length 5711;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTCGCTGAGACTTCTGGACCCCGCACAGGCTGTGGGGTTTCTCAGATAAAGTGGCC 60

Db 1 AGTCGCTGAGACTTCTGGACCCCGCACAGGCTGTGGGGTTTCTCAGATAAAGTGGCC 60

Qy 61 CTTGCGCTCAGAGGCTTCCACCTCTGCTCTGGTAAAGTTTCTTGGACAGAAAGAAA 120

Db 61 CTTGCGCTCAGAGGCTTCCACCTCTGCTCTGGTAAAGTTTCTTGGACAGAAAGAAA 120

Qy 121 TGGATTTATCTGCTCTTGGGTTTGAAGAGTACAAAATGTCATTATGCTATGCATGACAGAAA 180

Db 121 TGGATTTATCTGCTCTTGGGTTTGAAGAGTACAAAATGTCATTATGCTATGCATGACAGAAA 180

Qy 181 TCTTAGAGTGTCCCATCTGCTGAGTGTGATCAAGGAACCTGTCTCCAAAGTGTGACC 240

Db 181 TCTTAGAGTGTCCCATCTGCTGAGTGTGATCAAGGAACCTGTCTCCAAAGTGTGACC 240

Qy 241 ACATATTTTGCATTTTGCATGCTGAACTTCTCAACGAGAGAAAGGCGCTTCACAGT 300

Db 241 ACATATTTTGCATTTTGCATGCTGAACTTCTCAACGAGAGAAAGGCGCTTCACAGT 300

Qy 301 GTCTTTTATGTAAGAATGATATAACCAAGAGGAGCTTACAAAGAAAGTACAGATTTAGTC 360

Db 301 GTCTTTTATGTAAGAATGATATAACCAAGAGGAGCTTACAAAGAAAGTACAGATTTAGTC 360

Qy 361 AACTTGTGTAAGAGCTATTGAAAATCATTTGTGCTTTTCAAGTTGACACAGGTTTGGAGT 420

Db 361 AACTTGTGTAAGAGCTATTGAAAATCATTTGTGCTTTTCAAGTTGACACAGGTTTGGAGT 420

Qy 421 ATGCAACAGCTATAATTTTGGAAAAAGGAAAAATACTCTCTGAAACATCTTAAAGATG 480

Db 421 ATGCAACAGCTATAATTTTGGAAAAAGGAAAAATACTCTCTGAAACATCTTAAAGATG 480

Qy 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAAGAGCTTCTACAGAGTG 540

Db 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAAGAGCTTCTACAGAGTG 540

Qy 541 AACCCGAAAAATCTCTCTTGCAGGAAACCAAGTCTCAGTGTCCAACTCTCTAACTCTGAA 600

Db 541 AACCCGAAAAATCTCTCTTGCAGGAAACCAAGTCTCAGTGTCCAACTCTCTAACTCTGAA 600

Qy	601	CTGTGAGAACTCTCAGGACAAAGCAGCGGATACAACTCAAAAGACGCTCTGTCTACATTG	660
Dd	601	CTGTGAGAACTCTCAGGACAAAGCAGCGGATACAACTCAAAAGACGCTCTGTCTACATTG	660
Qy	661	AATTGGGATCTGATCTCTTGAAGATACCGTTAATAAGGCACACTTATTCAGTGTGGAG	720
Dd	661	AATTGGGATCTGATCTCTTGAAGATACCGTTAATAAGGCACACTTATTCAGTGTGGAG	720
Qy	721	ATCAAGAAATGTTTACAATACCCCTCAAGGAACAGGATGAATCAGTTTGGATTCTG	780
Dd	721	ATCAAGAAATGTTTACAATACCCCTCAAGGAACAGGATGAATCAGTTTGGATTCTG	780
Qy	781	CAAAAAAGGCTGCTTGTGAATTTTCTGAGACGGATGAACAAATPACTGAACATCATCAAC	840
Dd	781	CAAAAAAGGCTGCTTGTGAATTTTCTGAGACGGATGAACAAATPACTGAACATCATCAAC	840
Qy	841	CCAGTAATATGATTTGAACACCACTGAGAACGGCTGAGAGGATCCAGAAAGT	900
Dd	841	CCAGTAATATGATTTGAACACCACTGAGAACGGCTGAGAGGATCCAGAAAGT	900
Qy	901	ATCAGGCTAGTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCACAAATACTCATGCCA	960
Dd	901	ATCAGGCTAGTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCACAAATACTCATGCCA	960
Qy	961	GCTCATTTACAGCATGAGAACAGCAGTATTATTTACTCACTAAGACAGAAATGATAGAAA	1020
Dd	961	GCTCATTTACAGCATGAGAACAGCAGTATTATTTACTCACTAAGACAGAAATGATAGAAA	1020
Qy	1021	AGGCTGAATTTCTGTAATAAAGCAACAGCCTGTGCTAGCAAGGACCAACATTAACAGAT	1080
Dd	1021	AGGCTGAATTTCTGTAATAAAGCAACAGCCTGTGCTAGCAAGGACCAACATTAACAGAT	1080
Qy	1081	GGGCTGGAAGTAAGAAACATGTAATGATGGCGACTCCAGCACAGAAAGGATG	1140
Dd	1081	GGGCTGGAAGTAAGAAACATGTAATGATGGCGACTCCAGCACAGAAAGGATG	1140
Qy	1141	ATCTGAATGCTGATCCCTGTGTCAGAGAAAGAAATGGAATAAGCAGAAACCTGCATGCT	1200
Dd	1141	ATCTGAATGCTGATCCCTGTGTCAGAGAAAGAAATGGAATAAGCAGAAACCTGCATGCT	1200
Qy	1201	CAGAGAACTCTAGAGATACTGAAGATGTTCTTGGATAACAATAAGTAGCAGCATTCAGA	1260
Dd	1201	CAGAGAACTCTAGAGATACTGAAGATGTTCTTGGATAACAATAAGTAGCAGCATTCAGA	1260
Qy	1261	AAGTTAATGATGCTTTCCAGAGATGATGAATGTTAGGTTCTGATGACTCAATGATG	1320
Dd	1261	AAGTTAATGATGCTTTCCAGAGATGATGAATGTTAGGTTCTGATGACTCAATGATG	1320
Qy	1321	GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGATTTGGAGCTTCTAAATGAGGTAGATG	1380
Dd	1321	GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGATTTGGAGCTTCTAAATGAGGTAGATG	1380
Qy	1381	AATATTCCTGTTCTTCAGAGAAATAGACTTTACTGGCCAGTGATCCTCATGAGGCTTTAA	1440
Dd	1381	AATATTCCTGTTCTTCAGAGAAATAGACTTTACTGGCCAGTGATCCTCATGAGGCTTTAA	1440
Qy	1441	TATGTAAAGTGAAGAGTTCACTCCAAATCAGTAGAGATTAATATTGAAGACAAAATAT	1500
Dd	1441	TATGTAAAGTGAAGAGTTCACTCCAAATCAGTAGAGATTAATATTGAAGACAAAATAT	1500
Qy	1501	TTGGGAAACCTATCGGAAGAGCAAGCCCTCCCACTTAAGCCATGTAATCACTGAAATC	1560
Dd	1501	TTGGGAAACCTATCGGAAGAGCAAGCCCTCCCACTTAAGCCATGTAATCACTGAAATC	1560
Qy	1561	TAATTATAGGAGCATTTGTTACTGAGCCACAGATAATACAGAGCGTCCCCTCACAAATA	1620
Dd	1561	TAATTATAGGAGCATTTGTTACTGAGCCACAGATAATACAGAGCGTCCCCTCACAAATA	1620
Qy	1621	AATTAAGCGTAAAGGAGACCTTACATCAGGCTTTCATCTGAGGATTTTATCAAGAAAG	1680
Dd	1621	AATTAAGCGTAAAGGAGACCTTACATCAGGCTTTCATCTGAGGATTTTATCAAGAAAG	1680

Qy	1681	CAGATTTGGCAGTTCAAAAAGACTCCTGAAATGATAAATCAGGGAACATAACCAAAACGGAGC	1740
Dd	1681	CAGATTTGGCAGTTCAAAAAGACTCCTGAAATGATAAATCAGGGAACATAACCAAAACGGAGC	1740
Qy	1741	AGATGTGTCAAGTGAATTAATTAATAGTGTGTATGAGATAAACAACAAAGGTGATT	1800
Dd	1741	AGATGTGTCAAGTGAATTAATTAATAGTGTGTATGAGATAAACAACAAAGGTGATT	1800
Qy	1801	CTATTTCAGATGAGAAAAATCCTAAACCAATAGAAATCACTCGAAAAAGAAATCTCTTTCA	1860
Dd	1801	CTATTTCAGATGAGAAAAATCCTAAACCAATAGAAATCACTCGAAAAAGAAATCTCTTTCA	1860
Qy	1861	AAAGAAAGCTGAACTTAAAGCAGCAGTATAAGCAATATGAACTCGAAATTAATATCC	1920
Dd	1861	AAAGAAAGCTGAACTTAAAGCAGCAGTATAAGCAATATGAACTCGAAATTAATATCC	1920
Qy	1921	ACAAATTCAGAAAGCACTTAAAGAAAGTATAGGCTGAGGAGAAAGTCTTCTACAGGATATTC	1980
Dd	1921	ACAAATTCAGAAAGCACTTAAAGAAAGTATAGGCTGAGGAGAAAGTCTTCTACAGGATATTC	1980
Qy	1981	ATGGCTTGAATAGTAGTCACTAGTAAATCTTAAGCCCACTTAATTTGTACTGAAATTCGAAA	2040
Dd	1981	ATGGCTTGAATAGTAGTCACTAGTAAATCTTAAGCCCACTTAATTTGTACTGAAATTCGAAA	2040
Qy	2041	TTGATAGTTTCTAGCAGTGAAGATTAAGAAAAAAGTACAAACCAATGCCAGTCA	2100
Dd	2041	TTGATAGTTTCTAGCAGTGAAGATTAAGAAAAAAGTACAAACCAATGCCAGTCA	2100
Qy	2101	GGCAGCAGAGAACTTCAACTCATGGAAGTAAAGAACTGCAACTGGAGCCCAAGAGA	2160
Dd	2101	GGCAGCAGAGAACTTCAACTCATGGAAGTAAAGAACTGCAACTGGAGCCCAAGAGA	2160
Qy	2161	GTAACAAGCCAAATGAAACAGACAGTAAGTAAGACATGACAGTACTTTCCAGAGCTGA	2220
Dd	2161	GTAACAAGCCAAATGAAACAGACAGTAAGTAAGACATGACAGTACTTTCCAGAGCTGA	2220
Qy	2221	AGTTAAACAAATGCACTGGTTCTTTTACTAAGTGTTCAAATACCAGTGAACCTTAAAGAT	2280
Dd	2221	AGTTAAACAAATGCACTGGTTCTTTTACTAAGTGTTCAAATACCAGTGAACCTTAAAGAT	2280
Qy	2281	TTGTCAATCTAGCTTCCAGAGAGAAAGAAAGAGAAACTAGAAACAGTTAAAGTGT	2340
Dd	2281	TTGTCAATCTAGCTTCCAGAGAGAAAGAAAGAGAAACTAGAAACAGTTAAAGTGT	2340
Qy	2341	CTAATAATGCTGAAGACCCCAAGATCTCATGTTTAAAGTGAAGAAAGGTTTGCAAAAG	2400
Dd	2341	CTAATAATGCTGAAGACCCCAAGATCTCATGTTTAAAGTGAAGAAAGGTTTGCAAAAG	2400
Qy	2401	AAAGATCTGTAGAGTAGCAGTATTTTCACTGGTACCTGGTACTGATTTATGGCACTCAGG	2460
Dd	2401	AAAGATCTGTAGAGTAGCAGTATTTTCACTGGTACCTGGTACTGATTTATGGCACTCAGG	2460
Qy	2461	AAAGTATCTGTTACTGGAAAGTTAGCACTCTAGGGAAGGCAAAAACAGAACCAATAAAT	2520
Dd	2461	AAAGTATCTGTTACTGGAAAGTTAGCACTCTAGGGAAGGCAAAAACAGAACCAATAAAT	2520
Qy	2521	GTGTGAGTCTGAGTGCAGCATTTGAAACCCCAAGGAGCTAAATTCATGTTGTTCCAAAG	2580
Dd	2521	GTGTGAGTCTGAGTGCAGCATTTGAAACCCCAAGGAGCTAAATTCATGTTGTTCCAAAG	2580
Qy	2581	ATAATAGAAATGACACAGAAAGGCTTTAAAGTATCCATTTGGGACATGAAGTTAACCAAGTC	2640
Dd	2581	ATAATAGAAATGACACAGAAAGGCTTTAAAGTATCCATTTGGGACATGAAGTTAACCAAGTC	2640
Qy	2641	GGGAAAACAAGCATAGAAATGGAAGAAAGTGAATCTGATGCTCAGTATTTGAGAAATACAT	2700
Dd	2641	GGGAAAACAAGCATAGAAATGGAAGAAAGTGAATCTGATGCTCAGTATTTGAGAAATACAT	2700
Qy	2701	TCAAGGTTTCAAGGCGCAGTCAATTTGCTCTGTTTTCAAAATCCAGGAATCCAGAGAGG	2760
Dd	2701	TCAAGGTTTCAAGGCGCAGTCAATTTGCTCTGTTTTCAAAATCCAGGAATCCAGAGAGG	2760
Qy	2761	AATGTGCAACATTCTCTGCCACTCTGGGCTCTTTAAAGAAACAAAGTCCAAAAGTCACTT	2820

Db 2761 AATGTGCAACATTCTCTGCCCACTCTGGTCTTTAAAGAAACAAAGTCCAAAAGTCACTT 2820  
Qy 2821 TTGTAATGTGAACAAAGGAAGAAATCAAGAAAGAAATGAGTCTAAATATCAAGCCTGTAC 2880  
Db 2821 TTGTAATGTGAACAAAGGAAGAAATCAAGAAAGAAATGAGTCTAAATATCAAGCCTGTAC 2880  
Qy 2881 AGACAGTAAATATCACTGACGCTTTCTGTTGGTTGTTGAGAAAGATAAGCCAGTTCGATA 2940  
Db 2881 AGACAGTAAATATCACTGACGCTTTCTGTTGGTTGTTGAGAAAGATAAGCCAGTTCGATA 2940  
Qy 2941 ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTCCAGAGCA 3000  
Db 2941 ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTCCAGAGCA 3000  
Qy 3001 ACAGAACTGGACTCAATTTACTCCAAATAACATGAGCTTTTACAAAGCCATATCGTATAC 3060  
Db 3001 ACAGAACTGGACTCAATTTACTCCAAATAACATGAGCTTTTACAAAGCCATATCGTATAC 3060  
Qy 3061 CACCACCTTTTCCCATCAAGTCAATTTGTTAAACCTAAATGTAAAGAAATCTGCTAGAGG 3120  
Db 3061 CACCACCTTTTCCCATCAAGTCAATTTGTTAAACCTAAATGTAAAGAAATCTGCTAGAGG 3120  
Qy 3121 AAAACTTTGAGGAACATTCAATGTCACTGAAAGAGAAATGGGAAATGGAACATTTCCAA 3180  
Db 3121 AAAACTTTGAGGAACATTCAATGTCACTGAAAGAGAAATGGGAAATGGAACATTTCCAA 3180  
Qy 3181 GTACAGTGAGCACAAATAGCCGTAATTAACATTAGAGAAATGTTTTAAAGGAGCCAGCT 3240  
Db 3181 GTACAGTGAGCACAAATAGCCGTAATTAACATTAGAGAAATGTTTTAAAGGAGCCAGCT 3240  
Qy 3241 CAAGCAATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATCAAA 3300  
Db 3241 CAAGCAATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATCAAA 3300  
Qy 3301 TAGGTTCCAGTGATGAAAAACATTCAAGCAGAACTAGGTAGAAAACAGAGGSCAAAATTGA 3360  
Db 3301 TAGGTTCCAGTGATGAAAAACATTCAAGCAGAACTAGGTAGAAAACAGAGGSCAAAATTGA 3360  
Qy 3361 ATGCTATGCTTAGATTAGGGTTTTGCAACCTGAGGCTTATAAACAAGTCTTCTCGAA 3420  
Db 3361 ATGCTATGCTTAGATTAGGGTTTTGCAACCTGAGGCTTATAAACAAGTCTTCTCGAA 3420  
Qy 3421 GTAAATGTAGAGTCTTGAATAAAGCAAGAAATGAAGTAGTGTTCAGACTCTTA 3480  
Db 3421 GTAAATGTAGAGTCTTGAATAAAGCAAGAAATGAAGTAGTGTTCAGACTCTTA 3480  
Qy 3481 ATACAGATTTCTCTCCATATCTGATTTAGATAAATTTAGAACAGCCCTATGGGAAGTAGTC 3540  
Db 3481 ATACAGATTTCTCTCCATATCTGATTTAGATAAATTTAGAACAGCCCTATGGGAAGTAGTC 3540  
Qy 3541 ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAG 3600  
Db 3541 ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAG 3600  
Qy 3601 AAGATACCTAGTTTGTCTGAAATGACATTAAGGAAAGTCTGCTGTTTTAGCAAAAAGCG 3660  
Db 3601 AAGATACCTAGTTTGTCTGAAATGACATTAAGGAAAGTCTGCTGTTTTAGCAAAAAGCG 3660  
Qy 3661 TCCAGAGAGGAGCTTAGCAGGAGTCTAGCCCTTTCAACCAATACATTTGGCTCAGG 3720  
Db 3661 TCCAGAGAGGAGCTTAGCAGGAGTCTAGCCCTTTCAACCAATACATTTGGCTCAGG 3720  
Qy 3721 GTTACCAAGAGGGCCCAAGAAATAGAGTCTCAGAGAGAACTTATCTAGTGAGGATG 3780  
Db 3721 GTTACCAAGAGGGCCCAAGAAATAGAGTCTCAGAGAGAACTTATCTAGTGAGGATG 3780  
Qy 3781 AAGAGCTTCCCTGCTTCCAAACACTTGTATTTGGTAAAGTAAACAATATACCTTCTCAGT 3840  
Db 3781 AAGAGCTTCCCTGCTTCCAAACACTTGTATTTGGTAAAGTAAACAATATACCTTCTCAGT 3840  
Qy 3841 CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGTCTAAAGAACACAGAGGAGAAATTTAT 3900

Db 3841 CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGTCTAAAGAACACAGAGGAGAAATTTAT 3900  
Qy 3901 TATCATTTGAAGATAGCTTTAAATGACTGCGATTAACAGGTAATATTGGCAAGGCATCTC 3960  
Db 3901 TATCATTTGAAGATAGCTTTAAATGACTGCGATTAACAGGTAATATTGGCAAGGCATCTC 3960  
Qy 3961 AGGAACATCACTTTAGTGTAGGAAACAAATGTTCTGCTAGCTGTTTCTTTCAGGTGCA 4020  
Db 3961 AGGAACATCACTTTAGTGTAGGAAACAAATGTTCTGCTAGCTGTTTCTTTCAGGTGCA 4020  
Qy 4021 GTGAATTTGGAAGACTTGACTGCAAAATACAAACCCAGGATCCTTTCTGATTTGGTTCTT 4080  
Db 4021 GTGAATTTGGAAGACTTGACTGCAAAATACAAACCCAGGATCCTTTCTGATTTGGTTCTT 4080  
Qy 4081 CCAAAACAAATGAGGCATCAGTCTGAAAGCCAGGAGTTGCTGAGTGACAGGAATTTGG 4140  
Db 4081 CCAAAACAAATGAGGCATCAGTCTGAAAGCCAGGAGTTGCTGAGTGACAGGAATTTGG 4140  
Qy 4141 TTTTCAGATGATGAAGAAAGAGGAAACGGGCTTTGGAAGAAATTAATCAAGAAAGACAAAGCA 4200  
Db 4141 TTTTCAGATGATGAAGAAAGAGGAAACGGGCTTTGGAAGAAATTAATCAAGAAAGACAAAGCA 4200  
Qy 4201 TGGATTTCAAATCTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAAAACAAAGCTCTCTGAAG 4260  
Db 4201 TGGATTTCAAATCTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAAAACAAAGCTCTCTGAAG 4260  
Qy 4261 ACTGCTCAGGCTATCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGATACCAATGC 4320  
Db 4261 ACTGCTCAGGCTATCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGATACCAATGC 4320  
Qy 4321 AACATAACCTGATAAAGCTCCAGCAGGAATGGCTGAATAGAGCTGTGTAGAACAGC 4380  
Db 4321 AACATAACCTGATAAAGCTCCAGCAGGAATGGCTGAATAGAGCTGTGTAGAACAGC 4380  
Qy 4381 ATGGAGCCAGGCTTTAAACAGCTACCCCTTCCATCAATAAGTACTCTCTGCCCTTGAGG 4440  
Db 4381 ATGGAGCCAGGCTTTAAACAGCTACCCCTTCCATCAATAAGTACTCTCTGCCCTTGAGG 4440  
Qy 4441 ACCTGCGAATCCAGAACAGCAGCATCAGAAAAAGCAGTATTAACTTTCAGAAAAAGTA 4500  
Db 4441 ACCTGCGAATCCAGAACAGCAGCATCAGAAAAAGCAGTATTAACTTTCAGAAAAAGTA 4500  
Qy 4501 GTGAATACCCCTATAAGCCAGATCCAGAGGCTTTCTGCTGACAGTGTGAGTGCTG 4560  
Db 4501 GTGAATACCCCTATAAGCCAGATCCAGAGGCTTTCTGCTGACAGTGTGAGTGCTG 4560  
Qy 4561 CAGATAGTTCTACAGTAAATAAAGAACACAGAGTGGAAAGTCAATCCCTTCTAAAT 4620  
Db 4561 CAGATAGTTCTACAGTAAATAAAGAACACAGAGTGGAAAGTCAATCCCTTCTAAAT 4620  
Qy 4621 GCCCATCATTAGATGATAGTGGTCAATGACAGTGTCTCTGGGAGTCTTTCAGAAATAGAA 4680  
Db 4621 GCCCATCATTAGATGATAGTGGTCAATGACAGTGTCTCTGGGAGTCTTTCAGAAATAGAA 4680  
Qy 4681 ACTACCCATCTCAAGAGGAGCTCAATTAAGTGTGTGATGTGGAGGAGCAACAGCTGGAAG 4740  
Db 4681 ACTACCCATCTCAAGAGGAGCTCAATTAAGTGTGTGATGTGGAGGAGCAACAGCTGGAAG 4740  
Qy 4741 AGTCTGGGCCACACGATTTGACGGAAACATCTTACTTGCACAGCAAGATCTAGAGGAA 4800  
Db 4741 AGTCTGGGCCACACGATTTGACGGAAACATCTTACTTGCACAGCAAGATCTAGAGGAA 4800  
Qy 4801 CCCCTTACCTGGAAATCTGGAAATCAGCTCTTCTGATGACCTGTGATCTGATCTTCTG 4860  
Db 4801 CCCCTTACCTGGAAATCTGGAAATCAGCTCTTCTGATGACCTGTGATCTGATCTTCTG 4860  
Qy 4861 AAGACAGAGCCCGAGAGTCACTGCTGTGGCAACATACCATCTTCAACCTCTGCAATGA 4920  
Db 4861 AAGACAGAGCCCGAGAGTCACTGCTGTGGCAACATACCATCTTCAACCTCTGCAATGA 4920  
Qy 4921 AAGTTCCTCCAAATTTGAAGTTGAGAAATCTGCCAGGCTCAGCTGTGCTCATACTACTG 4980  
Db 4921 AAGTTCCTCCAAATTTGAAGTTGAGAAATCTGCCAGGCTCAGCTGTGCTCATACTACTG 4980







QY 361 AACCTGTTGAAGAGCTATGTAAATCATTTGTGCTTTTTCAGCTTGACACAGCTTTGGAGT 420  
DB 361 AACCTGTTGAAGAGCTATGTAAATCATTTGTGCTTTTTCAGCTTGACACAGCTTTGGAGT 420  
QY 421 ATGCAAAACAGCTATAATTTTTCGAAAGGAAATTAATCTCTCCTTGAAACATCTAAAGATG 480  
DB 421 ATGCAAAACAGCTATAATTTTTCGAAAGGAAATTAATCTCTCCTTGAAACATCTAAAGATG 480  
QY 481 AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCAAAGAGCTTCTACAGAGTG 540  
DB 481 AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCAAAGAGCTTCTACAGAGTG 540  
QY 541 AACCCGAAATCCCTTCTCCTTGAGAAACCACTCTCAGTGTCAAATCTCTAACCTTGAA 600  
DB 541 AACCCGAAATCCCTTCTCCTTGAGAAACCACTCTCAGTGTCAAATCTCTAACCTTGAA 600  
QY 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCAAAAGACGTCTGTCTACATTTG 660  
DB 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCAAAAGACGTCTGTCTACATTTG 660  
QY 661 AATTGGGATCTGATTTCTTCAAGATACCGTTAATAAGGCAACTTATTGCAAGTGTGGAG 720  
DB 661 AATTGGGATCTGATTTCTTCAAGATACCGTTAATAAGGCAACTTATTGCAAGTGTGGAG 720  
QY 721 ATCAAGAAATGTTTACAAATCAACCCCTCAAGGAAACCGGATGAAATCAGTTTGGATTTCTG 780  
DB 721 ATCAAGAAATGTTTACAAATCAACCCCTCAAGGAAACCGGATGAAATCAGTTTGGATTTCTG 780  
QY 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGACGGATGTAAACAAATCTGAACATCATCAAC 840  
DB 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGACGGATGTAAACAAATCTGAACATCATCAAC 840  
QY 841 CCAGTAAATATGATTTGAACACCACTGAGAGCGTGCAGCTGAGAGCATCCAGAAAGT 900  
DB 841 CCAGTAAATATGATTTGAACACCACTGAGAGCGTGCAGCTGAGAGCATCCAGAAAGT 900  
QY 901 ATCAGGCTAGTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCACAAATCTCATGCCA 960  
DB 901 ATCAGGCTAGTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCACAAATCTCATGCCA 960  
QY 961 GCTCATTTACAGCATGAGAACGACAGTATTATCTACTTAAGACAGAAATGAATGTAGAAA 1020  
DB 961 GCTCATTTACAGCATGAGAACGACAGTATTATCTACTTAAGACAGAAATGAATGTAGAAA 1020  
QY 1021 AGGCTGAATTTCTGTAATAAAGCAACACAGCTGCTGTAGCAAGGAGCAACATCAACAGAT 1080  
DB 1021 AGGCTGAATTTCTGTAATAAAGCAACACAGCTGCTGTAGCAAGGAGCAACATCAACAGAT 1080  
QY 1081 GGGCTGGAAGTAAAGAAACATGTAAATGATAGGCGGACTCCAGACAGAAAAAGGTAG 1140  
DB 1081 GGGCTGGAAGTAAAGAAACATGTAAATGATAGGCGGACTCCAGACAGAAAAAGGTAG 1140  
QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGGAATTAAGCAGAAATCGCATGCT 1200  
DB 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGGAATTAAGCAGAAATCGCATGCT 1200  
QY 1201 CAGAGAACTCTAGAGATCTGAAGATGTTCTTGGATAACACTAAATAGCAGCAATTCAGA 1260  
DB 1201 CAGAGAACTCTAGAGATCTGAAGATGTTCTTGGATAACACTAAATAGCAGCAATTCAGA 1260  
QY 1261 AAGTTAATGAGTGGTTTTTCCAGAAAGTATGAATCTGTTAGGTTCTGTGATGACTCATCATG 1320  
DB 1261 AAGTTAATGAGTGGTTTTTCCAGAAAGTATGAATCTGTTAGGTTCTGTGATGACTCATCATG 1320  
QY 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGTGAATGTATTGGAGCGTTCTAAATGAGGTAGATG 1380  
DB 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGTGAATGTATTGGAGCGTTCTAAATGAGGTAGATG 1380  
QY 1381 AATATCTGTTCTTTCAGAGAAATAGACTTTACTGGCCAGTGATCTCTCATGAGGCTTTAA 1440  
DB 1381 AATATCTGTTCTTTCAGAGAAATAGACTTTACTGGCCAGTGATCTCTCATGAGGCTTTAA 1440  
QY 1441 TATGTAAAGTGAAGAGTTCCTCCAAATCAGTAGAGATGAATATTGAAAGACAAATAT 1500

DB 1441 TATGTAAAGTGAAGAGTTCCTCCAAATCAGTAGAGATGAATATTGAAAGACAAATAT 1500  
QY 1501 TTGGGAAAACTTATCGGAAGAGGCAAGCCCTCCCAACTTAAGCATGTAACTGAAATC 1560  
DB 1501 TTGGGAAAACTTATCGGAAGAGGCAAGCCCTCCCAACTTAAGCATGTAACTGAAATC 1560  
QY 1561 TAATTATAGGAGCATTTGTTTACTGAGGCACAGATAATACAAAGAGCGTCCCTCACAATA 1620  
DB 1561 TAATTATAGGAGCATTTGTTTACTGAGGCACAGATAATACAAAGAGCGTCCCTCACAATA 1620  
QY 1621 AATTAAAGCGTAAAGAGGACCTACATCAGGCGCTTCTCTAGGATTTTATCAAGAAAG 1680  
DB 1621 AATTAAAGCGTAAAGAGGACCTACATCAGGCGCTTCTCTAGGATTTTATCAAGAAAG 1680  
QY 1681 CAGATTTGGCAGTTCAAAAGACTCTGAAATGATAAATCAGGNACTTAACCAACGAGC 1740  
DB 1681 CAGATTTGGCAGTTCAAAAGACTCTGAAATGATAAATCAGGNACTTAACCAACGAGC 1740  
QY 1741 AGAATGCTCAAGTATGAATATTACTAATAGTGTCTATGAGATAAATAAAGAGTGTATT 1800  
DB 1741 AGAATGCTCAAGTATGAATATTACTAATAGTGTCTATGAGATAAATAAAGAGTGTATT 1800  
QY 1801 CTATTCAAGATGAGAAAAATCTTAACCCCAATAGAAATCACTCGAAAAAGAAATCTGCTTTCA 1860  
DB 1801 CTATTCAAGATGAGAAAAATCTTAACCCCAATAGAAATCACTCGAAAAAGAAATCTGCTTTCA 1860  
QY 1861 AAACGAAAGCTGAACCTTAAAGCAGCATATAGCAATATGGAACCTCGAAATTAATATCC 1920  
DB 1861 AAACGAAAGCTGAACCTTAAAGCAGCATATAGCAATATGGAACCTCGAAATTAATATCC 1920  
QY 1921 ACAATTCAAAAGCACCTTAAAGAAATAGGCTGAGGAGGAAGTCTTTACCAAGGATATTC 1980  
DB 1921 ACAATTCAAAAGCACCTTAAAGAAATAGGCTGAGGAGGAAGTCTTTACCAAGGATATTC 1980  
QY 1981 ATGCGCTTGAACCTAGTAGTCAAGTAAAGTCTTAAGCCACCTAATTTGTAATTCGAAA 2040  
DB 1981 ATGCGCTTGAACCTAGTAGTCAAGTAAAGTCTTAAGCCACCTAATTTGTAATTCGAAA 2040  
QY 2041 TTGATAGTGTCTTCTAGCAGTGAAGATAAGAAAAAAGTACAACTGCACTCA 2100  
DB 2041 TTGATAGTGTCTTCTAGCAGTGAAGATAAGAAAAAAGTACAACTGCACTCA 2100  
QY 2101 GGACACAGCAAACTTACAACTCATGGAAGTAAAGAACTGCACTGGAAGCCAAAGA 2160  
DB 2101 GGACACAGCAAACTTACAACTCATGGAAGTAAAGAACTGCACTGGAAGCCAAAGA 2160  
QY 2161 GTAAACAGCCAAATGAAACAGCAAGTAAAGACATGACAGYGATCTTTCCAGAGCTGA 2220  
DB 2161 GTAAACAGCCAAATGAAACAGCAAGTAAAGACATGACAGYGATCTTTCCAGAGCTGA 2220  
QY 2221 AGTTACAAATGCACCTGGTCTTTTACTAAGTGTTCAAATACCACTTAAAGAT 2280  
DB 2221 AGTTACAAATGCACCTGGTCTTTTACTAAGTGTTCAAATACCACTTAAAGAT 2280  
QY 2281 TTGTCAATCTAGCTTCCAAAGAGAAAGAAAGAGAACTAGAAACAGTTTAAAGTGT 2340  
DB 2281 TTGTCAATCTAGCTTCCAAAGAGAAAGAAAGAGAACTAGAAACAGTTTAAAGTGT 2340  
QY 2341 CTAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGTTTTCGAAACTG 2400  
DB 2341 CTAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGTTTTCGAAACTG 2400  
QY 2401 AAAGATCTGAGAGTAGCAGTATTTCACTGGTACTCTGCTACTGATTTGGCACTCAGG 2460  
DB 2401 AAAGATCTGAGAGTAGCAGTATTTCACTGGTACTCTGCTACTGATTTGGCACTCAGG 2460  
QY 2461 AAAGTATCTGTTTACTGGAAGTAGCACTCTAGGGAAGGCAAAAACAGAACTAAAT 2520  
DB 2461 AAAGTATCTGTTTACTGGAAGTAGCACTCTAGGGAAGGCAAAAACAGAACTAAAT 2520  
QY 2521 GTGTGAGTCAAGTGTGACAGCATTTGAAAAACCCCAAGGAGCTAATTTCTGTTGTTCCAAAG 2580



Qy	4741	AGTCTGGGCCACACAGATTTGACGAAACATCTTACTTCTGCCAAGCCAGATCTAGAGGAA	4800
Db	4741	AGTCTGGGCCACACAGATTTGACGAAACATCTTACTTCTGCCAAGCCAGATCTAGAGGAA	4800
Qy	4801	CCCCTTACTGGAATCTGGAAATCAGCCTTCTCTGTATGATGACCCGTGAATCTGATCCTTCTG	4860
Db	4801	CCCCTTACTGGAATCTGGAAATCAGCCTTCTCTGTATGATGACCCGTGAATCTGATCCTTCTG	4860
Qy	4861	AAGACAGAGCCCGCCAGAGTCAGCTCGTGTGTGGCAAACATACCATCTTCAACTCTG	4920
Db	4861	AAGACAGAGCCCGCCAGAGTCAGCTCGTGTGTGGCAAACATACCATCTTCAACTCTG	4920
Qy	4921	AAGTTCCGCCAAATGAAAGTTGACAGAACTTGCCTCCAGGGTCCAGCTGCTCATACTG	4980
Db	4921	AAGTTCCGCCAAATGAAAGTTGACAGAACTTGCCTCCAGGGTCCAGCTGCTCATACTG	4980
Qy	4981	ATACTGCTGGGTATAATTCGAATGAAGAAAGTGTGACAGGGAGAACCCAGAAATTGACAG	5040
Db	4981	ATACTGCTGGGTATAATTCGAATGGAAGAAAGTGTGACAGGGAGAACCCAGAAATTGACAG	5040
Qy	5041	CTTCAAACAGAAAGGGTCAACAAAAGAAATGCCATGGTGGTGTCTGGCCTGACCCAGAAG	5100
Db	5041	CTTCAAACAGAAAGGGTCAACAAAAGAAATGCCATGGTGGTGTCTGGCCTGACCCAGAAG	5100
Qy	5101	AAATTTATGCTCGTGTACAAAGTTTGCAGAAAACACACATCACTTTAACTAACTAATTA	5160
Db	5101	AAATTTATGCTCGTGTACAAAGTTTGCAGAAAACACACATCACTTTAACTAACTAATTA	5160
Qy	5161	CTGAAGAGACTACTCATCTGTTGTTATGAAAACAGATGCTGAGTTTGTGTGTGAACGGACAC	5220
Db	5161	CTGAAGAGACTACTCATCTGTTGTTATGAAAACAGATGCTGAGTTTGTGTGTGAACGGACAC	5220
Qy	5221	TGAAATAATTTTCTAGGAATTTGCGGGAGGAAAAATGGGTAGTACTATTTCTGGGTGACCC	5280
Db	5221	TGAAATAATTTTCTAGGAATTTGCGGGAGGAAAAATGGGTAGTACTATTTCTGGGTGACCC	5280
Qy	5281	AGTCTATTAAAGAAAGAAAAATGCTGAAATGAGCATGATTTTGAAGTCAGAGGAGATGTGG	5340
Db	5281	AGTCTATTAAAGAAAGAAAAATGCTGAAATGAGCATGATTTTGAAGTCAGAGGAGATGTGG	5340
Qy	5341	TCAATGAAGAAACCCCAAGGTCCTGAAAGCGAGCAAGAGAAATCCAGGACAGAAAGATCT	5400
Db	5341	TCAATGAAGAAACCCCAAGGTCCTGAAAGCGAGCAAGAGAAATCCAGGACAGAAAGATCT	5400
Qy	5401	TCAGGGGCTAGAAATCTGTGCTATGCGGCCCTTCAACAATGCCCAAGATCAACTGG	5460
Db	5401	TCAGGGGCTAGAAATCTGTGCTATGCGGCCCTTCAACAATGCCCAAGATCAACTGG	5460
Qy	5461	AAATGGATGTGACAGCTGTGTGGTGCTTCTGTGGTGAAGGAGCTTTTCAATCAATCACCCCTTG	5520
Db	5461	AAATGGATGTGACAGCTGTGTGGTGCTTCTGTGGTGAAGGAGCTTTTCAATCAATCACCCCTTG	5520
Qy	5521	GCACAGTGTCCACCCCAATTTGTGTTGTGACCGCAGATGCTGTGACAGAGCAATAGGCT	5580
Db	5521	GCACAGTGTCCACCCCAATTTGTGTTGTGACCGCAGATGCTGTGACAGAGCAATAGGCT	5580
Qy	5581	TCCATGCAATTTGGGCAGATGTGTGAGGCACTGTGTGGTGAACCGAGAGTGGGTGTGGACA	5640
Db	5581	TCCATGCAATTTGGGCAGATGTGTGAGGCACTGTGTGGTGAACCGAGAGTGGGTGTGGACA	5640
Qy	5641	GTGTAGCACTCTACAGTGGCCAGAGCTGGACACACTTACCTGATACCCAGATCCCCCACA	5700
Db	5641	GTGTAGCACTCTACAGTGGCCAGAGCTGGACACACTTACCTGATACCCAGATCCCCCACA	5700
Qy	5701	GCCACTACTGA	5711
Db	5701	GCCACTACTGA	5711

RESULT 7

RESULI /  
AAV46452

AAV46452  
ID AAV46452 standard: cDNA: 5711 BP.

XX

AC	AAV46452;	
XX		
DT	18-NOV-1998 (first entry)	
XX		
DE	Human BRCA1 omil polymorphism #2 cDNA.	
XX		
KW	BRCA1; omil; human; breast and ovarian cancer predisposing gene;	
KW	polymorphism; susceptibility; anti-oncogene; tumour suppressor;	
KW	chromosome 17q; ss.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	120..5711
FT		/*tag= a
FT		/product= "BRCA1 omil protein"
FT	variation	2430
FT		/*tag= b
FT		/note= "This polymorphic variation can be a T or C nucleotide"
XX		
FN	US5750400-A.	
XX		
PD	12-MAY-1998.	
XX		
PF	12-FEB-1997; 97US-0798691.	
XX		
PR	12-FEB-1996; 96US-0598591.	
PR	12-FEB-1997; 97US-0798691.	
XX		
PA	(ONCO-) ONCORMED INC.	
XX		
PI	Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SU;	
PI	Schelter DB, Zeng B;	
XX		
DE	WPI; 1998-296774/26.	
XX		
PT	BRCA1 omi gene coding sequences - useful for distinguishing between	
PT	polymorphisms and mutation(s) in the screening for disposition to	
PT	breat or ovarian cancer	
XX		
PS	Claim 2e; Page -; 54pp; English.	

RESULT 7

RESULI /  
AAV46452

AAV46452  
ID AAV46452 standard: cDNA: 5711 BP.

XX

Db 121 TGGATTTATCGCTCTTCGCCGTTGAAGAAGTACAAAATGTCAATTAATGCTATGCATGCAGAAAA 180  
Qy 181 TCTTAGAGTGCCCATCTGTCTGGAGTTGATCAAGGAACCTGTCTCCACAAAAGTGTGACC 240  
Db 181 TCTTAGAGTGCCCATCTGTCTGGAGTTGATCAAGGAACCTGTCTCCACAAAAGTGTGACC 240  
Qy 241 ACATATTTGGCAAAATTTTGCATGTCTGAAATCTTCTCAACAGAGAAAGGGGCTTCAAGT 300  
Db 241 ACATATTTGGCAAAATTTTGCATGTCTGAAATCTTCTCAACAGAGAAAGGGGCTTCAAGT 300  
Qy 301 GTCCCTTATGTAAGATGATATACCAAAAGGAGCCTACAGAAAGTACAGAGATTTAGTC 360  
Db 301 GTCCCTTATGTAAGATGATATACCAAAAGGAGCCTACAGAAAGTACAGAGATTTAGTC 360  
Qy 361 AACTTGTGTGAAGAGCTATTGAAAATCATTTTGTGCTTTTTCAGCTTTGACACAGGTTTGGAGT 420  
Db 361 AACTTGTGTGAAGAGCTATTGAAAATCATTTTGTGCTTTTTCAGCTTTGACACAGGTTTGGAGT 420  
Qy 421 ATGCAAAACAGCTATAATTTTGCAGAAAAGGAAAATAACTCTCTGAAACATCTAAAAGATG 480  
Db 421 ATGCAAAACAGCTATAATTTTGCAGAAAAGGAAAATAACTCTCTGAAACATCTAAAAGATG 480  
Qy 481 AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCAAAAGACTTCTACAGAGTG 540  
Db 481 AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCAAAAGACTTCTACAGAGTG 540  
Qy 541 AACCAGAAAATCTTCTTGCAGGAAACCACTCTCAGTGTCCAACTCTCTAACCTTGGAA 600  
Db 541 AACCAGAAAATCTTCTTGCAGGAAACCACTCTCAGTGTCCAACTCTCTAACCTTGGAA 600  
Qy 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCTCAAAAGACGCTGTGTACATTG 660  
Db 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCTCAAAAGACGCTGTGTACATTG 660  
Qy 661 AATTGGGATCTGATCTTCTGAAGATACCGTTAATAGGCAACTTATTTGCGAGTGTGGAG 720  
Db 661 AATTGGGATCTGATCTTCTGAAGATACCGTTAATAGGCAACTTATTTGCGAGTGTGGAG 720  
Qy 721 ATCAAGAAATCTTACAAATCACCCCTCAAGGAAACAGGGATGAAATCAGTTTGGATCTG 780  
Db 721 ATCAAGAAATCTTACAAATCACCCCTCAAGGAAACAGGGATGAAATCAGTTTGGATCTG 780  
Qy 781 CAAAAAGGCTGCTGTGTAATTTTCTGAGACGGATGTAAACAAATCTGAAACATCATCAAC 840  
Db 781 CAAAAAGGCTGCTGTGTAATTTTCTGAGACGGATGTAAACAAATCTGAAACATCATCAAC 840  
Qy 841 CCAGTAATATGATTTGAAACCACTGAGAAAGCGTGAGAGGATCCAGAAAAGT 900  
Db 841 CCAGTAATATGATTTGAAACCACTGAGAAAGCGTGAGAGGATCCAGAAAAGT 900  
Qy 901 ATCAGGGTAGTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCACAATACTCATGCCA 960  
Db 901 ATCAGGGTAGTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCACAATACTCATGCCA 960  
Qy 961 GCTCATTTACAGCATGAGAAACAGCAGTTTATTTACTCACTTAAGACAGAAATGTAGAAA 1020  
Db 961 GCTCATTTACAGCATGAGAAACAGCAGTTTATTTACTCACTTAAGACAGAAATGTAGAAA 1020  
Qy 1021 AGGCTGAATTTCTGTAATAAAGCAAAACAGCTGTGCTTAGAAGGAGCCAAACATTAACAGAT 1080  
Db 1021 AGGCTGAATTTCTGTAATAAAGCAAAACAGCTGTGCTTAGAAGGAGCCAAACATTAACAGAT 1080  
Qy 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGCGGACTCCAGCAGCAAGAAAAGGTAG 1140  
Db 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGCGGACTCCAGCAGCAAGAAAAGGTAG 1140  
Qy 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGGAATAAGCAGAAAACCTGCCATGCT 1200  
Db 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGGAATAAGCAGAAAACCTGCCATGCT 1200  
Qy 1201 CAGAGAAATCTTAGAGATATCTGAAGATGTTCTTGGATAACTAATAATAGCAGCAATTCAGA 1260

Db 1201 CAGAGAAATCTTAGAGATATCTGAAGATGTTCTCTGGATAAACACTAAATAGCAGCAATTCAGA 1260  
Qy 1261 AAGTTAATAGTGGTGTTCAGAAAGTGAATGAACTGTGTAGGTTCTGTAGACTCAACATGATG 1320  
Db 1261 AAGTTAATAGTGGTGTTCAGAAAGTGAATGAACTGTGTAGGTTCTGTAGACTCAACATGATG 1320  
Qy 1321 GGGAGTCTGAATCAAAATGCCCAGAGTAGCTGATGATTTTGGAGCTTCTAAATGAGGTAGATG 1380  
Db 1321 GGGAGTCTGAATCAAAATGCCCAGAGTAGCTGATGATTTTGGAGCTTCTAAATGAGGTAGATG 1380  
Qy 1381 AATATTCTGTGTTCTTCAGAGAAAATAGACTTACTTGGCCAGTGATCTCTCATGAGGCTTTAA 1440  
Db 1381 AATATTCTGTGTTCTTCAGAGAAAATAGACTTACTTGGCCAGTGATCTCTCATGAGGCTTTAA 1440  
Qy 1441 TATGTAAAGTGAAGAGTTCACCTCCAAATCAGTAGAGAGTAATATTGAAGACAAAATAT 1500  
Db 1441 TATGTAAAGTGAAGAGTTCACCTCCAAATCAGTAGAGAGTAATATTGAAGACAAAATAT 1500  
Qy 1501 TTGGGAAAACCTATCGGAAGAGGCAAGCCCTCCCAACTTTAAGCCATGTAACTGAAAATC 1560  
Db 1501 TTGGGAAAACCTATCGGAAGAGGCAAGCCCTCCCAACTTTAAGCCATGTAACTGAAAATC 1560  
Qy 1561 TAATTATAGGAGCATTTGTTACTTGAGCCACAGATAATACAGAGCGTCCCTCACAATA 1620  
Db 1561 TAATTATAGGAGCATTTGTTACTTGAGCCACAGATAATACAGAGCGTCCCTCACAATA 1620  
Qy 1621 AATTAAAGCGTAAAGAGAGACCTACATCAGGCGCTTCTCTGAGGATTTTATCAAGAAAG 1680  
Db 1621 AATTAAAGCGTAAAGAGAGACCTACATCAGGCGCTTCTCTGAGGATTTTATCAAGAAAG 1680  
Qy 1681 CAGATTTGGCAGTTCAAAAGACTCTCGAATGATAAATCAGGGAACTAACCAACGGAGC 1740  
Db 1681 CAGATTTGGCAGTTCAAAAGACTCTCGAATGATAAATCAGGGAACTAACCAACGGAGC 1740  
Qy 1741 AGAATGCTCAAGTGAATTAATTTACTTAATAGTGTGTCATGAGAAATAAACAAGAGTGAT 1800  
Db 1741 AGAATGCTCAAGTGAATTAATTTACTTAATAGTGTGTCATGAGAAATAAACAAGAGTGAT 1800  
Qy 1801 CTATTTCAGATGAGAAAATCTTAAACCAATAGAAATCACTCGAAAAGAAATCTGCTTTCA 1860  
Db 1801 CTATTTCAGATGAGAAAATCTTAAACCAATAGAAATCACTCGAAAAGAAATCTGCTTTCA 1860  
Qy 1861 AAACGAAAGCTGAACCTTAAAGCAGAGTAAAGCAATATGGAACCTCGAATTAATAATCC 1920  
Db 1861 AAACGAAAGCTGAACCTTAAAGCAGAGTAAAGCAATATGGAACCTCGAATTAATAATCC 1920  
Qy 1921 ACAATTCAAAAGCAGCTTAAAGAAATAGGCTGAGGAGGAAAGTCTTCTACAGGAGATATTC 1980  
Db 1921 ACAATTCAAAAGCAGCTTAAAGAAATAGGCTGAGGAGGAAAGTCTTCTACAGGAGATATTC 1980  
Qy 1981 ATGGCTTGAACCTAGTAGTAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 2040  
Db 1981 ATGGCTTGAACCTAGTAGTAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 2040  
Qy 2041 TTGATAGTGTCTTACAGTGAAGAGATAAAGAAAAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 2100  
Db 2041 TTGATAGTGTCTTACAGTGAAGAGATAAAGAAAAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 2100  
Qy 2101 GGCACACAGAAAACCTTCAAACTCATGGAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 2160  
Db 2101 GGCACACAGAAAACCTTCAAACTCATGGAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 2160  
Qy 2161 GTAAACAGCCAAATGAAACAGACAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 2220  
Db 2161 GTAAACAGCCAAATGAAACAGACAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 2220  
Qy 2221 AGTTAAACAAATGCAACCTGCTGTTTCTTAAAGTGTCAAATACAGTGAACCTTAAAGTAAAGT 2280  
Db 2221 AGTTAAACAAATGCAACCTGCTGTTTCTTAAAGTGTCAAATACAGTGAACCTTAAAGTAAAGT 2280  
Qy 2281 TTGTCAATCTTAGCCTTCCAGAGAGAAAAGAGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 2340  
Db 2281 TTGTCAATCTTAGCCTTCCAGAGAGAAAAGAGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 2340

QY 2341 CTAATAATGCTGAAGACCCCAAGATCTCATGTTAAAGTGAAGAAAGGGTTTTGCAAACTG 2400  
DB 2341 CTAATAATGCTGAAGACCCCAAGATCTCATGTTAAAGTGAAGAAAGGGTTTTGCAAACTG 2400  
QY 2401 AAAGATCTGTAGAGAGTAGCAGTATTTTCACTGGTACCTGGTACTGATTTATGGCACTCAGG 2460  
DB 2401 AAAGATCTGTAGAGAGTAGCAGTATTTTCACTGGTACTGATTTATGGCACTCAGG 2460  
QY 2461 AAAGTATCTGGTTACTGGAAGTTAGCACTCTAGGGAAGGCCAAAACAGAACCAATAAAT 2520  
DB 2461 AAAGTATCTGGTTACTGGAAGTTAGCACTCTAGGGAAGGCCAAAACAGAACCAATAAAT 2520  
QY 2521 GTGTGAGTCAGTGTGACGATTTTCAAAACCCCAAGGACATAATTCATGGTTGTTCCAAAG 2580  
DB 2521 GTGTGAGTCAGTGTGACGATTTTCAAAACCCCAAGGACATAATTCATGGTTGTTCCAAAG 2580  
QY 2581 ATAATAGAAATGACACAGAGGCTTTAAAGTATCCATTTGGGACATGAAGTTAAACCAAGTC 2640  
DB 2581 ATAATAGAAATGACACAGAGGCTTTAAAGTATCCATTTGGGACATGAAGTTAAACCAAGTC 2640  
QY 2641 GGGAAACAGCATAGAAATGGAAGAAAGTGAACCTTGATGCTCAGTATTTGACAGAAATACAT 2700  
DB 2641 GGGAAACAGCATAGAAATGGAAGAAAGTGAACCTTGATGCTCAGTATTTGACAGAAATACAT 2700  
QY 2701 TCAAGGTTTCAAAGGCCAGTCATTTGCTCTGTTTTTCAAATCCAGGAAATGCGAAGAGG 2760  
DB 2701 TCAAGGTTTCAAAGGCCAGTCATTTGCTCTGTTTTTCAAATCCAGGAAATGCGAAGAGG 2760  
QY 2761 AATGTGCAACATCTCTGCCCCACTCTGGTCTTAAAGAAACAAAGTCCAAAAGTCACTT 2820  
DB 2761 AATGTGCAACATCTCTGCCCCACTCTGGTCTTAAAGAAACAAAGTCCAAAAGTCACTT 2820  
QY 2821 TTGAATGTGAACAAAGGAGAAATCAAGAAAGAAATGAGTCTAAATATCAAGCCCTGTAC 2880  
DB 2821 TTGAATGTGAACAAAGGAGAAATCAAGAAAGAAATGAGTCTAAATATCAAGCCCTGTAC 2880  
QY 2881 AGACAGTTAATATCACTGCGAGGCTTTCTGCTGGTGTGTCAGAAAGATAAGCCAGTTGATA 2940  
DB 2881 AGACAGTTAATATCACTGCGAGGCTTTCTGCTGGTGTGTCAGAAAGATAAGCCAGTTGATA 2940  
QY 2941 ATGCCAAATGAGTATCAAGAGGCTCTAGGTTTTGCTATCATCTCAGTTACAGAGGCA 3000  
DB 2941 ATGCCAAATGAGTATCAAGAGGCTCTAGGTTTTGCTATCATCTCAGTTACAGAGGCA 3000  
QY 3001 ACGBAACTGGACTCATTTACTCCAAATAAACATGCACTTTTACAAAACCCATATCGTATAC 3060  
DB 3001 ACGBAACTGGACTCATTTACTCCAAATAAACATGCACTTTTACAAAACCCATATCGTATAC 3060  
QY 3061 CACCACCTTTTCCCATCAAGTCATTTGTTAAACTAAATGTAAGAAAAATCTGCTAGAGG 3120  
DB 3061 CACCACCTTTTCCCATCAAGTCATTTGTTAAACTAAATGTAAGAAAAATCTGCTAGAGG 3120  
QY 3121 AAAACTTTGAGGAACATTCATGTCACCTGAAGAGAAATGGGAAATGAGAACAATTCCAA 3180  
DB 3121 AAAACTTTGAGGAACATTCATGTCACCTGAAGAGAAATGGGAAATGAGAACAATTCCAA 3180  
QY 3181 GTACAGTGACACAAATTAGCCGTAATTAACATTAGAGAAATGTTTTTAAAGGAGCCAGCT 3240  
DB 3181 GTACAGTGACACAAATTAGCCGTAATTAACATTAGAGAAATGTTTTTAAAGGAGCCAGCT 3240  
QY 3241 CAAGCAATATTAATGAATAGGTTCCAGTATTAATGAAGTGGGCTCCAGTATTAATGAAA 3300  
DB 3241 CAAGCAATATTAATGAATAGGTTCCAGTATTAATGAAGTGGGCTCCAGTATTAATGAAA 3300  
QY 3301 TAGGTTCCAGTATGAAAAATTCAGACAGAACTAGGTAGAAAAACAGAGGCCAAAATTTGA 3360  
DB 3301 TAGGTTCCAGTATGAAAAATTCAGACAGAACTAGGTAGAAAAACAGAGGCCAAAATTTGA 3360  
QY 3361 ATGCTATGCTTAGATTAGGGGTTTTGCAACTGAGGCTCTATAACAAAGTCTTCCCTGGAA 3420  
DB 3361 ATGCTATGCTTAGATTAGGGGTTTTGCAACTGAGGCTCTATAACAAAGTCTTCCCTGGAA 3420

QY 3421 GTAATTGTAGCATCTCGAAATAAAAAGCAAGAAATATGAAGAGTAGTTAGTTTCAGACTGTTA 3480  
DB 3421 GTAATTGTAGCATCTCGAAATAAAAAGCAAGAAATATGAAGAGTAGTTAGTTTCAGACTGTTA 3480  
QY 3481 ATACAGATTTTCTCTCCATATCTGATTTTTCAGATAACTTTAGAACAGCCTATGGGAAGTAGTC 3540  
DB 3481 ATACAGATTTTCTCTCCATATCTGATTTTTCAGATAACTTTAGAACAGCCTATGGGAAGTAGTC 3540  
QY 3541 ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTTTAGATGATGGGAAGTAGTC 3600  
DB 3541 ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTTTAGATGATGGGAAGTAGTC 3600  
QY 3601 AAGATCTAGTCTTGTCTGAAAAATGACATTAAGGAAAGTCTGCTGTTTTTGTAGCAAAAGCG 3660  
DB 3601 AAGATCTAGTCTTGTCTGAAAAATGACATTAAGGAAAGTCTGCTGTTTTTGTAGCAAAAGCG 3660  
QY 3661 TCCAGAGAGGAGAGCTTTAGCAGGAGTCTTAGCCCTTTTCAACCCTATACACATTTGGCTCAGG 3720  
DB 3661 TCCAGAGAGGAGAGCTTTAGCAGGAGTCTTAGCCCTTTTCAACCCTATACACATTTGGCTCAGG 3720  
QY 3721 GTTACCGAAGAGGGCCCAAGAAATTAGAGTCTCTCAGAAAGAACTTATCTAGTGAGGATG 3780  
DB 3721 GTTACCGAAGAGGGCCCAAGAAATTAGAGTCTCTCAGAAAGAACTTATCTAGTGAGGATG 3780  
QY 3781 AAGAGCTTCCCTGCTTCCAAACACTTTGTTATTTGTTAAAGTAAACAATATACCTTCTCAGT 3840  
DB 3781 AAGAGCTTCCCTGCTTCCAAACACTTTGTTATTTGTTAAAGTAAACAATATACCTTCTCAGT 3840  
QY 3841 CTACTAGGCATAGCACCGTTTGTACCGAGTGTCTGTCTAAGAAACACAGAGGAGAAATTTAT 3900  
DB 3841 CTACTAGGCATAGCACCGTTTGTACCGAGTGTCTGTCTAAGAAACACAGAGGAGAAATTTAT 3900  
QY 3901 TATCATTAAGAAATAGCTTAAATGACTGAGTAAACAGGTAATTTGGCAAGGATCTC 3960  
DB 3901 TATCATTAAGAAATAGCTTAAATGACTGAGTAAACAGGTAATTTGGCAAGGATCTC 3960  
QY 3961 AGCAACATCACTTAGTGAGGAAACAAAATGTTCTGCTAGCTTGTGTTTTTTCACAGTGCA 4020  
DB 3961 AGCAACATCACTTAGTGAGGAAACAAAATGTTCTGCTAGCTTGTGTTTTTTCACAGTGCA 4020  
QY 4021 GTGAATTTGGAAGACTTGACTGCAAAATACAAACCCAGGATCCTTTCTGATTTGGTTCTT 4080  
DB 4021 GTGAATTTGGAAGACTTGACTGCAAAATACAAACCCAGGATCCTTTCTGATTTGGTTCTT 4080  
QY 4081 CCAACAAATGAGGCATCTGCTGAAAGCCAGGAGTTGCTCTGAGTGACAAGAAATTTG 4140  
DB 4081 CCAACAAATGAGGCATCTGCTGAAAGCCAGGAGTTGCTCTGAGTGACAAGAAATTTG 4140  
QY 4141 TTTTCAGATGATGAAGAAAGAGGAAACGGGCTTTGGAAGAAAATAATCAAGAAAGACAAAGCA 4200  
DB 4141 TTTTCAGATGATGAAGAAAGAGGAAACGGGCTTTGGAAGAAAATAATCAAGAAAGACAAAGCA 4200  
QY 4201 TGGATTCAAACTTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAAACAAAGCGTCTCTGAAG 4260  
DB 4201 TGGATTCAAACTTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAAACAAAGCGTCTCTGAAG 4260  
QY 4261 ACTGCTCAGGGCTATCCTCTCAGAGTACATTTTAAACCACTCAGCAGAGGATACCAATGC 4320  
DB 4261 ACTGCTCAGGGCTATCCTCTCAGAGTACATTTTAAACCACTCAGCAGAGGATACCAATGC 4320  
QY 4321 AACATAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACTAGAAAGCTGTGTAGAACAGC 4380  
DB 4321 AACATAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACTAGAAAGCTGTGTAGAACAGC 4380  
QY 4381 ATGGGAGCCAGCCTTCTAAACAGTACCCCTTCCATCAATAGTGACTCTCTGCTGCCCTTGAGG 4440  
DB 4381 ATGGGAGCCAGCCTTCTAAACAGTACCCCTTCCATCAATAGTGACTCTCTGCTGCCCTTGAGG 4440  
QY 4441 ACCTGCGAATCCAGAACAGCAGATCAGAAAAAGCAGTATTAACTTCACAGAAAGTA 4500  
DB 4441 ACCTGCGAATCCAGAACAGCAGATCAGAAAAAGCAGTATTAACTTCACAGAAAGTA 4500  
QY 4501 GTGAATACCCCTATAAGCCAGAAATCCAGAGGGCCCTTTCTGCTGACAAAGTTTTCAGGTGCTG 4560

```
Db 4501 GTGAATACCCCTATAGCCAGAAATCCAGAGGCCCTTTCTGCTGCAAGTTTGGGTGCTG 4560
Qy 4561 CAGATAGTTCTACAGTAATAAAGAAACAGAGAGTGGAAAGTTCATCCCTTCTAAAT 4620
Db 4561 CAGATAGTTCTACAGTAATAAAGAAACAGAGAGTGGAAAGTTCATCCCTTCTAAAT 4620
Qy 4621 GCCCATCAATAGATAGAGTGGTACATGCAAGTGTCTGGAGTCTTCAGAAATAGAA 4680
Db 4621 GCCCATCAATAGATAGAGTGGTACATGCAAGTGTCTGGAGTCTTCAGAAATAGAA 4680
Qy 4681 ACTACCCATCTCAGAGAGAGCTCAATTAAGTTGTTGATGTCGAGAGCAACAGCTGGAAG 4740
Db 4681 ACTACCCATCTCAGAGAGAGCTCAATTAAGTTGTTGATGTCGAGAGCAACAGCTGGAAG 4740
Qy 4741 AGTCTGGGCCACACGATTTGACGGAACATCTTACTTGCACAGGCAAGATCTAGAGGAA 4800
Db 4741 AGTCTGGGCCACACGATTTGACGGAACATCTTACTTGCACAGGCAAGATCTAGAGGAA 4800
Qy 4801 CCCCTTACCTGGAATCTGGAATCAGCCTCTTCTCTGATGACCCCTGAATCTGATCTCTG 4860
Db 4801 CCCCTTACCTGGAATCTGGAATCAGCCTCTTCTCTGATGACCCCTGAATCTGATCTCTG 4860
Qy 4861 AAGACAGAGCCCCAGAGTCACTGCTGTTGGCAACATACCATCTTCAACCTCTGCATGA 4920
Db 4861 AAGACAGAGCCCCAGAGTCACTGCTGTTGGCAACATACCATCTTCAACCTCTGCATGA 4920
Qy 4921 AAGTTCCCAATTCGAAGTTCAGAAATCTGCCAGGCTCAGAGTCTGCTCATACTCTG 4980
Db 4921 AAGTTCCCAATTCGAAGTTCAGAAATCTGCCAGGCTCAGAGTCTGCTCATACTCTG 4980
Qy 4981 ATACTGCTGGGTATAATCAATGGAAGAAAGTGTGAGCAGGAGAAAGCCAGAAATGACAG 5040
Db 4981 ATACTGCTGGGTATAATCAATGGAAGAAAGTGTGAGCAGGAGAAAGCCAGAAATGACAG 5040
Qy 5041 CTTCAACAGAAAGGGTCAACAAAAGATGTCATGCTGGTGTCTGGCTGACCCAGAGAG 5100
Db 5041 CTTCAACAGAAAGGGTCAACAAAAGATGTCATGCTGGTGTCTGGCTGACCCAGAGAG 5100
Qy 5101 AATTTATGCTGCTGACAAAGTTCCAGAAACAGATGCTGAGTTGTGTGTAACGGACAC 5160
Db 5101 AATTTATGCTGCTGACAAAGTTCCAGAAACAGATGCTGAGTTGTGTGTAACCTAATTA 5160
Qy 5161 CTGAAGAGACTACTCATCTGTTATGAAAACAGATGCTGAGTTGTGTGTAACGGACAC 5220
Db 5161 CTGAAGAGACTACTCATCTGTTATGAAAACAGATGCTGAGTTGTGTGTAACGGACAC 5220
Qy 5221 TGAATATTTTCTAGGAATTCGGAGGAAATGGTATGCTATTTCTGGGTGACCC 5280
Db 5221 TGAATATTTTCTAGGAATTCGGAGGAAATGGTATGCTATTTCTGGGTGACCC 5280
Qy 5281 AGTCTATTAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGAGATGTTGG 5340
Db 5281 AGTCTATTAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGAGATGTTGG 5340
Qy 5341 TCAATGGAAGAAACCAACAGCTCCAAAGCAGAGCAAGAGATCCAGGACAGAAAGATCT 5400
Db 5341 TCAATGGAAGAAACCAACAGCTCCAAAGCAGAGCAAGAGATCCAGGACAGAAAGATCT 5400
Qy 5401 TCAGGGGCTAGAAATCTGTTGCTATGAGCCCTTCCACCAATGCCCCACAGATCAACTGG 5460
Db 5401 TCAGGGGCTAGAAATCTGTTGCTATGAGCCCTTCCACCAATGCCCCACAGATCAACTGG 5460
Qy 5461 AATGATGGTACAGTGTGGTCTCTGTTGGTGAAGAGCTTTCATCATTTACCCCTG 5520
Db 5461 AATGATGGTACAGTGTGGTCTCTGTTGGTGAAGAGCTTTCATCATTTACCCCTG 5520
Qy 5521 GCACAGGTGTCACCCCAATGTTGTTGTCAGCCAGATGCTGGACAGAGCAATGCT 5580
Db 5521 GCACAGGTGTCACCCCAATGTTGTTGTCAGCCAGATGCTGGACAGAGCAATGCT 5580
Qy 5581 TCCATGCAATTTGGGCAGATGTTGAGGCACTGTGTCAGCCAGAGAGTGGGTGTTGGACA 5640
Db 5581 TCCATGCAATTTGGGCAGATGTTGAGGCACTGTGTCAGCCAGAGAGTGGGTGTTGGACA 5640
```

```
Db 5581 TCCATGCAATTTGGGCAGATGTTGAGGCACTGTGTTGACCCGAGAGTGGGTGTTGGACA 5640
Qy 5641 GTGTAGCACTCTACCACTGCCAGAGCTGGACACCTACCTGATATCCCGAGATCCCCCACA 5700
Db 5641 GTGTAGCACTCTACCACTGCCAGAGCTGGACACCTACCTGATATCCCGAGATCCCCCACA 5700
Qy 5701 GCCACTACTGA 5711
Db 5701 GCCACTACTGA 5711

RESULT 8
AAV46453
ID AAV46453 standard; cDNA; 5711 BP.
XX
AC AAV46453;
XX
DT 18-NOV-1998 (first entry)
XX
DE Human BRCA1 omil polymorphism #3 cDNA.
XX
KW BRCA1; omil; human; breast and ovarian cancer predisposing gene;
KW polymorphism; susceptibility; anti-oncogene; tumour suppressor;
KW chromosome 17q; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 120..5711
FT /*tag= a
FT product= "BRCA1 omil protein"
FT variation 2731
FT /*tag= b
FT /note= "This polymorphic variation can be a C or T.
XX
XX US750400-A.
XX
XX 12-MAY-1998.
XX
XX 12-FEB-1997; 97US-0798691.
XX
XX 12-FEB-1996; 96US-0598591.
XX 12-FEB-1997; 97US-0798691.
XX (ONCO-) ONCORMED INC.
XX
XX Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ;
XX Schelter DB, Zeng B;
XX
XX WPI; 1998-296774/26.
XX
XX BRCA1 omi gene coding sequences - useful for distinguishing between
XX polymorphisms and mutation(s) in the screening for disposition to
XX breast or ovarian cancer
XX
XX Claim 2e; Page -; 54pp; English.
XX
XX This sequence encodes a human BRCA1 (breast and ovarian cancer
XX predisposing gene) omil gene in which a polymorphic variation occurs at
XX nucleotide 2731. This sequence and other polymorphic variations of this
XX sequence are useful for the identification of an individual who may or
XX may not have an increased susceptibility to breast or ovarian cancer.
XX The sequences used identify gene changes which are due to polymorphisms,
XX rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
XX suppressor) which is involved in genetic inheritance of cancers,
XX especially breast and ovarian cancer. It is found at human chromosome
XX 17q which is known to be linked to cancer susceptibility, especially
XX breast cancer. Cells containing a mutation in this gene lose the
XX wild-type function of BRCA1 and are more susceptible to cancers.
XX NOTE: This sequence does not appear in the specification but has been
XX created from the wild type BRCA1 omil gene represented in AAV46448.
XX
```



SQ Sequence 5711 BP; 1953 A; 1099 C; 1277 G; 1381 T; 1 other;									
Query Match 100.0%; Score 5710.6; DB 19; Length 5711;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	AGCTCGCTGAGACTTCCTGGACCCCGCACAGGCTGTGGGTTTCTCAGATAAATGGGCC	60						
Db	1	AGCTCGCTGAGACTTCCTGGACCCCGCACAGGCTGTGGGTTTCTCAGATAAATGGGCC	60						
Qy	61	CTCGGCTCAGAGGCTTCAACCTCTGCTCTGGGTAAAGTTCAATGGAAACAGAAAGAAA	120						
Db	61	CTCGGCTCAGAGGCTTCAACCTCTGCTCTGGGTAAAGTTCAATGGAAACAGAAAGAAA	120						
Qy	121	TGGATTTATCTGCTCTTCGCGTTGAGAAAGTACAAAATGCTAATTAAGTCTATGAGAAA	180						
Db	121	TGGATTTATCTGCTCTTCGCGTTGAGAAAGTACAAAATGCTAATTAAGTCTATGAGAAA	180						
Qy	181	TCCTAGAGTGTCCCATCTGCTGGAGTTGATCAAGGAACCTGTCTCCACAAAGTGTGACC	240						
Db	181	TCCTAGAGTGTCCCATCTGCTGGAGTTGATCAAGGAACCTGTCTCCACAAAGTGTGACC	240						
Qy	241	ACATATTTTGCAAAATTTTGATGTGAAAATCTTCTCAACAGAAAGGGCCITTCACAGT	300						
Db	241	ACATATTTTGCAAAATTTTGATGTGAAAATCTTCTCAACAGAAAGGGCCITTCACAGT	300						
Qy	301	GTCCCTTTATGTAAGATATATACCAAAAGGACCTACAGAAAGTACAGATTTAGTC	360						
Db	301	GTCCCTTTATGTAAGATATATACCAAAAGGACCTACAGAAAGTACAGATTTAGTC	360						
Qy	361	AACCTGTTGAGAGCTATTGAAAATCAATTTGTGCTTTTACGCTTGACACAGGTTTGAGT	420						
Db	361	AACCTGTTGAGAGCTATTGAAAATCAATTTGTGCTTTTACGCTTGACACAGGTTTGAGT	420						
Qy	421	ATGCAAAACAGCTATAATTTTGCAAAAAGGAAAATAAATCTCTCTGAAACATCTAAAGATG	480						
Db	421	ATGCAAAACAGCTATAATTTTGCAAAAAGGAAAATAAATCTCTCTGAAACATCTAAAGATG	480						
Qy	481	AAGTTTCTATCATCAAGATATGGCTACAGAAACCGTGCCAAAGACTTCTACAGAGTG	540						
Db	481	AAGTTTCTATCATCAAGATATGGCTACAGAAACCGTGCCAAAGACTTCTACAGAGTG	540						
Qy	541	AACCCGAAATCTCTCTGAGGAAACCAAGTCTCAGTGTCCAACTCTTAACCTTGAA	600						
Db	541	AACCCGAAATCTCTCTGAGGAAACCAAGTCTCAGTGTCCAACTCTTAACCTTGAA	600						
Qy	601	CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCTGAAAGACGCTGTCTACATTG	660						
Db	601	CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCTGAAAGACGCTGTCTACATTG	660						
Qy	661	AATTGGGATCTGATTTCTGAAGATACCGTTAATAGGCAACTTATTCAGTGTGGAG	720						
Db	661	AATTGGGATCTGATTTCTGAAGATACCGTTAATAGGCAACTTATTCAGTGTGGAG	720						
Qy	721	ATCAAGAAATGTTTACAAATCACCCCTCAAGGAACCGGATGAAATCAGTTTGGATTCTG	780						
Db	721	ATCAAGAAATGTTTACAAATCACCCCTCAAGGAACCGGATGAAATCAGTTTGGATTCTG	780						
Qy	781	CAAAAAGGCTGCTGTGAAATTTCTGAGCGGATGAAACATACTGATCAATCAAC	840						
Db	781	CAAAAAGGCTGCTGTGAAATTTCTGAGCGGATGAAACATACTGATCAATCAAC	840						
Qy	841	CCAGTAATATGATTTGAAACCACTGAGAGCGGTGAGTCCAGAGGATCCAGAAAGT	900						
Db	841	CCAGTAATATGATTTGAAACCACTGAGAGCGGTGAGTCCAGAGGATCCAGAAAGT	900						
Qy	901	ATCAGGCTAGTTCCTGTTTCAAACTTGATGTGGAGCCATGTGGCACAAATACATGCCA	960						
Db	901	ATCAGGCTAGTTCCTGTTTCAAACTTGATGTGGAGCCATGTGGCACAAATACATGCCA	960						
Qy	961	GCTCATTACAGATGAGAACAGCAGTTTATTTACTCTCTAAAGACAGAAATGATGAGAA	1020						
Db	961	GCTCATTACAGATGAGAACAGCAGTTTATTTACTCTCTAAAGACAGAAATGATGAGAA	1020						

Qy	1021	AGGCTGAATTTCTGTAATAAAGCAAAACAGCGCTGCTTAGCAAGGAGCCACATACAGAT	1080						
Db	1021	AGGCTGAATTTCTGTAATAAAGCAAAACAGCGCTGCTTAGCAAGGAGCCACATACAGAT	1080						
Qy	1081	GGGCTGGAAGTAAGAAACATGTAAATGATAGCGCGACTCCAGACACAGAAAAAGGTAG	1140						
Db	1081	GGGCTGGAAGTAAGAAACATGTAAATGATAGCGCGACTCCAGACACAGAAAAAGGTAG	1140						
Qy	1141	ATCTGAATGCTGATCCCTCTGTGTGAGAGAAAGAAATGGAATAGCAGAAAATGCTGCT	1200						
Db	1141	ATCTGAATGCTGATCCCTCTGTGTGAGAGAAAGAAATGGAATAGCAGAAAATGCTGCT	1200						
Qy	1201	CAGAGAACTCTAGAGATCTGAAAGATCTTCTTGATGAAACACTAAATAGCAGCAATTG	1260						
Db	1201	CAGAGAACTCTAGAGATCTGAAAGATCTTCTTGATGAAACACTAAATAGCAGCAATTG	1260						
Qy	1261	AAGTTAATGATGCTGTTTCCAGAAAGTGAATCAATCTGTTAGGTTCTGATGACTCAGATG	1320						
Db	1261	AAGTTAATGATGCTGTTTCCAGAAAGTGAATCAATCTGTTAGGTTCTGATGACTCAGATG	1320						
Qy	1321	GGGAGTCTGAATCAAAATGCGCAAGTACTGATGATTTGGACGTTCTAAATGAGTAGATG	1380						
Db	1321	GGGAGTCTGAATCAAAATGCGCAAGTACTGATGATTTGGACGTTCTAAATGAGTAGATG	1380						
Qy	1381	AATATTCTGCTGTTCTCAGAGAAATAGACTTACTGGCCAGTGATCTCTCATGAGGCTTAA	1440						
Db	1381	AATATTCTGCTGTTCTCAGAGAAATAGACTTACTGGCCAGTGATCTCTCATGAGGCTTAA	1440						
Qy	1441	TATGTAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGAGTAATATTGAAGACAAAATAT	1500						
Db	1441	TATGTAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGAGTAATATTGAAGACAAAATAT	1500						
Qy	1501	TTGGGAAAACCTATCGGAAGAGCGCTCCGCCAATCTTAAGCATGTAACTGAAATC	1560						
Db	1501	TTGGGAAAACCTATCGGAAGAGCGCGCTCCGCCAATCTTAAGCATGTAACTGAAATC	1560						
Qy	1561	TAATTTAGGAGATTTGTTTACTGAGCCACAGATAATACAGAGCGTCCCTCACAATA	1620						
Db	1561	TAATTTAGGAGATTTGTTTACTGAGCCACAGATAATACAGAGCGTCCCTCACAATA	1620						
Qy	1621	AATTTAAGCGTAAAGGAGACCTACATCAGCGCTTCTATCTGAGGATTTTATCAAGAAAG	1680						
Db	1621	AATTTAAGCGTAAAGGAGACCTACATCAGCGCTTCTATCTGAGGATTTTATCAAGAAAG	1680						
Qy	1681	CAGATTGGCAGTTCAAAAGACTCTCGAAATGATAATCAGGAACTAAACAAACGGAGC	1740						
Db	1681	CAGATTGGCAGTTCAAAAGACTCTCGAAATGATAATCAGGAACTAAACAAACGGAGC	1740						
Qy	1741	AGAATGCTCAAGTGATGAATATTACTAATAGTGGTCAATGAGATAAACAAGGTCATT	1800						
Db	1741	AGAATGCTCAAGTGATGAATATTACTAATAGTGGTCAATGAGATAAACAAGGTCATT	1800						
Qy	1801	CTATTCAAGATGAGAAAAATCTTAAACCAATAGAACTACCTCGAAAAAGAACTCTGCTTCA	1860						
Db	1801	CTATTCAAGATGAGAAAAATCTTAAACCAATAGAACTACCTCGAAAAAGAACTCTGCTTCA	1860						
Qy	1861	AAACGAAAGCTGAAACCTTAAAGCAGAGTAAAGCAATATGGAATCTGAAATTAATATCC	1920						
Db	1861	AAACGAAAGCTGAAACCTTAAAGCAGAGTAAAGCAATATGGAATCTGAAATTAATATCC	1920						
Qy	1921	ACAAATTTCAAAAGCACTTAAAGAAATAGGCTGAGGAGGAGTCTTCTACAGGCAATATTC	1980						
Db	1921	ACAAATTTCAAAAGCACTTAAAGAAATAGGCTGAGGAGGAGTCTTCTACAGGCAATATTC	1980						
Qy	1981	ATGCGCTTGAATCTAGTAGTCAAGTAGAAATCTAAGCCCACTTAATTTGACTGAATTCGAAA	2040						
Db	1981	ATGCGCTTGAATCTAGTAGTCAAGTAGAAATCTAAGCCCACTTAATTTGACTGAATTCGAAA	2040						
Qy	2041	TTGATAGTTGTTCTAGCAGTGAAGAGATAAAGAAAAAGTACAAACCAATGCGAGTCA	2100						
Db	2041	TTGATAGTTGTTCTAGCAGTGAAGAGATAAAGAAAAAGTACAAACCAATGCGAGTCA	2100						



QY 2101 GGCACAGCAAAACCTTCAACTCATGGAAGTAAAGAAACCTGCAACTGGAGCCCAAGAAGA 2160  
DB 2101 GGCACAGCAAAACCTTCAACTCATGGAAGTAAAGAAACCTGCAACTGGAGCCCAAGAAGA 2160  
QY 2161 GTAAACAGCCAAATGAACAGACAGTAAAGACATGACATGATCTTTCCCGAGCTGA 2220  
DB 2161 GTAAACAGCCAAATGAACAGACAGTAAAGACATGACATGATCTTTCCCGAGCTGA 2220  
QY 2221 AGTTAAACAAATGCACTGGTCTTTTACTAAGTGTTCAAATATACCAGTGAACCTTAAAGAAAT 2280  
DB 2221 AGTTAAACAAATGCACTGGTCTTTTACTAAGTGTTCAAATATACCAGTGAACCTTAAAGAAAT 2280  
QY 2281 TTGTCAATCTAGCCCTTCCAGAGAGAAAGAAAGAAACCTAGAAACAGTAAAGTGT 2340  
DB 2281 TTGTCAATCTAGCCCTTCCAGAGAGAAAGAAAGAAACCTAGAAACAGTAAAGTGT 2340  
QY 2341 CTAAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAGAAAGGTTTGCACAACTG 2400  
DB 2341 CTAAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAGAAAGGTTTGCACAACTG 2400  
QY 2401 AAAGATCTGTAGAGAGTAGCAGTATTTCACTGGTACCTGGTACTGATTTATGGCACTCAGG 2460  
DB 2401 AAAGATCTGTAGAGAGTAGCAGTATTTCACTGGTACCTGGTACTGATTTATGGCACTCAGG 2460  
QY 2461 AAAGTATCTGTTACTGGAAGTTAGCACTCTAGGGAAGGCCAAACAGAAACCAAAATAAT 2520  
DB 2461 AAAGTATCTGTTACTGGAAGTTAGCACTCTAGGGAAGGCCAAACAGAAACCAAAATAAT 2520  
QY 2521 GTGTGAGTCAAGTGCAGCATTGAAACCCCAAGGACTAAATTCATGGTGTTCCAAAG 2580  
DB 2521 GTGTGAGTCAAGTGCAGCATTGAAACCCCAAGGACTAAATTCATGGTGTTCCAAAG 2580  
QY 2581 ATAAATAGAAATGACACAGAGGCTTTAAGTATCCATTTGGGACATGAAAGTTAAACACAGTC 2640  
DB 2581 ATAAATAGAAATGACACAGAGGCTTTAAGTATCCATTTGGGACATGAAAGTTAAACACAGTC 2640  
QY 2641 GGGAAACCAAGCATAGAAATGGAAGAAAGTGAATCTGATTTTGCAGAAATACAT 2700  
DB 2641 GGGAAACCAAGCATAGAAATGGAAGAAAGTGAATCTGATTTTGCAGAAATACAT 2700  
QY 2701 TCAAGGTTTCAAGCGGCAGTCATTTGCTCTGTTTTCAATCCAGGAAATGCAGAAAGG 2760  
DB 2701 TCAAGGTTTCAAGCGGCAGTCATTTGCTCTGTTTTCAATCCAGGAAATGCAGAAAGG 2760  
QY 2761 AATGTGCAACATCTCTGCCCCACTCTGGTCTTAAAGAAACCAAGTCCAAAGTCACTT 2820  
DB 2761 AATGTGCAACATCTCTGCCCCACTCTGGTCTTAAAGAAACCAAGTCCAAAGTCACTT 2820  
QY 2821 TTGAATGTGAACAAAAGGAAGAAATCAAGGAAAGAAATGAGTCTTAATATCAAGCCTGTAC 2880  
DB 2821 TTGAATGTGAACAAAAGGAAGAAATCAAGGAAAGAAATGAGTCTTAATATCAAGCCTGTAC 2880  
QY 2881 AGACAGTTAATATCACTGCGAGGCTTCTGTTGGTTGGTCAGAAAGATAAGCCAGTTGATA 2940  
DB 2881 AGACAGTTAATATCACTGCGAGGCTTCTGTTGGTTGGTCAGAAAGATAAGCCAGTTGATA 2940  
QY 2941 ATGCCAAATGTAGTATCAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTTCAGAGGCA 3000  
DB 2941 ATGCCAAATGTAGTATCAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTTCAGAGGCA 3000  
QY 3001 ACGAAATCTGGAATCACTTCAATTAACATGGAATTTTACAAACCCATATCGTATAC 3060  
DB 3001 ACGAAATCTGGAATCACTTCAATTAACATGGAATTTTACAAACCCATATCGTATAC 3060  
QY 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAACCTAAATGTAAGAAATCTGCTAGAGG 3120  
DB 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAACCTAAATGTAAGAAATCTGCTAGAGG 3120  
QY 3121 AAAATTTTGAAGAACATTCATGTCACCTGAAGAGAAATGGGAAATGAGAACATTCNA 3180  
DB 3121 AAAATTTTGAAGAACATTCATGTCACCTGAAGAGAAATGGGAAATGAGAACATTCNA 3180  
QY 3181 GTACAGTGAGCACAATTAGCCGTAATAACATTAGAGAAATGTTTTTAAAGGAGCCAGCT 3240

DB 3181 GTACAGTGAGCACAATTAGCCGTAATAACATTAGAGAAATGTTTTTAAAGGAGCCAGCT 3240  
QY 3241 CAAGCAATATTAATGAAGTAGGTTCCAGTACTTAATGAAGTGGGCTCCAGTATTAAATGAAA 3300  
DB 3241 CAAGCAATATTAATGAAGTAGGTTCCAGTACTTAATGAAGTGGGCTCCAGTATTAAATGAAA 3300  
QY 3301 TAGGTTCCAGTGATGAAAAACATTCAAGCAGAACTAGGTAGAAAACAGAGGGCCAAAATTGA 3360  
DB 3301 TAGGTTCCAGTGATGAAAAACATTCAAGCAGAACTAGGTAGAAAACAGAGGGCCAAAATTGA 3360  
QY 3361 ATGCTATGCTTAGATTAGGGGTTTTGCAACTGAGGCTTATAAACAAGTCTTCTCGAA 3420  
DB 3361 ATGCTATGCTTAGATTAGGGGTTTTGCAACTGAGGCTTATAAACAAGTCTTCTCGAA 3420  
QY 3421 GTAATTTGAAGCACTCTGAAATAAAAAAGCAAGAAATATGAAGAAAGTACTGAGACTGTTA 3480  
DB 3421 GTAATTTGAAGCACTCTGAAATAAAAAAGCAAGAAATATGAAGAAAGTACTGAGACTGTTA 3480  
QY 3481 ATACAGATTTCTCTCCATATCTGATTTCAAGATACTTAGAAACAGCCTATGGAAGTAGTC 3540  
DB 3481 ATACAGATTTCTCTCCATATCTGATTTCAAGATACTTAGAAACAGCCTATGGAAGTAGTC 3540  
QY 3541 ATGCACTCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGTTGAAATAAAGG 3600  
DB 3541 ATGCACTCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGTTGAAATAAAGG 3600  
QY 3601 AAGATCTCTAGTTTGTCTGAAAAATGACATTAAGGAAAGTCTGCTGTTTTTGTAGCAAAAGCG 3660  
DB 3601 AAGATCTCTAGTTTGTCTGAAAAATGACATTAAGGAAAGTCTGCTGTTTTTGTAGCAAAAGCG 3660  
QY 3661 TCCAGAGAGGAGAGCTTTAGCAGGAGTCTTAGCCCTTTCAACCATACACATTTGCTCAGG 3720  
DB 3661 TCCAGAGAGGAGAGCTTTAGCAGGAGTCTTAGCCCTTTCAACCATACACATTTGCTCAGG 3720  
QY 3721 GTTACCGAAGAGGGGCCAAGAAATTAGAGTCTCTCAGAAAGAACTTATCTAGTGAGGATG 3780  
DB 3721 GTTACCGAAGAGGGGCCAAGAAATTAGAGTCTCTCAGAAAGAACTTATCTAGTGAGGATG 3780  
QY 3781 AAGAGCTTCCCTGCTTCCACACCTGTTATTTGGTAAAGTAAACAATATCTTCTCAGT 3840  
DB 3781 AAGAGCTTCCCTGCTTCCACACCTGTTATTTGGTAAAGTAAACAATATCTTCTCAGT 3840  
QY 3841 CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGCTTAAGAAACACAGAGAGAGAAATTTAT 3900  
DB 3841 CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGCTTAAGAAACACAGAGAGAGAAATTTAT 3900  
QY 3901 TATCATTGAAGAAATAGCTTAAATGACTGCGATTAACAGGTTAATTTGGCAAGGCACTCTC 3960  
DB 3901 TATCATTGAAGAAATAGCTTAAATGACTGCGATTAACAGGTTAATTTGGCAAGGCACTCTC 3960  
QY 3961 AGGAAACATCACTTAGTGAGGAAACAAATGTTCTGCTAGCTGTTTCTTCAAGTGCA 4020  
DB 3961 AGGAAACATCACTTAGTGAGGAAACAAATGTTCTGCTAGCTGTTTCTTCAAGTGCA 4020  
QY 4021 GTGAATTTGGAAGACTTCACTGCAAAATCAACACCCAGGATCCTTTCTTGATTTGTTCTT 4080  
DB 4021 GTGAATTTGGAAGACTTCACTGCAAAATCAACACCCAGGATCCTTTCTTGATTTGTTCTT 4080  
QY 4081 CCAACAAATAGGCACTCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGACAAGGAATTTGG 4140  
DB 4081 CCAACAAATAGGCACTCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGACAAGGAATTTGG 4140  
QY 4141 TTTTCAGATGATGAAGAAAGAGGACCGGCTTGGAGAAATTAATCAAGAGAGCAAGCA 4200  
DB 4141 TTTTCAGATGATGAAGAAAGAGGACCGGCTTGGAGAAATTAATCAAGAGAGCAAGCA 4200  
QY 4201 TGGATTTCAAACTTAGGTGAAGCAGCATCTGGTGTGAGAGTGAACAGCGCTCTCTGAAG 4260  
DB 4201 TGGATTTCAAACTTAGGTGAAGCAGCATCTGGTGTGAGAGTGAACAGCGCTCTCTGAAG 4260  
QY 4261 ACTGCTCAGGCTATCTCTCAGAGTGAACATTTTAAACCACTCAGCAGAGGATACCATGTC 4320

Db 4261 ACTGCTCAGGGCTATCCTCTCAGAGTGACATTTTAAACCATCTCAGCAGAGGATACCATGC 4320  
Qy 4321 AACATAACCTGATAAAGCTCCAGCAGGAATGGCTGAACATAGAAAGCTGTGTAGAACAGC 4380  
Db 4321 AACATAACCTGATAAAGCTCCAGCAGGAATGGCTGAACATAGAAAGCTGTGTAGAACAGC 4380  
Qy 4381 ATGGAGCAGCCTTCTAAACAGCTAACCTTCCATCAATAGTGAATCTCTGCTGCCCTTGAGG 4440  
Db 4381 ATGGAGCAGCCTTCTAAACAGCTAACCTTCCATCAATAGTGAATCTCTCTGCCCTTGAGG 4440  
Qy 4441 ACCTGCCAATCCAGAAACAGCATCAGAAAAGCAGATTAATCTTCAAGAAAAGTA 4500  
Db 4441 ACCTGCCAATCCAGAAACAGCATCAGAAAAGCAGATTAATCTTCAAGAAAAGTA 4500  
Qy 4501 GTGAATACCTTATAAGCCAGAAATCCAGAAAGCCTTCTGCTGACAAAGTTTGTAGGTGCTG 4560  
Db 4501 GTGNATACCTTATAAGCCAGAAATCCAGAAAGCCTTCTGCTGACAAAGTTTGTAGGTGCTG 4560  
Qy 4561 CAGATAGTTCTACAGTAAATAAAGAACCCAGAGTGGAAAGTCTATCCCTTCTAAAT 4620  
Db 4621 GCGCATCATTAGATGATAGTGGTACATGACAGTGTGCTCTGGAGTCTTCAGAAATAGAA 4680  
Qy 4621 GCGCATCATTAGATGATAGTGGTACATGACAGTGTGCTCTGGAGTCTTCAGAAATAGAA 4680  
Qy 4681 ACTACCCATCTCAAGAGGAGCTCAATTAAGTTGTTGATGTGGAGGACCAACAGCTGGAAG 4740  
Db 4681 ACTACCCATCTCAAGAGGAGCTCAATTAAGTTGTTGATGTGGAGGACCAACAGCTGGAAG 4740  
Qy 4741 AGTCTGGCCACAGATTTGACGGAAACATCTTACTTGGCCAAAGCAAGATCTAGAGGGAA 4800  
Db 4741 AGTCTGGCCACAGATTTGACGGAAACATCTTACTTGGCCAAAGCAAGATCTAGAGGGAA 4800  
Qy 4801 CCCCTTACCTGGATCTGGATCAGCCTCTCTCTGATGACCTGATCTGATCTCTCTG 4860  
Db 4801 CCCCTTACCTGGATCTGGATCAGCCTCTCTCTGATGACCTGATCTGATCTCTCTG 4860  
Qy 4861 AAGACAGAGCCAGAGTCTGCTGCTGGCAACATACCATCTTCAACCTCTGCAATTGA 4920  
Db 4861 AAGACAGAGCCAGAGTCTGCTGCTGGCAACATACCATCTTCAACCTCTGCAATTGA 4920  
Qy 4921 AAGTTCCTCCAAATGAAAGTTGCAAGATCTGCCAGGCTCAGCTGCTGCTCATACTACTG 4980  
Db 4921 AAGTTCCTCCAAATGAAAGTTGCAAGATCTGCCAGGCTCAGCTGCTGCTCATACTACTG 4980  
Qy 4981 ATACTGCTGGTATATGCAATGGAAGAAAGTGTGAGCAGGAGAGCCAGAAATTGACAG 5040  
Db 4981 ATACTGCTGGTATATGCAATGGAAGAAAGTGTGAGCAGGAGAGCCAGAAATTGACAG 5040  
Qy 5041 CTTCAACAGAAAGGCTCAACAAAGAAATGTCATGTTGTTGCTGGCTCAGCCCGAGAAG 5100  
Db 5041 CTTCAACAGAAAGGCTCAACAAAGAAATGTCATGTTGTTGCTGGCTCAGCCCGAGAAG 5100  
Qy 5101 AATTTATGCTCGTGTAACAAGTTGGCCAGAAACACCATCACTTTAACTAACTAATTA 5160  
Db 5101 AATTTATGCTCGTGTAACAAGTTGGCCAGAAACACCATCACTTTAACTAACTAATTA 5160  
Qy 5161 CTGAAGAGACTACTCATGTTGTTATGAAAACAGATGCTGATGTTGTGTGTAACGGACAC 5220  
Db 5161 CTGAAGAGACTACTCATGTTGTTATGAAAACAGATGCTGATGTTGTGTGTAACGGACAC 5220  
Qy 5221 TGAATAATTTTCTAGGAATTCGGGAGAAATGGGTAGTTAGTATTTCTGGGTGACCC 5280  
Db 5221 TGAATAATTTTCTAGGAATTCGGGAGAAATGGGTAGTTAGTATTTCTGGGTGACCC 5280  
Qy 5281 AGTCTATTAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAGAGGAGATGCG 5340  
Db 5281 AGTCTATTAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAGAGGAGATGCG 5340  
Qy 5341 TCAATGGAAGAAACCACAGGTCCAAAGGAGCAAGATCCAGGACAGAAAGTCT 5400  
Db 5341 TCAATGGAAGAAACCACAGGTCCAAAGGAGCAAGATCCAGGACAGAAAGTCT 5400

RESULT 9  
AAV46454

ID AAV46454 standard; cDNA; 5711 BP.

XX AAV46454;

XX AC AC  
XX XX  
DT 18-NOV-1998 (first entry)

XX Human BRCA1 omil polymorphism #4 cDNA.

XX BRCA1; omil; human; breast and ovarian cancer predisposing gene;  
XX polymorphism; susceptibility; anti-oncogene; tumour suppressor;  
XX chromosome 17q; ss.

XX Homo sapiens.

Key	Location/Qualifiers
PH	120..5711
FT	/*tag= a
FT	/product= "BRCA1 omil protein"
FT	3232
FT	/*tag= b
FT	/note= "This polymorphic variation can be an A or G nucleotide"

XX US5750400-A.

XX 12-MAY-1998.

XX 12-FEB-1997; 97US-0798691.

XX 12-FEB-1996; 96US-0598591.

XX 12-FEB-1997; 97US-0798691.

XX (ONCO-) ONCORMED INC.

XX Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ;

XX Schelter DB, Zeng B;

XX WPI; 1998-296774/26.

XX BRCA1 omi gene coding sequences - useful for distinguishing between

XX polymorphisms and mutation(s) in the screening for disposition to

XX breast or ovarian cancer

XX Claim 2e; Page -; 54pp; English.

CC This sequence encodes a human BRCA1 (breast and ovarian cancer  
CC predisposing gene) omli gene in which a polymorphic variation occurs at  
CC nucleotide 3232. This sequence and other polymorphic variations of this  
CC sequence are useful for the identification of an individual who may or  
CC may not have an increased susceptibility to breast or ovarian cancer.  
CC The sequences used identify gene changes which are due to polymorphisms,  
CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour  
CC suppressor) which is involved in genetic inheritance of cancers,  
CC especially breast and ovarian cancer. It is found at human chromosome  
CC 17q which is known to be linked to cancer susceptibility, especially  
CC breast cancer. Cells containing a mutation in this gene lose the  
CC wild-type function of BRCA1 and are more susceptible to cancers.  
CC NOTE: This sequence does not appear in the specification but has been  
CC created from the wild type BRCA1 omli gene represented in AAV46448.  
XX

SQ Sequence 5711 BP; 1953 A; 1099 C; 1276 G; 1382 T; 1 other;

Query Match 100.0%; Score 5710.6; DB 19; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGCTCGCTGAGACTTCCTGGACCCCGCACAGGCTGTGGGTTTCTCAGATAAAGTGGGCC 60  
DB 1 AGCTCGCTGAGACTTCCTGGACCCCGCACAGGCTGTGGGTTTCTCAGATAAAGTGGGCC 60  
QY 61 CCTGCGCTCAGGAGGCGCTTCAACCTCTGCTCTGGGTAAAGTTTCAATGGAAACAGAAAGAAA 120  
DB 61 CCTGCGCTCAGGAGGCGCTTCAACCTCTGCTCTGGGTAAAGTTTCAATGGAAACAGAAAGAAA 120  
QY 121 TGGATTTATCTGCTTCCTGGGTTGAAGAAGTACAAAATGCTTAATGCTATGAGAAAAA 180  
DB 121 TGGATTTATCTGCTTCCTGGGTTGAAGAAGTACAAAATGCTTAATGCTATGAGAAAAA 180  
QY 181 TCTTAGAGTGCCTATCTGCTGAGTTGATCAAGGAACTGTCTCCACAAAGTGTGACC 240  
DB 181 TCTTAGAGTGCCTATCTGCTGAGTTGATCAAGGAACTGTCTCCACAAAGTGTGACC 240  
QY 241 ACATATTTTGCATATTTGCTGCTGAACTTCTCAACAGAAAGGCGCTTTCACAGT 300  
DB 241 ACATATTTTGCATATTTGCTGCTGAACTTCTCAACAGAAAGGCGCTTTCACAGT 300  
QY 301 GTCTTTTATGATGATATACCAAAAGGAGCTTACAGAAAGTACAGATTTAGTC 360  
DB 301 GTCTTTTATGATGATATACCAAAAGGAGCTTACAGAAAGTACAGATTTAGTC 360  
QY 361 AACTTGTGAGAGCTATTTGAAATATCAATTTGTGCTTTTCAGCTTGACACAGGTTTGAGT 420  
DB 361 AACTTGTGAGAGCTATTTGAAATATCAATTTGTGCTTTTCAGCTTGACACAGGTTTGAGT 420  
QY 421 ATGCAACAGCTATAATTTTCAAAAAGGAAATAAATCTCTCTGAACTCTAAAGATG 480  
DB 421 ATGCAACAGCTATAATTTTCAAAAAGGAAATAAATCTCTCTGAACTCTAAAGATG 480  
QY 481 AAGTTTCTCATATCCAAAGTATGGGCTACAGAAACCGTGCCAAAGACTTCTACAGAGTG 540  
DB 481 AAGTTTCTCATATCCAAAGTATGGGCTACAGAAACCGTGCCAAAGACTTCTACAGAGTG 540  
QY 541 AACCCGAAATCTCTTCTGAGGAAACAGTCTCAGTGTCCAATCTCTAACCTTGGAA 600  
DB 541 AACCCGAAATCTCTTCTGAGGAAACAGTCTCAGTGTCCAATCTCTAACCTTGGAA 600  
QY 601 CTGTGAGAACTCTGAGGAAACAGGAGGATACAACTCTCAAAAGAGCTCTGTCTACATG 660  
DB 601 CTGTGAGAACTCTGAGGAAACAGGAGGATACAACTCTCAAAAGAGCTCTGTCTACATG 660  
QY 661 AATTGGGATCTGATTTCTCTGAGATACCGTTAATAAGCAACTTATTGTCAGTGTGGAG 720  
DB 661 AATTGGGATCTGATTTCTCTGAGATACCGTTAATAAGCAACTTATTGTCAGTGTGGAG 720  
QY 721 ATCAAGAAATGTTTCAAAATCAACCTCAAGGAAACAGGAGTGAATCAATGTTGATTTCTG 780  
DB 721 ATCAAGAAATGTTTCAAAATCAACCTCAAGGAAACAGGAGTGAATCAATGTTGATTTCTG 780

QY 781 CAAAAAAGGCTGCTGTGTAATTTTCTGAGACGGATGTAAACAAATACTGAACATCATCAAC 840  
DB 781 CAAAAAAGGCTGCTGTGTAATTTTCTGAGACGGATGTAAACAAATACTGAACATCATCAAC 840  
QY 841 CCAGTAAATATGATTTTGAACACCACTGAGAAAGCGTGCAGCTGAGAGGCGATCCAGAAAGT 900  
DB 841 CCAGTAAATATGATTTTGAACACCACTGAGAAAGCGTGCAGCTGAGAGGCGATCCAGAAAGT 900  
QY 901 ATCAGGGTAGTCTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCACAATACTCATGCCA 960  
DB 901 ATCAGGGTAGTCTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCACAATACTCATGCCA 960  
QY 961 GCTCATTTACAGATGAGACAGAGCTTTTATCTCCTAATAAGACAGAGATGATGATAGAAA 1020  
DB 961 GCTCATTTACAGATGAGACAGAGCTTTTATCTCCTAATAAGACAGAGATGATGATAGAAA 1020  
QY 1021 AGGCTGAATTTCTGTAATAAAGCAACAGCTGTGCTTAGCAAGGAGCAACATACAGAT 1080  
DB 1021 AGGCTGAATTTCTGTAATAAAGCAACAGCTGTGCTTAGCAAGGAGCAACATACAGAT 1080  
QY 1081 GGGCTGGAAGTAAAGGAAACATGTAATGATAGGCGGACTCCAGCACAGAAAAAGGTAG 1140  
DB 1081 GGGCTGGAAGTAAAGGAAACATGTAATGATAGGCGGACTCCAGCACAGAAAAAGGTAG 1140  
QY 1141 ATCTGAATGCTGATCCCTCTGTGTGAGAGAAAGAAATGGAATAGCAGAAATCTGCATGCT 1200  
DB 1141 ATCTGAATGCTGATCCCTCTGTGTGAGAGAAAGAAATGGAATAGCAGAAATCTGCATGCT 1200  
QY 1201 CAGAGATCTCAGAGATCTGAGAGTCTCTCTGGATAACACATAAATAGCAGCAATTGAGA 1260  
DB 1201 CAGAGATCTCAGAGATCTGAGAGTCTCTCTGGATAACACATAAATAGCAGCAATTGAGA 1260  
QY 1261 AAGTTAATGATGTTGTTTCCAGAAAGTGAATGATGATGTTTCTGATGACTCAGATGATG 1320  
DB 1261 AAGTTAATGATGTTGTTTCCAGAAAGTGAATGATGATGTTTCTGATGACTCAGATGATG 1320  
QY 1321 GGGAGTCTGAATCAAAATGCGCAAGTGTGATGTTTGGAGCTTTCTAAATGAGGTAGATG 1380  
DB 1321 GGGAGTCTGAATCAAAATGCGCAAGTGTGATGTTTGGAGCTTTCTAAATGAGGTAGATG 1380  
QY 1381 AATATTTCTGTTTCTCAGAGAAATAGACTTCTGCGCAGTGATCTCTCATGAGGCTTTAA 1440  
DB 1381 AATATTTCTGTTTCTCAGAGAAATAGACTTCTGCGCAGTGATCTCTCATGAGGCTTTAA 1440  
QY 1441 TATGTAAGTGAAGAGTTCACCTCCAAATCAGTAGAGAGTAATATTGAAGACAAAATAT 1500  
DB 1441 TATGTAAGTGAAGAGTTCACCTCCAAATCAGTAGAGAGTAATATTGAAGACAAAATAT 1500  
QY 1501 TTGGAAAAA CCTATCGGAAGAGGCAAGCTCCCAACTTAAAGCCATGTAACTGAAAAATC 1560  
DB 1501 TTGGAAAAA CCTATCGGAAGAGGCAAGCTCCCAACTTAAAGCCATGTAACTGAAAAATC 1560  
QY 1561 TAATTTAGAGCAATTTGTTACTGAGCCACAGATAATACAGAGGCTCCCTCACAATA 1620  
DB 1561 TAATTTAGAGCAATTTGTTACTGAGCCACAGATAATACAGAGGCTCCCTCACAATA 1620  
QY 1621 AATTTAAAGCGTAAAGGAGACCTACATCAGGCTTTCTCTGAGAGTTTATCAAGAAAG 1680  
DB 1621 AATTTAAAGCGTAAAGGAGACCTACATCAGGCTTTCTCTGAGAGTTTATCAAGAAAG 1680  
QY 1681 CAGATTTGGCAGTTCAAAAGACTCTCTGAAATGATAAATCAGGGAACCTAACCAACGGAGC 1740  
DB 1681 CAGATTTGGCAGTTCAAAAGACTCTCTGAAATGATAAATCAGGGAACCTAACCAACGGAGC 1740  
QY 1741 AGAATGTCAGTGAATGAAATTAATTAATAGTGTGATGAGAAATAAACAAGAGTGAT 1800  
DB 1741 AGAATGTCAGTGAATGAAATTAATTAATAGTGTGATGAGAAATAAACAAGAGTGAT 1800  
QY 1801 CTATTTCAAGATGAGAAATCTTAACCCCAATAGAAATCACTCGAAAAAGAAATCTGCTTCA 1860  
DB 1801 CTATTTCAAGATGAGAAATCTTAACCCCAATAGAAATCACTCGAAAAAGAAATCTGCTTCA 1860  
QY 1861 AAACGAAAGCTGAACCTATTAAGCAGCAGTAAAGCAATATGGAATCGAAATTAATATCC 1920

Db 1861 ||||| AAAGCAAGCTGAACTATAAGCAGCAGTAAAGCAATATGGAACCTCGAATTAATAATATCC 1920  
Qy 1921 ACRATTCGAAAGCACCTTAAAGAAATAGGCTGAGGAGGAAGCTTCTACAGGCGATATTC 1980  
Db 1921 ACRATTCGAAAGCACCTTAAAGAAATAGGCTGAGGAGGAAGCTTCTACAGGCGATATTC 1980  
Qy 1981 ATGGCTTGAACCTAGTAGTCAAGTAAATCAAGCCACCTAAATGTGCTGAAATGGCAAA 2040  
Db 1981 ATGGCTTGAACCTAGTAGTCAAGTAAATCTAAGCCACCTAATGTGCTGAAATGGCAAA 2040  
Qy 2041 TTGATAGTGTCTAGCAGTGAAGATPAAAGAAAAAAGTACAAACCAATGGCAGTCA 2100  
Db 2041 TTGATAGTGTCTAGCAGTGAAGATPAAAGAAAAAAGTACAAACCAATGGCAGTCA 2100  
Qy 2101 GGCAAGCAGAAACCTTACACTCATGAGTAAAGTAAAGCACTGAGGAGCCAAAGAGA 2160  
Db 2101 GGCAAGCAGAAACCTTACACTCATGAGTAAAGTAAAGCACTGAGGAGCCAAAGAGA 2160  
Qy 2161 GTAAACAGCCAAATGAACAGACAGTAAAGACATGACAGTGATCTTCCAGAGCTGA 2220  
Db 2161 GTAAACAGCCAAATGAACAGACAGTAAAGACATGACAGTGATCTTCCAGAGCTGA 2220  
Qy 2221 AGTTAAACAAATGCACCTGGTCTTTTACTAAGTGTCAAATPACCAAGTCAACTTAAAGAA 2280  
Db 2221 AGTTAAACAAATGCACCTGGTCTTTTACTAAGTGTCAAATPACCAAGTCAACTTAAAGAA 2280  
Qy 2281 TTGTCAATCTAGCTTCCAGAGAGAAAGAAAGAGAACTAGAAACAGTCTTAAAGTGT 2340  
Db 2281 TTGTCAATCTAGCTTCCAGAGAGAAAGAAAGAGAACTAGAAACAGTCTTAAAGTGT 2340  
Qy 2341 CTAATAATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAAGAAAGGTTTGCACAACTG 2400  
Db 2341 CTAATAATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAAGAAAGGTTTGCACAACTG 2400  
Qy 2401 AAAGATCTGTAGAGAGTAGCAGTATTTCACTGGTACCTGGTACTGATTTATGGCACTCAGG 2460  
Db 2401 AAAGATCTGTAGAGAGTAGCAGTATTTCACTGGTACCTGGTACTGATTTATGGCACTCAGG 2460  
Qy 2461 AAAGTATCTGTTACTGGAAGTAGCAGTCTAGGGAAGGCAAAACAGAACCAATTAAT 2520  
Db 2461 AAAGTATCTGTTACTGGAAGTAGCAGTCTAGGGAAGGCAAAACAGAACCAATTAAT 2520  
Qy 2521 GTGTGAGTCAAGTGTGACGATTTGAAACCCCAAGGAGCTAAATCATGTTGTTTCCAAAG 2580  
Db 2521 GTGTGAGTCAAGTGTGACGATTTGAAACCCCAAGGAGCTAAATCATGTTGTTTCCAAAG 2580  
Qy 2581 ATAAATAGAAATGACACAGAAAGGCTTTAAGTATCCATTTGGGACATGAAGTTAAACCAAGTC 2640  
Db 2581 ATAAATAGAAATGACACAGAAAGGCTTTAAGTATCCATTTGGGACATGAAGTTAAACCAAGTC 2640  
Qy 2641 GGGAAACAGCATAGAAATGGAAGAAAGTGAACCTTGATGCTCAGTATTTGAGAAATACAT 2700  
Db 2641 GGGAAACAGCATAGAAATGGAAGAAAGTGAACCTTGATGCTCAGTATTTGAGAAATACAT 2700  
Qy 2701 TCAAGGTTTCAAGCGCCAGCTCATTTGCTCTGTTTCCAAATCCAGGAAATGCGAAGAGG 2760  
Db 2701 TCAAGGTTTCAAGCGCCAGCTCATTTGCTCTGTTTCCAAATCCAGGAAATGCGAAGAGG 2760  
Qy 2761 AATGTGCAACATCTCTGCCACTCTGGTCTTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
Db 2761 AATGTGCAACATCTCTGCCACTCTGGTCTTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
Qy 2821 TTGATGTGAACAAAGGAGAAATCAAGAAAGAAATGAGTCTAATATCAAGCTGTAC 2880  
Db 2821 TTGATGTGAACAAAGGAGAAATCAAGAAAGAAATGAGTCTAATATCAAGCTGTAC 2880  
Qy 2881 AGACAGTTAATATCACTGCGAGGCTTCTCTGTTGTTGTCAGAAAGATGAAGCCAGTTGATA 2940  
Db 2881 AGACAGTTAATATCACTGCGAGGCTTCTCTGTTGTTGTCAGAAAGATGAAGCCAGTTGATA 2940  
Qy 2941 ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTTCAGAGGCA 3000  
Db |||||

Db 2941 ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTTCAGAGGCA 3000  
Qy 3001 ACGAAACTGGACTCATTTACTTCCAAATPAAACATGAGACTTTTACAAACCCCATATCGTATAC 3060  
Db 3001 ACGAAACTGGACTCATTTACTTCCAAATPAAACATGAGACTTTTACAAACCCCATATCGTATAC 3060  
Qy 3061 CACCACATTTTCCCATCAAGTCAATTTGTTAAACTAAATGTAAGAAAAATCTGCTAGAGG 3120  
Db 3061 CACCACATTTTCCCATCAAGTCAATTTGTTAAACTAAATGTAAGAAAAATCTGCTAGAGG 3120  
Qy 3121 AAAATTTTGAGGAACATTTCAATGTCACTGAAAGAGAAATGGGAAATGAGAAACATTCCAA 3180  
Db 3121 AAAATTTTGAGGAACATTTCAATGTCACTGAAAGAGAAATGGGAAATGAGAAACATTCCAA 3180  
Qy 3181 GTACAGTGAGCACAAATTAGCCGTAATPAAACATTAGAGAAAAATGTTTTTAAAGGAGCCAGCT 3240  
Db 3181 GTACAGTGAGCACAAATTAGCCGTAATPAAACATTAGAGAAAAATGTTTTTAAAGGAGCCAGCT 3240  
Qy 3241 CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAAATGAAA 3300  
Db 3241 CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAAATGAAA 3300  
Qy 3301 TAGGTTCCAGTGATGAAAAACATTTCAAGCAGAACTAGGTAGAAAAACAGAGGGCCAAAAATGA 3360  
Db 3301 TAGGTTCCAGTGATGAAAAACATTTCAAGCAGAACTAGGTAGAAAAACAGAGGGCCAAAAATGA 3360  
Qy 3361 ATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGGCTCTATAAACAAGTCTTCTCTGGAA 3420  
Db 3361 ATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGGCTCTATAAACAAGTCTTCTCTGGAA 3420  
Qy 3421 GTAAATCTGAAGCACTCTGAAATAAAAAGCAAGAAATGAAGAGTAGTAGTTTCAGACTGTGA 3480  
Db 3421 GTAAATCTGAAGCACTCTGAAATAAAAAGCAAGAAATGAAGAGTAGTAGTTTCAGACTGTGA 3480  
Qy 3481 ATACAGATTTCTCTCCATATCTGATTTTCAGATAAATTTAGAACAGCCTATGGAAGTAGTC 3540  
Db 3481 ATACAGATTTCTCTCCATATCTGATTTTCAGATAAATTTAGAACAGCCTATGGAAGTAGTC 3540  
Qy 3541 ATGCACTCAGGTTTGTCTTGAGACACCTGATGACCTGTTTAGATGATGGTGAATAAAGG 3600  
Db 3541 ATGCACTCAGGTTTGTCTTGAGACACCTGATGACCTGTTTAGATGATGGTGAATAAAGG 3600  
Qy 3601 AAGATCTAGTGTGCTGAAAAATGACATTAAGGAAAGTCTGCTGTTTTTAGCAAAAAGCG 3660  
Db 3601 AAGATCTAGTGTGCTGAAAAATGACATTAAGGAAAGTCTGCTGTTTTTAGCAAAAAGCG 3660  
Qy 3661 TCCAGAGAGGAGAGCTTTAGCAGGAGTCTTAGCCCTTTTACCCTATACACATTTGCTCAGG 3720  
Db 3661 TCCAGAGAGGAGAGCTTTAGCAGGAGTCTTAGCCCTTTTACCCTATACACATTTGCTCAGG 3720  
Qy 3721 GTTACCGAAGAGGGGCCAAGAAATTTAGAGTCTCTCAGAAAGAACTTATCTAGTGAGGATG 3780  
Db 3721 GTTACCGAAGAGGGGCCAAGAAATTTAGAGTCTCTCAGAAAGAACTTATCTAGTGAGGATG 3780  
Qy 3781 AAGAGCTTCTCCTGCTTCCAAACATCTGTTATTGTTGAAGTAAACAATATACCTTCTCAGT 3840  
Db 3781 AAGAGCTTCTCCTGCTTCCAAACATCTGTTATTGTTGAAGTAAACAATATACCTTCTCAGT 3840  
Qy 3841 CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGCTAAGAAACACAGAGGAGAAATTTAT 3900  
Db 3841 CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGCTAAGAAACACAGAGGAGAAATTTAT 3900  
Qy 3901 TATCATTTGAAGAATAGCTTAAATGACTGAGTAAACCCAGGTAATTTGGCAAGGCACTCTC 3960  
Db 3901 TATCATTTGAAGAATAGCTTAAATGACTGAGTAAACCCAGGTAATTTGGCAAGGCACTCTC 3960  
Qy 3961 AGGAAACATCACTTAGTGAGGAAAAAATAATGTTCTGCTAGCTGTTTTTCTTTCAGAGTGCA 4020  
Db 3961 AGGAAACATCACTTAGTGAGGAAAAAATAATGTTCTGCTAGCTGTTTTTCTTTCAGAGTGCA 4020  
Qy 4021 GTGAAATTTGGAAGACTTGACTGCAAAATACAAACCCAGGATCCTTTCTTGATTTGGTCTT 4080  
Db GTGAAATTTGGAAGACTTGACTGCAAAATACAAACCCAGGATCCTTTCTTGATTTGGTCTT 4080







Db 1621 AATTAAAGCGTAAAGAGGACCTACATCAGGCCCTTCATCTGAGGATTTTATCAAGAAAG 1680  
Qy 1681 CAGATTTGGCAGTTCAAAAGACTCCTGAAATGATAAATACAGGGAACCTAACCAACCGGAGC 1740  
Db 1681 CAGATTTGGCAGTTCAAAAGACTCCTGAAATGATAAATACAGGGAACCTAACCAACCGGAGC 1740  
Qy 1741 AGAATGCTCAAGTCAGTGAATTAATTAATTAATGCTCATGAGATTAACCAACCAAGGTCAT 1800  
Db 1741 AGAATGCTCAAGTCAGTGAATTAATTAATTAATGCTCATGAGATTAACCAACCAAGGTCAT 1800  
Qy 1801 CTATTCAGAATGAGAAAATCCTAACCCAATAGAAATCACTCGAAAAAGAAATCTGCTTTCA 1860  
Db 1801 CTATTCAGAATGAGAAAATCCTAACCCAATAGAAATCACTCGAAAAAGAAATCTGCTTTCA 1860  
Qy 1861 AAACGAAAGCTGAACCTATTAAGCAGCAGTATAAGCAATATGGAACTCGAAATTAATATCC 1920  
Db 1861 AAACGAAAGCTGAACCTATTAAGCAGCAGTATAAGCAATATGGAACTCGAAATTAATATCC 1920  
Qy 1921 ACAATTCAAAAGCAGCTTAAAGAAATAGGCTGAGGAGGAAGTCTTCTACCGGCATATTC 1980  
Db 1921 ACAATTCAAAAGCAGCTTAAAGAAATAGGCTGAGGAGGAAGTCTTCTACCGGCATATTC 1980  
Qy 1981 ATGGCTTTGAACCTAGTAGTCACTAGTAAGAACTTAAGCCCACTTAATTTGACTGAATTCGAAA 2040  
Db 1981 ATGGCTTTGAACCTAGTAGTCACTAGTAAGAACTTAAGCCCACTTAATTTGACTGAATTCGAAA 2040  
Qy 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATTAAGAAAAGAAAGTACAACTGAGTCCAGTCA 2100  
Db 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATTAAGAAAAGAAAGTACAACTGAGTCCAGTCA 2100  
Qy 2101 GGCAACAGAGAAACCTCAACTCATGGAAGTAAAGAACTGGAACCTGGAAGCCAAAGAA 2160  
Db 2101 GGCAACAGAGAAACCTCAACTCATGGAAGTAAAGAACTGGAACCTGGAAGCCAAAGAA 2160  
Qy 2161 GTACAGACCAATGAACAGCAAGTAAAGACATGACATGATACCTTTCCAGAGCTGA 2220  
Db 2161 GTACAGACCAATGAACAGCAAGTAAAGACATGACATGATACCTTTCCAGAGCTGA 2220  
Qy 2221 AGTTAAACAATGCACTGGTCTTTTACTAAGTGTCAAAATACCAATGCACTTAAGAAAT 2280  
Db 2221 AGTTAAACAATGCACTGGTCTTTTACTAAGTGTCAAAATACCAATGCACTTAAGAAAT 2280  
Qy 2281 TTGTCATCTCCTAGCCTTCCAGAGAGAGAAAAGAGAGAAACTAGAAAACAGTCTAAAGTGT 2340  
Db 2281 TTGTCATCTCCTAGCCTTCCAGAGAGAGAAAAGAGAGAAACTAGAAAACAGTCTAAAGTGT 2340  
Qy 2341 CTAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGTTTTCGAAACTG 2400  
Db 2341 CTAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGTTTTCGAAACTG 2400  
Qy 2401 AAAGATCTGTAGAGAGTAGCAGTATTTCACTGGTACCTGGTACTGATTTATGGCACTCAGG 2460  
Db 2401 AAAGATCTGTAGAGAGTAGCAGTATTTCACTGGTACCTGGTACTGATTTATGGCACTCAGG 2460  
Qy 2461 AAAGTATCTCGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAACAGAACCAATTAAT 2520  
Db 2461 AAAGTATCTCGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAACAGAACCAATTAAT 2520  
Qy 2521 GTGTGAGTCAGTGTGACAGATTTGAAAACCCCAAGGAGCTAAATTCATGGTTTTCGAAAG 2580  
Db 2521 GTGTGAGTCAGTGTGACAGATTTGAAAACCCCAAGGAGCTAAATTCATGGTTTTCGAAAG 2580  
Qy 2581 ATATAGAAATGACACAGAGGCTTAAAGTATCAATTTGGGACATGAAGTTAAACACAGTC 2640  
Db 2581 ATATAGAAATGACACAGAGGCTTAAAGTATCAATTTGGGACATGAAGTTAAACACAGTC 2640  
Qy 2641 GGGAAAACAGCATAGAAATGGAAGAGTGAATTTGATGCTCAGTATTTGAGAAATACAT 2700  
Db 2641 GGGAAAACAGCATAGAAATGGAAGAGTGAATTTGATGCTCAGTATTTGAGAAATACAT 2700  
Qy 2701 TCAAGGTTTCAAAGCGCCAGTCATTTGCTCTGTTTTCAAATCCAGGAAATGACAGAGG 2760  
Db 2701 TCAAGGTTTCAAAGCGCCAGTCATTTGCTCTGTTTTCAAATCCAGGAAATGACAGAGG 2760

Qy 2761 AATGTGCAACATTTCTCTGCCCACTCTGGGTCCTTTAAAGAAAACAAAGTCCAAAAGTCACTT 2820  
Db 2761 AATGTGCAACATTTCTCTGCCCACTCTGGGTCCTTTAAAGAAAACAAAGTCCAAAAGTCACTT 2820  
Qy 2821 TTGAATCTGAAACAAAAGGAGAAAATCAAGAAAGAAATGAGTCTTAATATCAAGCCTGTAC 2880  
Db 2821 TTGAATCTGAAACAAAAGGAGAAAATCAAGAAAGAAATGAGTCTTAATATCAAGCCTGTAC 2880  
Qy 2881 AGACAGTTAATATACATCTGACAGGCTTTCTCTGGTTGCTCAGAAAAGATAAGCCAGTTGATA 2940  
Db 2881 AGACAGTTAATATACATCTGACAGGCTTTCTCTGGTTGCTCAGAAAAGATAAGCCAGTTGATA 2940  
Qy 2941 ATGCCAAATCTAGTATCAAAAGGAGGCTCTAGGTTTCTCTATCATCTCAGTTTCAGAGGCA 3000  
Db 2941 ATGCCAAATCTAGTATCAAAAGGAGGCTCTAGGTTTCTCTATCATCTCAGTTTCAGAGGCA 3000  
Qy 3001 ACCGAACTGACCTCATTTACTCCAAATAAACATGGACTTTTACAAAACCCATATCGTATAC 3060  
Db 3001 ACCGAACTGACCTCATTTACTCCAAATAAACATGGACTTTTACAAAACCCATATCGTATAC 3060  
Qy 3061 CACCACCTTTTCCCATCAAGTCAATTTGTTAAACCTAAATGTAAGAAAATCTGCTAGAGG 3120  
Db 3061 CACCACCTTTTCCCATCAAGTCAATTTGTTAAACCTAAATGTAAGAAAATCTGCTAGAGG 3120  
Qy 3121 AAAAATTTGAGGAAACATTTCAATGTCACTGAAAGAGAAAATGGGAAAATGAGAAATTCGAA 3180  
Db 3121 AAAAATTTGAGGAAACATTTCAATGTCACTGAAAGAGAAAATGGGAAAATGAGAAATTCGAA 3180  
Qy 3181 GTACAGTGACACAAATTTAGCCGCTAAATCAATTAGAGAAAATGTTTTTAAAGGAGCCAGCT 3240  
Db 3181 GTACAGTGACACAAATTTAGCCGCTAAATCAATTAGAGAAAATGTTTTTAAAGGAGCCAGCT 3240  
Qy 3241 CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA 3300  
Db 3241 CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA 3300  
Qy 3301 TAGGTTCCAGTGATGAAAAACATTTCAAGCAGAACTAGGTAGAAAACAGAGGGCCAAAATTTGA 3360  
Db 3301 TAGGTTCCAGTGATGAAAAACATTTCAAGCAGAACTAGGTAGAAAACAGAGGGCCAAAATTTGA 3360  
Qy 3361 ATGCTATGCTTAGATTTAGGGGTTTTGCAACTGAGGCTCTATAAACAAAGTCTTCTCGGAA 3420  
Db 3361 ATGCTATGCTTAGATTTAGGGGTTTTGCAACTGAGGCTCTATAAACAAAGTCTTCTCGGAA 3420  
Qy 3421 GTAAATCTGAGCACTCTGAAATAAAGCAAGAAATATGAAGTAGTCTCAGACTGTTA 3480  
Db 3421 GTAAATCTGAGCACTCTGAAATAAAGCAAGAAATATGAAGTAGTCTCAGACTGTTA 3480  
Qy 3481 ATACAGATTTCTCTCCATATCTGATTTTCAAGTAACTTAGAACAGCCTATGGGAAAGTAGTC 3540  
Db 3481 ATACAGATTTCTCTCCATATCTGATTTTCAAGTAACTTAGAACAGCCTATGGGAAAGTAGTC 3540  
Qy 3541 ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTTAGATGATGGTGAATAAAGG 3600  
Db 3541 ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTTAGATGATGGTGAATAAAGG 3600  
Qy 3601 AAGTACTAGTTTGTCTGAAAATGACATTAAGGAAAGTCTGCTGTTTTTAAAGCAAGGCG 3660  
Db 3601 AAGTACTAGTTTGTCTGAAAATGACATTAAGGAAAGTCTGCTGTTTTTAAAGCAAGGCG 3660  
Qy 3661 TCCAGAGAGGAGGAGTCTTAGCAGGAGTCTTAGCCCTTTTCAACCATACATTTGGCTCAGG 3720  
Db 3661 TCCAGAGAGGAGGAGTCTTAGCAGGAGTCTTAGCCCTTTTCAACCATACATTTGGCTCAGG 3720  
Qy 3721 GTTACCGAAGAGGGGCCCAAGAAATTTAGAGTCTCAGAAAGAGAACTTATCTAGTGAGGATG 3780  
Db 3721 GTTACCGAAGAGGGGCCCAAGAAATTTAGAGTCTCAGAAAGAGAACTTATCTAGTGAGGATG 3780  
Qy 3781 AAGAGCTTCCCTGCTTCCAAACATTTGTTTATTTGGTAAAGTAAACAATATACCTTCTCAGT 3840  
Db 3781 AAGAGCTTCCCTGCTTCCAAACATTTGTTTATTTGGTAAAGTAAACAATATACCTTCTCAGT 3840



QY	3841	CTACTAGCATAGACCGTGTCTACCGAGTGTCTGTCTAAGAAACACACAGAGAGAAATTTAT	3900
DB	3841	CTACTAGCATAGACCGTGTCTACCGAGTGTCTGTCTAAGAAACACACAGAGAGAAATTTAT	3900
QY	3901	TATCATTGAAGATAGCTTAAATGACCTGCAGTACACAGGTAATATTTGGGAAAGGCATCTC	3960
DB	3901	TATCATTGAAGATAGCTTAAATGACCTGCAGTACACAGGTAATATTTGGGAAAGGCATCTC	3960
QY	3961	AGGAACATCACCTTAGTGGAGAAACAAATGTTCTGCTAGCTGTGTTTCTTTCACAGTGCA	4020
DB	3961	AGGAACATCACCTTAGTGGAGAAACAAATGTTCTGCTAGCTGTGTTTCTTTCACAGTGCA	4020
QY	4021	GTGAATTTGGAAGCTTGCATGCAATAACAAACCCAGGATCCTTTCTTGATTTGGTTCTT	4080
DB	4021	GTGAATTTGGAAGCTTGCATGCAATAACAAACCCAGGATCCTTTCTTGATTTGGTTCTT	4080
QY	4081	CCAAACAATAGGCGATCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGCAACGAATTTGG	4140
DB	4081	CCAAACAATAGGCGATCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGCAACGAATTTGG	4140
QY	4141	TTTCAGATGATGAAGAAAGAGGACGGCTTTGGAAGAAATATATCAAGAGAGCAAGCA	4200
DB	4141	TTTCAGATGATGAAGAAAGAGGACGGCTTTGGAAGAAATATATCAAGAGAGCAAGCA	4200
QY	4201	TGGATTTCAAACTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAAACAAAGCGTCTCTGAAG	4260
DB	4201	TGGATTTCAAACTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAAACAAAGCGTCTCTGAAG	4260
QY	4261	ACTGCTCAGGCTATCCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGATACCATGC	4320
DB	4261	ACTGCTCAGGCTATCCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGATACCATGC	4320
QY	4321	AACATACCTGATAAAGCTCCAGCAGGAATGGCTGAATAGAGCTGTGTTAGAACAGC	4380
DB	4321	AACATACCTGATAAAGCTCCAGCAGGAATGGCTGAATAGAGCTGTGTTAGAACAGC	4380
QY	4381	ATGGAGCCAGCCTTCTAAACAGCTACCCCTTCCATATAAGTGAATCTCTGCGCCCTTGAGG	4440
DB	4381	ATGGAGCCAGCCTTCTAAACAGCTACCCCTTCCATATAAGTGAATCTCTGCGCCCTTGAGG	4440
QY	4441	ACCTGGAAATCCAGAACAAAGCNCATCAGAAAAAGCAGTATTTAACTTCAAGAAAGTA	4500
DB	4441	ACCTGGAAATCCAGAACAAAGCNCATCAGAAAAAGCAGTATTTAACTTCAAGAAAGTA	4500
QY	4501	GTGAATACCTTATAAGCCAGAAATCCAGAGGCTTTCTGCTGACAAAGTTTGGAGTGCTG	4560
DB	4501	GTGAATACCTTATAAGCCAGAAATCCAGAGGCTTTCTGCTGACAAAGTTTGGAGTGCTG	4560
QY	4561	CAGATAGTTCTACCAAGTAAATAAAGAACCCAGAGTGGAAAGTCAATCCCTTCTAAAT	4620
DB	4561	CAGATAGTTCTACCAAGTAAATAAAGAACCCAGAGTGGAAAGTCAATCCCTTCTAAAT	4620
QY	4621	GCCCATCATTTAGATGATAGTGTTATGACAGAGTGTCTCTGGAGTCTTTCAGAAATAGAA	4680
DB	4621	GCCCATCATTTAGATGATAGTGTTATGACAGAGTGTCTCTGGAGTCTTTCAGAAATAGAA	4680
QY	4681	ACTACCCATCTCAAGAGGAGCTCATTAAGTGTGTTGATGTTGGAGGAGCAACAGCTGGAAG	4740
DB	4681	ACTACCCATCTCAAGAGGAGCTCATTAAGTGTGTTGATGTTGGAGGAGCAACAGCTGGAAG	4740
QY	4741	AGTCTGGGCCACACGATTTGACCGAAACATCTTACTTTGCCAAGGCAAGATCTAGAGGGAA	4800
DB	4741	AGTCTGGGCCACACGATTTGACCGAAACATCTTACTTTGCCAAGGCAAGATCTAGAGGGAA	4800
QY	4801	CCCTTACTTGGAAATCTGGAATCAGCCTTCTCTGATGACCCCTGAAATCTGATCTCTG	4860
DB	4801	CCCTTACTTGGAAATCTGGAATCAGCCTTCTCTGATGACCCCTGAAATCTGATCTCTG	4860
QY	4861	AAGACAGAGCCCGAGAGTCTGCTGTTGGCAACATACCATCTTCAACCTCTGCAATGA	4920
DB	4861	AAGACAGAGCCCGAGAGTCTGCTGTTGGCAACATACCATCTTCAACCTCTGCAATGA	4920
QY	4921	AAGTTCCTCCAAATTTGAAAGTTGCAGAAATCTGCCAGGGTCCAGCTGTGCTCATACTACTG	4980

DB	4921	AAGTTCCTCCAAATTTGAAAGTTGCAGAAATCTGCCAGGGTCCAGCTGTGCTCATACTACTG	4980
QY	4981	ATACTCTGGTATATGCAATGGAAGAAAGTGTGAGCAGGAGGAGCAAGATTTGACAG	5040
DB	4981	ATACTCTGGTATATGCAATGGAAGAAAGTGTGAGCAGGAGGAGCAAGATTTGACAG	5040
QY	5041	CTTCAACAGAAAGGGTCAACAAAGAAATGTCATGTTGGTGTCTGGCTTCACCCAGAG	5100
DB	5041	CTTCAACAGAAAGGGTCAACAAAGAAATGTCATGTTGGTGTCTGGCTTCACCCAGAG	5100
QY	5101	AATTTATGCTCGTGTACAAAGTTTGCAGAAAAACCAACATCACTTTAACTTAATTA	5160
DB	5101	AATTTATGCTCGTGTACAAAGTTTGCAGAAAAACCAACATCACTTTAACTTAATTA	5160
QY	5161	CTGAAGAGACTACTCATGTTGTTATGAAAAACAGATGCTGAGTTTGTGTGAACGGACAC	5220
DB	5161	CTGAAGAGACTACTCATGTTGTTATGAAAAACAGATGCTGAGTTTGTGTGAACGGACAC	5220
QY	5221	TGAAATATTTCTAGGAAATTTGCGGAGGAGAAATGGGTAGTGTAGCTATTCTTGGGTGACCC	5280
DB	5221	TGAAATATTTCTAGGAAATTTGCGGAGGAGAAATGGGTAGTGTAGCTATTCTTGGGTGACCC	5280
QY	5281	AGTCTTATTTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAGAGGAGATGTGG	5340
DB	5281	AGTCTTATTTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAGAGGAGATGTGG	5340
QY	5341	TCAATGGAAGAAACCAACCAAGGTCCAAAGCGCAGCAAGAAATCCAGGACAGAAAGATCT	5400
DB	5341	TCAATGGAAGAAACCAACCAAGGTCCAAAGCGCAGCAAGAAATCCAGGACAGAAAGATCT	5400
QY	5401	TCAGGGGGCTAGAAATCTGTTGCTATGGGCCCTTCCAAACATGCCACAGATCAACTGG	5460
DB	5401	TCAGGGGGCTAGAAATCTGTTGCTATGGGCCCTTCCAAACATGCCACAGATCAACTGG	5460
QY	5461	AATGGAATGTTACAGCTGTGTGGTGTCTTGTGTGGAAGGAGCTTTTCATCATTCACCCCTTG	5520
DB	5461	AATGGAATGTTACAGCTGTGTGGTGTCTTGTGTGGAAGGAGCTTTTCATCATTCACCCCTTG	5520
QY	5521	GCACAGGTGTCACCCCAATTTGGTGTGTCAGGCAGATGCTGTCGAGCAGAGGACAATGGCT	5580
DB	5521	GCACAGGTGTCACCCCAATTTGGTGTGTCAGGCAGATGCTGTCGAGCAGAGGACAATGGCT	5580
QY	5581	TCCATGCAATTTGGGCGAGATGTGTGAGGCACCTGTGTGTGACCCGAGAGTGGGTGAGACA	5640
DB	5581	TCCATGCAATTTGGGCGAGATGTGTGAGGCACCTGTGTGTGACCCGAGAGTGGGTGAGACA	5640
QY	5641	GTGTAGCACTCTACCAAGTCCAGGAGCTGGACACCTACCTGTATACCCAGATCCCCCACA	5700
DB	5641	GTGTAGCACTCTACCAAGTCCAGGAGCTGGACACCTACCTGTATACCCAGATCCCCCACA	5700
QY	5701	GCCACTACTGA 5711	
DB	5701	GCCACTACTGA 5711	

## RESULT 11

AAV46456  
ID AAV46456 standard; cDNA; 5711 BP.

XX AAV46456;

XX AC AC

XX 18-NOV-1998 (first entry)

XX Human BRCA1 omil polymorphism #6 cDNA.

XX BRCA1; omil; human; breast and ovarian cancer predisposing gene;  
XX polymorphism; susceptibility; anti-oncogene; tumour suppressor;  
XX chromosome 17q; ss.

XX Homo sapiens.

XX Key Location/Qualifiers  
FH

```

FT CDS 120..5711
FT /*tag= a
FT /product= "BRCA1 omi protein"
FT variation 4427
FT /*tag= b
FT /note= "This polymorphic variation can be a T or C
FT nucleotide"
XX US5750400-A.
XX
XX 12-MAY-1998. 97US-0798691.
XX
XX 12-FEB-1997;
XX
XX 12-FEB-1996; 96US-0598591.
XX 12-FEB-1997; 97US-0798691.
XX
XX (ONCO-) ONCORMED INC.
XX
XX Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ;
XX Schelter DB, Zeng B;
XX
XX WPI; 1998-296774/26.
XX
XX BRCA1 omi gene coding sequences - useful for distinguishing between
XX polymorphisms and mutation(s) in the screening for disposition to
XX breast or ovarian cancer
XX
XX Claim 2e; Page -; 54pp; English.
XX
XX This sequence encodes a human BRCA1 (breast and ovarian cancer
XX predisposing gene) omi gene in which a polymorphic variation occurs at
XX nucleotide 4427. This sequence and other polymorphic variations of this
XX sequence are useful for the identification of an individual who may or
XX may not have an increased susceptibility to breast or ovarian cancer.
XX The sequences used identify gene changes which are due to polymorphisms,
XX rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
XX suppressor) which is involved in genetic inheritance of cancers,
XX especially breast and ovarian cancer. It is found at human chromosome
XX 17q which is known to be linked to cancer susceptibility, especially
XX breast cancer. Cells containing a mutation in this gene lose the
XX wild-type function of BRCA1 and are more susceptible to cancers.
XX NOTE: This sequence does not appear in the specification but has been
XX created from the wild type BRCA1 omi gene represented in AAV46448.
XX
XX Sequence 5711 BP; 1953 A; 1098 C; 1277 G; 1382 T; 1 other;
XX
XX Query Match 100.0%; Score 5710.6; DB 19; Length 5711;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 AGCTCGCTGAGACTTCCTGGACCCCGCACAGGCTGTGGGTTTCTCAGATAACTGGGCC 60
XX |||||
XX 1 AGCTCGCTGAGACTTCCTGGACCCCGCACAGGCTGTGGGTTTCTCAGATAACTGGGCC 60
XX
XX 61 CCTCGCTCAGAGGCGCTTCAACCTCTGCTCTGGGTAAAGTTCAATGGAAACAGAAAGAAA 120
XX 61 CCTCGCTCAGAGGCGCTTCAACCTCTGCTCTGGGTAAAGTTCAATGGAAACAGAAAGAAA 120
XX
XX 121 TGGATTTATCTGCTCTTCGCGTTGAAGAGTACAAAATGTCATTAATGCTATGACAGAAA 180
XX 121 TGGATTTATCTGCTCTTCGCGTTGAAGAGTACAAAATGTCATTAATGCTATGACAGAAA 180
XX
XX 181 TCTTAGAGTGCCTCTGCTGAGTTGATCAAGGACCTGTCTCCACAAGTGTGACC 240
XX 181 TCTTAGAGTGCCTCTGCTGAGTTGATCAAGGACCTGTCTCCACAAGTGTGACC 240
XX
XX 241 ACATATTTGCAATTTTGCATGCTGAACTTCTCAACCAAGAAAGGGGCTTCAAGT 300
XX 241 ACATATTTGCAATTTTGCATGCTGAACTTCTCAACCAAGAAAGGGGCTTCAAGT 300
XX
XX 301 GTCCTTTATGATGATATATAACCAAAAGGACCTTACAAAGTAACGAGATTTAGTC 360
XX |||||

```

```

301 GTCCTTTATGATGATATATAACCAAAAGGACCTTACAAAGTAACGAGATTTAGTC 360
361 AACTTGTGAGAGCTATTGAAAATCATTTGTGCTTTTTCAGCTTTGACACAGGTTGGAGT 420
361 AACTTGTGAGAGCTATTGAAAATCATTTGTGCTTTTTCAGCTTTGACACAGGTTGGAGT 420
421 ATGCAACAGCTATATAATTTTGCAAAAGGAAAATAAATCTCTCCTGAAACATCTAAAGATG 480
421 ATGCAACAGCTATATAATTTTGCAAAAGGAAAATAAATCTCTCCTGAAACATCTAAAGATG 480
481 AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCAAAAGACTTCTACAGAGTG 540
481 AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCAAAAGACTTCTACAGAGTG 540
541 AACCCGAAAATCCTTCTCTGAGGAAACCAAGTCTCAGTGTCCAACTCTCTAACCTTGGAA 600
541 AACCCGAAAATCCTTCTCTGAGGAAACCAAGTCTCAGTGTCCAACTCTCTAACCTTGGAA 600
601 CTGTGAGAACTCTGAGGACAAAAGCAGCGGATACAACTCTAAAAGACGTCGTCTACATTG 660
601 CTGTGAGAACTCTGAGGACAAAAGCAGCGGATACAACTCTAAAAGACGTCGTCTACATTG 660
661 AATTGGGATCTGATTCTTCTGAGATACCGTTAATAAGGCAACTTATTGCAAGTGTGGAG 720
661 AATTGGGATCTGATTCTTCTGAGATACCGTTAATAAGGCAACTTATTGCAAGTGTGGAG 720
721 ATCAAGAAATTTGTACAAATCACCCCTCAAGGAAACAGGAGTGAATCAGTTTGGATTCTG 780
721 ATCAAGAAATTTGTACAAATCACCCCTCAAGGAAACAGGAGTGAATCAGTTTGGATTCTG 780
781 CAAAAAGGCTGCTTGTGAATTTTCTGAGACGGATGTAACAAATCTGAAACATCATCAAC 840
781 CAAAAAGGCTGCTTGTGAATTTTCTGAGACGGATGTAACAAATCTGAAACATCATCAAC 840
841 CCAGTAAATATGATTTTGAACACCACTGAGAGCGCTGAGCTGAGAGGATCCAGAAAGT 900
841 CCAGTAAATATGATTTTGAACACCACTGAGAGCGCTGAGCTGAGAGGATCCAGAAAGT 900
901 ATCAGGCTAGTTCTGTTTCAAACTTGTGAGCCATGTGGCAACAATACTCATGCCA 960
901 ATCAGGCTAGTTCTGTTTCAAACTTGTGAGCCATGTGGCAACAATACTCATGCCA 960
961 GCTCATTACAGCATGAGAAACAGAGTTTATTACTCATTAAAGACAGAAATGATGAGAAA 1020
961 GCTCATTACAGCATGAGAAACAGAGTTTATTACTCATTAAAGACAGAAATGATGAGAAA 1020
1021 AGGCTGAATTTCTGTAATAAAGCAACAGCTGCTTAGCAAGGAGCCCAACATACAGAT 1080
1021 AGGCTGAATTTCTGTAATAAAGCAACAGCTGCTTAGCAAGGAGCCCAACATACAGAT 1080
1081 GGGCTGGAAGTAAGGAAACATGTAATGATAGCGGACTCCAGCACAGAAAAAGGTAG 1140
1081 GGGCTGGAAGTAAGGAAACATGTAATGATAGCGGACTCCAGCACAGAAAAAGGTAG 1140
1141 ATCTGAATGCTGATCCCTCTGTGTGAGAGAAAGAAATGGAATAAGCAGAAACCTGCCATGCT 1200
1141 ATCTGAATGCTGATCCCTCTGTGTGAGAGAAAGAAATGGAATAAGCAGAAACCTGCCATGCT 1200
1201 CAGGAATCTTAGAGATCTGGAAGATGTTCTTGGATAACACTAAATAGCAGCATTCAGA 1260
1201 CAGGAATCTTAGAGATCTGGAAGATGTTCTTGGATAACACTAAATAGCAGCATTCAGA 1260
1261 AAGTTAATGATGTTGTTTTCCAGAAAGTATGAATGTTTCTGATGACTCACATGATG 1320
1261 AAGTTAATGATGTTGTTTTCCAGAAAGTATGAATGTTTCTGATGACTCACATGATG 1320
1321 GGGAGTCTGAATCAAAATGCCAAAGTAGTGTATTTGGACGTTCTAAATGAGGTAGATG 1380
1321 GGGAGTCTGAATCAAAATGCCAAAGTAGTGTATTTGGACGTTCTAAATGAGGTAGATG 1380
1381 AATATCTGGTTCTTACAGAGAAATAGACTTACTTGGCCAGTGTCTCATGAGGCTTTAA 1440
1381 AATATCTGGTTCTTACAGAGAAATAGACTTACTTGGCCAGTGTCTCATGAGGCTTTAA 1440

```

Qy	1441	TATGTAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGAGTAATATTGAAGACAAATAT	1500
Db	1441	TATGTAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGAGTAATATTGAAGACAAATAT	1500
Qy	1501	TTGGGAAAACCTATCGGAAGAGGCAAGCCCTCCCAACTTAAGCCATGTAACTGAAAATC	1560
Db	1501	TTGGGAAAACCTATCGGAAGAGGCAAGCCCTCCCAACTTAAGCCATGTAACTGAAAATC	1560
Qy	1561	TAATTATAGGAGCATTTGTTACTGAGGCACAGATAATACAAAGAGCGTCCCTCCAAATA	1620
Db	1561	TAATTATAGGAGCATTTGTTACTGAGGCACAGATAATACAAAGAGCGTCCCTCCAAATA	1620
Qy	1621	AATTTAAAGCGTAAAGAGAGCTTACATCAGCCCTTCACTCTGAGGATTTTATCAAGAAAG	1680
Db	1621	AATTTAAAGCGTAAAGAGAGCTTACATCAGCCCTTCACTCTGAGGATTTTATCAAGAAAG	1680
Qy	1681	CAGATTTGGCAGTTCAAAAAGACTCCTGAAATGATAAATCAGGAACTAAACCAACGGAGC	1740
Db	1681	CAGATTTGGCAGTTCAAAAAGACTCCTGAAATGATAAATCAGGAACTAAACCAACGGAGC	1740
Qy	1741	AGAATGTCAGTGATGAATATTACTAATAGTGTCTATGAGATATAAACAAGAGTGATT	1800
Db	1741	AGAATGTCAGTGATGAATATTACTAATAGTGTCTATGAGATATAAACAAGAGTGATT	1800
Qy	1801	CTATTCAAGATGAGAAAATCCTTAACCCAAATAGAACTCACTCGAAAAGAAATCTGCTTTCA	1860
Db	1801	CTATTCAAGATGAGAAAATCCTTAACCCAAATAGAACTCACTCGAAAAGAAATCTGCTTTCA	1860
Qy	1861	AAACGAAAGCTGAACTTAAAGCAGCAGTATAGCAATATGGAACCTCGAATTTAAATATCC	1920
Db	1861	AAACGAAAGCTGAACTTAAAGCAGCAGTATAGCAATATGGAACCTCGAATTTAAATATCC	1920
Qy	1921	ACAAATCAAAAGCCTTAAAGAGATAGGCTGAGGAGAGTCTTCTACCAGGCATATTC	1980
Db	1921	ACAAATCAAAAGCCTTAAAGAGATAGGCTGAGGAGAGTCTTCTACCAGGCATATTC	1980
Qy	1981	ATGGGCTTGAACCTAGTAGTCAGTAGAATCTTAAGCCCACTTAATTTGACTGAATTCGAAA	2040
Db	1981	ATGGGCTTGAACCTAGTAGTCAGTAGAATCTTAAGCCCACTTAATTTGACTGAATTCGAAA	2040
Qy	2041	TTGATAGTTGTTCTAGCAGTGAAGAGATAAAGAAAAAAGTACAACTGCAATGCGAGTCA	2100
Db	2041	TTGATAGTTGTTCTAGCAGTGAAGAGATAAAGAAAAAAGTACAACTGCAATGCGAGTCA	2100
Qy	2101	GGCACAGCAGAACTTCACTATGGAAGTAAAGAACTGCACTGGAAGCCCAAGAGA	2160
Db	2101	GGCACAGCAGAACTTCACTATGGAAGTAAAGAACTGCACTGGAAGCCCAAGAGA	2160
Qy	2161	GTAACAAGCCAAATGAACAGACAGTAAAGACATGACAGTACTTTCCAGAGCTGA	2220
Db	2161	GTAACAAGCCAAATGAACAGACAGTAAAGACATGACAGTACTTTCCAGAGCTGA	2220
Qy	2221	AGTTAAACAAATGCACTGGTCTTTTACTAAGTGTTCAAAATACCAAGTGAATTTAAAGAA	2280
Db	2221	AGTTAAACAAATGCACTGGTCTTTTACTAAGTGTTCAAAATACCAAGTGAATTTAAAGAA	2280
Qy	2281	TTGTCAATCTAGCCTTCCAGAGAGAAAGAAAGAGAACTAGAAAACAGTTAAAGTGT	2340
Db	2281	TTGTCAATCTAGCCTTCCAGAGAGAAAGAAAGAGAACTAGAAAACAGTTAAAGTGT	2340
Qy	2341	CTAATAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAGAGAAAGGTTTTCGAAACTG	2400
Db	2341	CTAATAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAGAGAAAGGTTTTCGAAACTG	2400
Qy	2401	AAAGATCTGAGAGTAGCAGTATTTCACTGGTACTGTTAGTATGAGCACTCAGG	2460
Db	2401	AAAGATCTGAGAGTAGCAGTATTTCACTGGTACTGTTAGTATGAGCACTCAGG	2460
Qy	2461	AAAGTATCTGTTACTGGAAGTTAGCACTCTAGGGAAGGCCAAAACAGAACCAATTAAT	2520
Db	2461	AAAGTATCTGTTACTGGAAGTTAGCACTCTAGGGAAGGCCAAAACAGAACCAATTAAT	2520

Qy	2521	GTGTAGTCAGTGTGACGACATTTGAAAAACCCCAAGGACATAATTCATGGTTGTTCCAAAG	2580
Db	2521	GTGTAGTCAGTGTGACGACATTTGAAAAACCCCAAGGACATAATTCATGGTTGTTCCAAAG	2580
Qy	2581	ATAATAGAAATGACACAGAAAGGCTTTAAAGTATCCATTTGGGACATGAAGTTAAACACAGTC	2640
Db	2581	ATAATAGAAATGACACAGAAAGGCTTTAAAGTATCCATTTGGGACATGAAGTTAAACACAGTC	2640
Qy	2641	GGGAAAACAGCATAGAAAATGGAAGAGTGAATTCATGCTCAGTATTTTCAGAAATACAT	2700
Db	2641	GGGAAAACAGCATAGAAAATGGAAGAGTGAATTCATGCTCAGTATTTTCAGAAATACAT	2700
Qy	2701	TCAAGGTTTCAAAAGCGCCAGTCATTTGCTCTGTTTTCAAAATCCAGGAAATGCGAAGAGG	2760
Db	2701	TCAAGGTTTCAAAAGCGCCAGTCATTTGCTCTGTTTTCAAAATCCAGGAAATGCGAAGAGG	2760
Qy	2761	AATGTGCAACATTTCTCTGCCCTCTCTGGGCTCTTAAAGAAACAAAGTCCAAAAGTCACTT	2820
Db	2761	AATGTGCAACATTTCTCTGCCCTCTCTGGGCTCTTAAAGAAACAAAGTCCAAAAGTCACTT	2820
Qy	2821	TTGAATGTGAACAAAAGGAAAGAAATCAAGGAAAGAAATGAGTCTAATATCAAGCCTGTAC	2880
Db	2821	TTGAATGTGAACAAAAGGAAAGAAATCAAGGAAAGAAATGAGTCTAATATCAAGCCTGTAC	2880
Qy	2881	AGACAGTTAATATACCTGACAGGCTTTCTCTGTTGGTTCAGAAAGATAAGCCAGTTCGATA	2940
Db	2881	AGACAGTTAATATACCTGACAGGCTTTCTCTGTTGGTTCAGAAAGATAAGCCAGTTCGATA	2940
Qy	2941	ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGGCA	3000
Db	2941	ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGGCA	3000
Qy	3001	ACGAAATGGAACCTTACTTCCAAATAAAGATGAGCTTTTACAAAACCAATATCGTATAC	3060
Db	3001	ACGAAATGGAACCTTACTTCCAAATAAAGATGAGCTTTTACAAAACCAATATCGTATAC	3060
Qy	3061	CACACATTTTCCCATCAAGTCAATTTGTTAAAACTAAATCTAAGAAAAATCTGTCAGAGG	3120
Db	3061	CACACATTTTCCCATCAAGTCAATTTGTTAAAACTAAATCTAAGAAAAATCTGTCAGAGG	3120
Qy	3121	AAAACTTTGAGGAACTTCAATGTCACTGAAAGAGAAATGGGAAATGAGAAACATTCCTAA	3180
Db	3121	AAAACTTTGAGGAACTTCAATGTCACTGAAAGAGAAATGGGAAATGAGAAACATTCCTAA	3180
Qy	3181	GTACAGTGAGCACAATTTAGCCGTAATAACATTAAGAGAAATGTTTTTAAAGGAGCCAGCT	3240
Db	3181	GTACAGTGAGCACAATTTAGCCGTAATAACATTAAGAGAAATGTTTTTAAAGGAGCCAGCT	3240
Qy	3241	CAAGCAATATTAAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA	3300
Db	3241	CAAGCAATATTAAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA	3300
Qy	3301	TAGGTTCCAGTGATGAAAAACATTTCAAGCAGAACTAGGTAGAAAACAGAGGCCAAATTTGA	3360
Db	3301	TAGGTTCCAGTGATGAAAAACATTTCAAGCAGAACTAGGTAGAAAACAGAGGCCAAATTTGA	3360
Qy	3361	ATGCTATGCTTAGATTTAGGGTTTTTGCACCTGAGTCTATAACAAAGTCTTCTCTGGAA	3420
Db	3361	ATGCTATGCTTAGATTTAGGGTTTTTGCACCTGAGTCTATAACAAAGTCTTCTCTGGAA	3420
Qy	3421	GTAATTTGAAGCATCTGAAAATAAAAAACGAAGTATGAAGAGTAGTTTCAGACTGTTA	3480
Db	3421	GTAATTTGAAGCATCTGAAAATAAAAAACGAAGTATGAAGAGTAGTTTCAGACTGTTA	3480
Qy	3481	ATAAGATTTCTCTCATATCTCATTTTCAGATAAATTTAGAACAGCCCTATCGGAGAGTAGTC	3540
Db	3481	ATAAGATTTCTCTCATATCTCATTTTCAGATAAATTTAGAACAGCCCTATCGGAGAGTAGTC	3540
Qy	3541	ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGG	3600
Db	3541	ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGG	3600
Qy	3601	AAGATACTAGTTTTTGTGCTGAAAATGACATTAAGGAAAAGTTCTGCTGTTTTTGTAGCAAAAGCG	3660

Db ||||| 3601 AAGTACTAGTTTGTGAAATGACATTAAGAAAGTTCTGCTGTTTTTGTAGCAAAAGCG 3660  
Qy ||||| 3661 TCCAGAGAGAGAGCTTTAGCAGGAGTCTCAGCCCTTTCAACCATAACATTTGCTCAGG 3720  
Db ||||| 3661 TCCAGAGAGAGAGCTTTAGCAGGAGTCTCAGCCCTTTCAACCATAACATTTGCTCAGG 3720  
Qy ||||| 3721 GTTACCGAAGAGGGCCCAAGAAATAGAGTCTCAGAGAGAACTTATCTAGTAGAGATG 3780  
Db ||||| 3721 GTTACCGAAGAGGGCCCAAGAAATAGAGTCTCAGAGAGAACTTATCTAGTAGAGATG 3780  
Qy ||||| 3781 AAGAGCTTCCCTGCTTCCACACATGTTATTTGTTAAAGTAAACAATATACCTTCTCAGT 3840  
Db ||||| 3781 AAGAGCTTCCCTGCTTCCACACATGTTATTTGTTAAAGTAAACAATATACCTTCTCAGT 3840  
Qy ||||| 3841 CTACTAGGCATAGCACCGTTGCTACCGAGTCTGTTCTAAGAAACACAGAGAGAAATTTAT 3900  
Db ||||| 3841 CTACTAGGCATAGCACCGTTGCTACCGAGTCTGTTCTAAGAAACACAGAGAGAAATTTAT 3900  
Qy ||||| 3901 TATCATTTGAAGATAGCTTAAATGACTGCAAGTAAACCAAGGTAAATTTGGCAAGCATCTC 3960  
Db ||||| 3901 TATCATTTGAAGATAGCTTAAATGACTGCAAGTAAACCAAGGTAAATTTGGCAAGCATCTC 3960  
Qy ||||| 3961 AGGAACATCACCCTTAGTGAGGAAACAAAATGTTCTGCTAGCTTTTCTTCAAGTGCA 4020  
Db ||||| 3961 AGGAACATCACCCTTAGTGAGGAAACAAAATGTTCTGCTAGCTTTTCTTCAAGTGCA 4020  
Qy ||||| 4021 GTGAATTTGGAAGACTTGACTGCAAAATCAAAACACCCAGGATCCCTTTCTTGATTTGGTCTT 4080  
Db ||||| 4021 GTGAATTTGGAAGACTTGACTGCAAAATCAAAACACCCAGGATCCCTTTCTTGATTTGGTCTT 4080  
Qy ||||| 4081 CCAAAACAAATGAGGCATCAGTCTGAAAGCCAGGAGTTGTTGCTGAGTGACAAGGAAATGG 4140  
Db ||||| 4081 CCAAAACAAATGAGGCATCAGTCTGAAAGCCAGGAGTTGTTGCTGAGTGACAAGGAAATGG 4140  
Qy ||||| 4141 TTTGAGATGATGAAGAAAGAGAAACGGGCTTTGGAAGAAAATAATCAAGAGAGCAAAAGCA 4200  
Db ||||| 4141 TTTGAGATGATGAAGAAAGAGAAACGGGCTTTGGAAGAAAATAATCAAGAGAGCAAAAGCA 4200  
Qy ||||| 4201 TGGATTCAAACTAGGTGAAAGCAGCATCTGGGTGTGAGAGTGAACAGGCTCTCTGAAG 4260  
Db ||||| 4201 TGGATTCAAACTAGGTGAAAGCAGCATCTGGGTGTGAGAGTGAACAGGCTCTCTGAAG 4260  
Qy ||||| 4261 ACTGCTCAGGCTATCCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGATACCATGC 4320  
Db ||||| 4261 ACTGCTCAGGCTATCCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGATACCATGC 4320  
Qy ||||| 4321 AACATAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACCTAGAGCTGTGTTAGAAACAGC 4380  
Db ||||| 4321 AACATAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACCTAGAGCTGTGTTAGAAACAGC 4380  
Qy ||||| 4381 ATGGAGGCCACCTTCTTAACAGCTACCTTCCATCATAGTGACTCTCTGCCCTTGAGG 4440  
Db ||||| 4381 ATGGAGGCCACCTTCTTAACAGCTACCTTCCATCATAGTGACTCTCTGCCCTTGAGG 4440  
Qy ||||| 4441 ACCTGCGAAATCCAGAACAAAGCAGCATCAGAAAAAGCAGATTAACCTTCAAGAAAAAGTA 4500  
Db ||||| 4441 ACCTGCGAAATCCAGAACAAAGCAGCATCAGAAAAAGCAGATTAACCTTCAAGAAAAAGTA 4500  
Qy ||||| 4501 GTGAATACCTTATAAGCCAGAAATCCAGAAAGCCCTTTCTGCTGACAAGTTTGGAGTGCTG 4560  
Db ||||| 4501 GTGAATACCTTATAAGCCAGAAATCCAGAAAGCCCTTTCTGCTGACAAGTTTGGAGTGCTG 4560  
Qy ||||| 4561 CAGATAGTTCTACAGGTAATAAAGAAACAGAGGTGGAAGGTCTATCCCTTCTTAAT 4620  
Db ||||| 4561 CAGATAGTTCTACAGGTAATAAAGAAACAGAGGTGGAAGGTCTATCCCTTCTTAAT 4620  
Qy ||||| 4621 GCGCATCATAGATGATAGGTGGTACATGACAGTTGCTCTGGGAGCTTCTCAGATAGAA 4680  
Db ||||| 4621 GCGCATCATAGATGATAGGTGGTACATGACAGTTGCTCTGGGAGCTTCTCAGATAGAA 4680  
Qy ||||| 4681 ACTACCCATCTCAAGAGAGCTCAATTAAGTTGTTGATGTGAGGAGCAACAGCTGGAAG 4740

Db ||||| 4681 ACTACCCATCTCAAGAGAGCTCATTAAGGTTGTTGATGTGGAGGAGCAACAGCTGGAAG 4740  
Qy ||||| 4741 AGTCTGGGCCACACGATTTTGAACGAAACATCTTATCTTCCAAAGCAAGATCTAGAGGAA 4800  
Db ||||| 4741 AGTCTGGGCCACACGATTTTGAACGAAACATCTTATCTTCCAAAGCAAGATCTAGAGGAA 4800  
Qy ||||| 4801 CCCCTTACCTGGAAATCTGGAATCAGCCTCTCTCTGATGACCCCTGAATCTGATCTTCTG 4860  
Db ||||| 4801 CCCCTTACCTGGAAATCTGGAATCAGCCTCTCTCTGATGACCCCTGAATCTGATCTTCTG 4860  
Qy ||||| 4861 AAGACAGAGCCCAAGAGTCAAGTCTGTGTGGCAACATACCATCTTCAACCTCTGCATTGA 4920  
Db ||||| 4861 AAGACAGAGCCCAAGAGTCAAGTCTGTGTGGCAACATACCATCTTCAACCTCTGCATTGA 4920  
Qy ||||| 4921 AAGTTCCCAATTTGAAAGTTGCAGAACTGCCCCAGGCTCCAGCTGCTCATACTCTG 4980  
Db ||||| 4921 AAGTTCCCAATTTGAAAGTTGCAGAACTGCCCCAGGCTCCAGCTGCTCATACTCTG 4980  
Qy ||||| 4981 ATACTGCTGGGTATAATGCAATGGAAGAAAGTGTGAGCAGGGAGAGCCAGAAATTGACAG 5040  
Db ||||| 4981 ATACTGCTGGGTATAATGCAATGGAAGAAAGTGTGAGCAGGGAGAGCCAGAAATTGACAG 5040  
Qy ||||| 5041 CTTCAACAGAAAGGCTCAACAAAGAAATGTCATGTTGTTCTGCTGCTGCTGCTGCTGCTG 5100  
Db ||||| 5041 CTTCAACAGAAAGGCTCAACAAAGAAATGTCATGTTGTTCTGCTGCTGCTGCTGCTGCTG 5100  
Qy ||||| 5101 AATTTATGCTCGTGACAAAGTTTCCAGAAACACACATCACCTTAACTTAATCTAATTA 5160  
Db ||||| 5101 AATTTATGCTCGTGACAAAGTTTCCAGAAACACACATCACCTTAACTTAATCTAATTA 5160  
Qy ||||| 5161 CTGAAGAGACTACTCATGTTGTTATGAAAAACAGATGCTGAGTTTGTGTGAAACGACAC 5220  
Db ||||| 5161 CTGAAGAGACTACTCATGTTGTTATGAAAAACAGATGCTGAGTTTGTGTGAAACGACAC 5220  
Qy ||||| 5221 TGAATAATTTTCTAGGAATTCGCGGAGAAATCGGTAGTTAGCTATTCTTCTGGGTGACCC 5280  
Db ||||| 5221 TGAATAATTTTCTAGGAATTCGCGGAGAAATCGGTAGTTAGCTATTCTTCTGGGTGACCC 5280  
Qy ||||| 5281 AGTCTATTAAGAAAGAAATGCTGATGAGCATGATTTTGAAGTCAAGAGAGATGTGG 5340  
Db ||||| 5281 AGTCTATTAAGAAAGAAATGCTGATGAGCATGATTTTGAAGTCAAGAGAGATGTGG 5340  
Qy ||||| 5341 TCAATGGAAGAAACCAAGGTTCCAAAGGAGCAAGAAATCCAGGACAGAAAGATCT 5400  
Db ||||| 5341 TCAATGGAAGAAACCAAGGTTCCAAAGGAGCAAGAAATCCAGGACAGAAAGATCT 5400  
Qy ||||| 5401 TCAGGGGCTAGAAATCTGTTGCTATGGGCCCTTCAACCAATGCCACAGATCAACTGG 5460  
Db ||||| 5401 TCAGGGGCTAGAAATCTGTTGCTATGGGCCCTTCAACCAATGCCACAGATCAACTGG 5460  
Qy ||||| 5461 AATGATGGTACAGCTGTGTGCTCTTCTGTGGTGAAGGAGCTTTCATCTTACCCCTTG 5520  
Db ||||| 5461 AATGATGGTACAGCTGTGTGCTCTTCTGTGGTGAAGGAGCTTTCATCTTACCCCTTG 5520  
Qy ||||| 5521 GCACAGGTGTCACCCCAATTTGTGTTGTGACAGCAGATGCTTGGACAGAGGACAAATGGCT 5580  
Db ||||| 5521 GCACAGGTGTCACCCCAATTTGTGTTGTGACAGCAGATGCTTGGACAGAGGACAAATGGCT 5580  
Qy ||||| 5581 TCCATGCAATTTGGCAGATGTGAGGACCTGTGTGTGACCCGAGAGTGGGTGTTGGACA 5640  
Db ||||| 5581 TCCATGCAATTTGGCAGATGTGAGGACCTGTGTGTGACCCGAGAGTGGGTGTTGGACA 5640  
Qy ||||| 5641 GTGTAGCACTTACAGTCCAGGAGCTGGACACTTACCTGATACCCAGATCCCCCACA 5700  
Db ||||| 5641 GTGTAGCACTTACAGTCCAGGAGCTGGACACTTACCTGATACCCAGATCCCCCACA 5700  
Qy ||||| 5701 GCCACTACTGA 5711  
Db ||||| 5701 GCCACTACTGA 5711

ID AAV46457 standard; cDNA; 5711 BP.  
 AC AAV46457;  
 XX 18-NOV-1998 (first entry)  
 DT  
 XX Human BRCA1 omil polymorphism #7 cDNA.  
 XX  
 XX BRCA1; omil; human; breast and ovarian cancer predisposing gene;  
 KW polymorphism; susceptibility; anti-oncogene; tumour suppressor;  
 KW chromosome 17q; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 PH 120..5711  
 FT /tag= a  
 FT /product= "BRCA1 omil protein"  
 FT 4956  
 FT variation  
 FT /tag= b  
 FT /note= "This polymorphic variation can be an A or G  
 nucleotide."  
 XX  
 PN US5750400-A.  
 XX  
 XX 12-MAY-1998. 97US-0798691.  
 PD  
 XX  
 PF 12-FEB-1997;  
 XX  
 PR 12-FEB-1996; 96US-0598591.  
 PR 12-FEB-1997; 97US-0798691.  
 XX  
 XX (ONCO-) ONCORMED INC.  
 XX  
 XX Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ;  
 PI Schelter DB, Zeng B;  
 PI  
 XX WPI; 1998-296774/26.  
 DR  
 XX  
 XX BRCA1 omi gene coding sequences - useful for distinguishing between  
 PT polymorphisms and mutation(s) in the screening for disposition to  
 PT breast or ovarian cancer  
 PT  
 XX  
 PS Claim 2e; Page -; 54pp; English.  
 XX  
 XX This sequence encodes a human BRCA1 (breast and ovarian cancer  
 CC predisposing gene) omil gene in which a polymorphic variation occurs at  
 CC nucleotide 4956. This sequence and other polymorphic variations of this  
 CC sequence are useful for the identification of an individual who may or  
 CC may not have an increased susceptibility to breast or ovarian cancer.  
 CC The sequences used identify gene changes which are due to polymorphisms,  
 CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour  
 CC suppressor) which is involved in genetic inheritance of cancers,  
 CC especially breast and ovarian cancer. It is found at human chromosome  
 CC 17q which is known to be linked to cancer susceptibility, especially  
 CC breast cancer. Cells containing a mutation in this gene lose the  
 CC wild-type function of BRCA1 and are more susceptible to cancers.  
 CC NOTE: This sequence does not appear in the specification but has been  
 CC created from the wild type BRCA1 omil gene represented in AAV46448.  
 XX  
 SQ Sequence 5711 BP; 1953 A; 1099 C; 1276 G; 1382 T; 1 other;  
 Query Match 100.0%; Score 5710.6; DB 19; Length 5711;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGCTCGCTGAGACTTCCTGACCCCGCACCAGGCTGTGGGTTCTCAGATAACTGGGCC 60  
 DB  
 DB 1 AGCTCGCTGAGACTTCCTGACCCCGCACCAGGCTGTGGGTTCTCAGATAACTGGGCC 60  
 QY 61 CTTGGCTCAGGAGGCTTCACCTCTGTCTGTGGTAAAGTTTCATTGGAAACAGAAAGAAA 120  
 DB 61 CTTGGCTCAGGAGGCTTCACCTCTGTCTGTGGTAAAGTTTCATTGGAAACAGAAAGAAA 120

Qy	1201	CAGAAATCCTAGAGATACGAAATGTTCTTGGATAAACCTAAATAGCGGATTCAGA	1260
Db	1201	CAGAAATCCTAGAGATACGAAATGTTCTTGGATAAACCTAAATAGCAGCATTCAGA	1260
Qy	1261	AAGTTAATGAGTGTTTTCAGAAAGTGAATGAATGTTAGGTTCTGATGACTCAGATG	1320
Db	1261	AAGTTAATGAGTGTTTTCAGAAAGTGAATGAATGTTAGGTTCTGATGACTCAGATG	1320
Qy	1321	GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGATTTGGAGCTTCTAAATGAGGTAGATG	1380
Db	1321	GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGATTTGGAGCTTCTAAATGAGGTAGATG	1380
Qy	1381	AATATTCGTGTTCTTCAGAGAAATAGACTTACTTGGCCAGTGATCCTCAAGAGCTTTAA	1440
Db	1381	AATATTCGTGTTCTTCAGAGAAATAGACTTACTTGGCCAGTGATCCTCAAGAGCTTTAA	1440
Qy	1441	TATGTAAAGTGAAGAGTTCACCTCCAAATCAGTAGAGAGTAATATTGAAGACAAATAT	1500
Db	1441	TATGTAAAGTGAAGAGTTCACCTCCAAATCAGTAGAGAGTAATATTGAAGACAAATAT	1500
Qy	1501	TTGGGAAATCCTATCGGAAGAGGCAAGCCTCCCAACTTAAGCCATGTAACCTGAAATC	1560
Db	1501	TTGGGAAATCCTATCGGAAGAGGCAAGCCTCCCAACTTAAGCCATGTAACCTGAAATC	1560
Qy	1561	TAATTTATGAGAGCAATTTGTTACTGAGCCACAGATAATACAGAGCGTCCCTCAAAATA	1620
Db	1561	TAATTTATGAGAGCAATTTGTTACTGAGCCACAGATAATACAGAGCGTCCCTCAAAATA	1620
Qy	1621	AATTTAAAGCTTAAAGGAGCTACATCAGCGCTTCATCCTGAGGATTTTATCAAGAAAG	1680
Db	1621	AATTTAAAGCTTAAAGGAGCTACATCAGCGCTTCATCCTGAGGATTTTATCAAGAAAG	1680
Qy	1681	CAGATTTGGCAGTTCAAAAGACTCTGAAATGATAAATCAGGGAATTAACCAACGGAGC	1740
Db	1681	CAGATTTGGCAGTTCAAAAGACTCTGAAATGATAAATCAGGGAATTAACCAACGGAGC	1740
Qy	1741	AGAAATGTCAGTGAATTAATTAATAGTGTGTCATGAGAAATAAACAAGAGTGAT	1800
Db	1741	AGAAATGTCAGTGAATTAATTAATAGTGTGTCATGAGAAATAAACAAGAGTGAT	1800
Qy	1801	CTATTCAGATGAGAAATCCTAACCAATAGATCACTCGAAAGAAATCTGCTTCA	1860
Db	1801	CTATTCAGATGAGAAATCCTAACCAATAGATCACTCGAAAGAAATCTGCTTCA	1860
Qy	1861	AAACGAAGCTGAACCTATAAGCAGCAGTATAAGCAATATGGAATTAATAATCC	1920
Db	1861	AAACGAAGCTGAACCTATAAGCAGCAGTATAAGCAATATGGAATTAATAATCC	1920
Qy	1921	ACAAATTCAAAAGCACCTAAAAGAAATAGGCTGAGGAGGAGTCTTCTACAGGCAATTC	1980
Db	1921	ACAAATTCAAAAGCACCTAAAAGAAATAGGCTGAGGAGGAGTCTTCTACAGGCAATTC	1980
Qy	1981	ATGGCTTTGAATAGTAGTAGTAATCTAAGCCCACTAATTTGACTGAATGCAAA	2040
Db	1981	ATGGCTTTGAATAGTAGTAGTAATCTAAGCCCACTAATTTGACTGAATGCAAA	2040
Qy	2041	TTGATAGTGTCTTAGCAGTGAAGATAAAGAAAGTACAAACCAATGCCAGTCA	2100
Db	2041	TTGATAGTGTCTTAGCAGTGAAGATAAAGAAAGTACAAACCAATGCCAGTCA	2100
Qy	2101	GGCAGCAGAGAAACCTCAACCTCATGGAAGGTAAAGAACCTGGACCTGAGCCCAAGAGA	2160
Db	2101	GGCAGCAGAGAAACCTCAACCTCATGGAAGGTAAAGAACCTGGACCTGAGCCCAAGAGA	2160
Qy	2161	GTAAACAGCCAAATGAAACAGTAAAGACATGACAGTGATCTTTCCAGAGCTGA	2220
Db	2161	GTAAACAGCCAAATGAAACAGTAAAGACATGACAGTGATCTTTCCAGAGCTGA	2220
Qy	2221	AGTTTAAACAAATGCACTGTTCTTTTACTAGTGTTCAAATCAGCTGAACTTAAAGAA	2280
Db	2221	AGTTTAAACAAATGCACTGTTCTTTTACTAGTGTTCAAATCAGCTGAACTTAAAGAA	2280
Qy	2281	TTGTCAATCCTAGGCTTCCAGAGAGAGAGAGAGAACTAGAGAACTAGAAAGTGT	2340

Db	2281	TTGTCAATCCTAGGCTTCCAGAGAGAGAGAGAGAACTAGAGAACTAGTTAAAGTGT	2340
Qy	2341	CTAATATGCTGAAGACCCCAAGATCTCATGTTAACTGAGAAAGGTTTTCGAAACTG	2400
Db	2341	CTAATATGCTGAAGACCCCAAGATCTCATGTTAACTGAGAAAGGTTTTCGAAACTG	2400
Qy	2401	AAAGATCTGAGAGTAGCAGTATTTCACTGGTACCTGGTACTGATTTATGGCACTCAGG	2460
Db	2401	AAAGATCTGAGAGTAGCAGTATTTCACTGGTACCTGGTACTGATTTATGGCACTCAGG	2460
Qy	2461	AAAGTATCTGTTACTGGAGTTAGCACTCTAGGGAAGGCAAAACAGAACCAATTAAT	2520
Db	2461	AAAGTATCTGTTACTGGAGTTAGCACTCTAGGGAAGGCAAAACAGAACCAATTAAT	2520
Qy	2521	GTGTGAGTCAGTGTGAGCAATTTGAAAACCCCAAGGACATAATTCATGGTGTTCCTCAAG	2580
Db	2521	GTGTGAGTCAGTGTGAGCAATTTGAAAACCCCAAGGACATAATTCATGGTGTTCCTCAAG	2580
Qy	2581	ATAATAGAAATGACACAGAAAGGCTTTAAGTATCCATTTGGGACATGAAAGTAAACACAGTC	2640
Db	2581	ATAATAGAAATGACACAGAAAGGCTTTAAGTATCCATTTGGGACATGAAAGTAAACACAGTC	2640
Qy	2641	GGGAAACAGCATAGAAATGGAGAAAGTGAACCTTGATGCTCAGTATTTGCAGAAATACAT	2700
Db	2641	GGGAAACAGCATAGAAATGGAGAAAGTGAACCTTGATGCTCAGTATTTGCAGAAATACAT	2700
Qy	2701	TCAGAGTTTCAAGGCGCAGTCATTGCTCTGTTTCAAAATCCAGGAAATGCAGAAAGG	2760
Db	2701	TCAGAGTTTCAAGGCGCAGTCATTGCTCTGTTTCAAAATCCAGGAAATGCAGAAAGG	2760
Qy	2761	AATGTGCAACATTTCTGCCCCACCTCTGGGCTCTTAAAGAAACAAAGTCCAAAAGTCACTT	2820
Db	2761	AATGTGCAACATTTCTGCCCCACCTCTGGGCTCTTAAAGAAACAAAGTCCAAAAGTCACTT	2820
Qy	2821	TTGATGTGAACAAAGAGAGAAATCAAGAAAGATGAGTCTAATATCAAGCCTGTAC	2880
Db	2821	TTGATGTGAACAAAGAGAGAAATCAAGAAAGATGAGTCTAATATCAAGCCTGTAC	2880
Qy	2881	AGACAGTTAATATACACTGCAGGCTTCTGTTGTTGTCAGAAAGATGAGTCTAATATCAAGCCTGTAC	2940
Db	2881	AGACAGTTAATATACACTGCAGGCTTCTGTTGTTGTCAGAAAGATGAGTCTAATATCAAGCCTGTAC	2940
Qy	2941	ATGCCAAATGTAGTATCAAGAGGAGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGGCA	3000
Db	2941	ATGCCAAATGTAGTATCAAGAGGAGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGGCA	3000
Qy	3001	ACGAAACTGAGTCAATTTCTCCAAATAAATGAGTCTTTTACAAACCCATATCGTATAC	3060
Db	3001	ACGAAACTGAGTCAATTTCTCCAAATAAATGAGTCTTTTACAAACCCATATCGTATAC	3060
Qy	3061	CACCACCTTTTCCCATCAAGTCAATTTGTTAAATCTAATGTAAGAAATCTGCTAGAGG	3120
Db	3061	CACCACCTTTTCCCATCAAGTCAATTTGTTAAATCTAATGTAAGAAATCTGCTAGAGG	3120
Qy	3121	AAAACTTTGAGGAACTTCAATGTCACTGAAAGAGAAATGGGAAATGAGAACTTCCAA	3180
Db	3121	AAAACTTTGAGGAACTTCAATGTCACTGAAAGAGAAATGGGAAATGAGAACTTCCAA	3180
Qy	3181	GTAAGTGAAGCAATTTAGCGGTAAATCAATTTAGAGAAATTTGTTTAAAGGAGCAGCT	3240
Db	3181	GTAAGTGAAGCAATTTAGCGGTAAATCAATTTAGAGAAATTTGTTTAAAGGAGCAGCT	3240
Qy	3241	CAAGCAATTTAATGAAAGTGGTTCAGTCTAATGAGTGGCTCCAGTATTAATGAAA	3300
Db	3241	CAAGCAATTTAATGAAAGTGGTTCAGTCTAATGAGTGGCTCCAGTATTAATGAAA	3300
Qy	3301	TAGTTCAGTGTGAAAACTTCAAGCAGAACTAGGTAGAAAAACAGAGGCGCAAAATGGA	3360
Db	3301	TAGTTCAGTGTGAAAACTTCAAGCAGAACTAGGTAGAAAAACAGAGGCGCAAAATGGA	3360
Qy	3361	ATGCTATCTGTTAGGAGTGGGTTTGGCAACTGAGGCTTATAAACAAGTCTTCTCGAA	3420
Db	3361	ATGCTATCTGTTAGGAGTGGGTTTGGCAACTGAGGCTTATAAACAAGTCTTCTCGAA	3420



Db 3361 ATGCTATGCTTAGAATAGGGGTTTTGCAACCTGAGGTCTATAAACAAGTCTTCTCTGAA 3420  
Qy 3421 GTAATTGTAGCATCTCGAATAAATAAAGCAAGATATGAAGAAGTAGTTTCAGACTGTGA 3480  
Db 3421 GTAATTGTAGCATCTCGAATAAATAAAGCAAGATATGAAGAAGTAGTTTCAGACTGTGA 3480  
Qy 3481 ATACAGATTTCTCTCCATATCTGATTTTTCAGATAAATCTTAGAACAGCCCTATGGAGTAGTC 3540  
Db 3481 ATACAGATTTCTCTCCATATCTGATTTTTCAGATAAATCTTAGAACAGCCCTATGGAGTAGTC 3540  
Qy 3541 ATGCACTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGG 3600  
Db 3541 ATGCACTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGG 3600  
Qy 3601 AAGATACCTAGTTTGTCTGAAATCACATTAAGGAAAGTTCTGCTGTTTTTAGCAAAAGCG 3660  
Db 3601 AAGATACCTAGTTTGTCTGAAATGACATTAAGGAAAGTTCTGCTGTTTTTAGCAAAAGCG 3660  
Qy 3661 TCCAGAGAGGAGCTTAGCAGGAGTCTAGCCCTTTTCAACCATAACATTTGGCTCAGG 3720  
Db 3661 TCCAGAGAGGAGCTTAGCAGGAGTCTAGCCCTTTTCAACCATAACATTTGGCTCAGG 3720  
Qy 3721 GTTACCAAGAGGGGCCAAGAAATAGAGTCTCAGAGGAACTTATCTAGTGAGGATG 3780  
Db 3721 GTTACCAAGAGGGGGCCAAAGAAATAGAGTCTCAGAGGAACTTATCTAGTGAGGATG 3780  
Qy 3781 AAGAGCTTCCCTGCTTCCACACCTGTTATTTGGTAAAGTAAACAATATACCTTCTCAGT 3840  
Db 3781 AAGAGCTTCCCTGCTTCCACACCTGTTATTTGGTAAAGTAAACAATATACCTTCTCAGT 3840  
Qy 3841 CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGCTAAGAAACACAGAGGAGAAATTTAT 3900  
Db 3841 CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGCTAAGAAACACAGAGGAGAAATTTAT 3900  
Qy 3901 TATCATTTGAAGATAGCTTAAATGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 3960  
Db 3901 TATCATTTGAAGATAGCTTAAATGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 3960  
Qy 3961 AGGAACATACCTTAGTGAGGAAACAAATGTTCTGCTAGCTGCTGCTGCTGCTGCTGCTG 4020  
Db 3961 AGGAACATACCTTAGTGAGGAAACAAATGTTCTGCTAGCTGCTGCTGCTGCTGCTGCTG 4020  
Qy 4021 GTGAATTTGGAAGACTTGAAGTGAAGGAAACAAATGTTCTGCTAGCTGCTGCTGCTGCTG 4080  
Db 4021 GTGAATTTGGAAGACTTGAAGTGAAGGAAACAAATGTTCTGCTAGCTGCTGCTGCTGCTG 4080  
Qy 4081 CCAACAAATAGGAGCATCTGAAAGCAGGAGTGTCTGAGTGAACAAGAAATGG 4140  
Db 4081 CCAACAAATAGGAGCATCTGAAAGCAGGAGTGTCTGAGTGAACAAGAAATGG 4140  
Qy 4141 TTTTCAGATGATGAAGAGGAGGAGGCTTGGAGGAAATTAATCAAGAGAGGAGCAAGCA 4200  
Db 4141 TTTTCAGATGATGAAGAGGAGGAGGCTTGGAGGAAATTAATCAAGAGAGGAGCAAGCA 4200  
Qy 4201 TGGATTTCAAACTTAGTGAAGCAGCATCTGGGTGAGAGTGAAACAAAGGCTCTCTGAAG 4260  
Db 4201 TGGATTTCAAACTTAGTGAAGCAGCATCTGGGTGAGAGTGAAACAAAGGCTCTCTGAAG 4260  
Qy 4261 ACTGCTCAGGCTATCTCTCAGAGTGAATTTTAAACCTCAGCAGAGGAGTACCATGC 4320  
Db 4261 ACTGCTCAGGCTATCTCTCAGAGTGAATTTTAAACCTCAGCAGAGGAGTACCATGC 4320  
Qy 4321 AACATAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACCTAGAGCTGTGTAGACAGC 4380  
Db 4321 AACATAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACCTAGAGCTGTGTAGACAGC 4380  
Qy 4381 ATGGAGCCAGCCTTTTAAACAGCTTACCTTTCCATCATAGTGAACCTCTGCTGCTGCTGAGG 4440  
Db 4381 ATGGAGCCAGCCTTTTAAACAGCTTACCTTTCCATCATAGTGAACCTCTGCTGCTGCTGAGG 4440  
Qy 4441 ACCTGCGAAATCCAGAAACAAAGCNCATCAGAAAGCAGTATTTAACTTCAAGAAAGTA 4500  
Db 4441 ACCTGCGAAATCCAGAAACAAAGCNCATCAGAAAGCAGTATTTAACTTCAAGAAAGTA 4500

Qy 4501 GTGAATACCTTATAAGCCAGAAATCCAGAGGCCCTTTCTGCTGACAAAGTTTGTAGGTGCTG 4560  
Db 4501 GTGAATACCTTATAAGCCAGAAATCCAGAGGCCCTTTCTGCTGACAAAGTTTGTAGGTGCTG 4560  
Qy 4561 CAGATAGTTCTACACAGTAAATAAAGAACACAGAGTGGAAAGTCAATCCCTTCTTAAT 4620  
Db 4561 CAGATAGTTCTACACAGTAAATAAAGAACACAGAGTGGAAAGTCAATCCCTTCTTAAT 4620  
Qy 4621 GCCCATCATTTAGATGATAGTGTGATCATGACAGTTGCTCTGGAGTCTTTCAGAAATGAA 4680  
Db 4621 GCCCATCATTTAGATGATAGTGTGATCATGACAGTTGCTCTGGAGTCTTTCAGAAATGAA 4680  
Qy 4681 ACTTACCCATCTCAAGAGGAGCTCATTAAGGTGTTGATGTTGGAGGACCAACAGCTGGAAG 4740  
Db 4681 ACTTACCCATCTCAAGAGGAGCTCATTAAGGTGTTGATGTTGGAGGACCAACAGCTGGAAG 4740  
Qy 4741 AGTCTGGGCCACACGATTTTTCAGCGAAACATCTTATTTGCCAAGGCAAGATCTAGAGGAA 4800  
Db 4741 AGTCTGGGCCACACGATTTTTCAGCGAAACATCTTATTTGCCAAGGCAAGATCTAGAGGAA 4800  
Qy 4801 CCCCTTACCTGGAATCTGGAATCAGGCTCTTCTGATGACCCCTGGAATCTGATCTCTG 4860  
Db 4801 CCCCTTACCTGGAATCTGGAATCAGGCTCTTCTGATGACCCCTGGAATCTGATCTCTG 4860  
Qy 4861 AAGACAGAGCCCGACAGTCTGCTGTTGGCAACATACCATCTTCAACCTCTGCAATTGA 4920  
Db 4861 AAGACAGAGCCCGACAGTCTGCTGTTGGCAACATACCATCTTCAACCTCTGCAATTGA 4920  
Qy 4921 AAGTCTCCCAATTTGAAAGTTTGCAGAAATCTGCCAGGCTCCAGCTGCTGCTCATACTG 4980  
Db 4921 AAGTCTCCCAATTTGAAAGTTTGCAGAAATCTGCCAGGCTCCAGCTGCTGCTCATACTG 4980  
Qy 4981 ATACTGCTGGTATATGCAATGGAAGAAAGTGTGAGCAGGAGGAGGACCAAGATTGACAG 5040  
Db 4981 ATACTGCTGGTATATGCAATGGAAGAAAGTGTGAGCAGGAGGAGGACCAAGATTGACAG 5040  
Qy 5041 CTTTCAACAGAAAGGGTCAACAAAGAAATGTCATGTTGGTGTCTGGCTCAGCCCAAG 5100  
Db 5041 CTTTCAACAGAAAGGGTCAACAAAGAAATGTCATGTTGGTGTCTGGCTCAGCCCAAG 5100  
Qy 5101 AATTTATGCTGCTGTAACAAGTTTCCAGAAACACCAACATCACTTTAACTTAATTA 5160  
Db 5101 AATTTATGCTGCTGTAACAAGTTTCCAGAAACACCAACATCACTTTAACTTAATTA 5160  
Qy 5161 CTGAAGAGACTACTCATGTTGTTATGAAACACATGCTGAGTTTGTGTGTAACGAGCAC 5220  
Db 5161 CTGAAGAGACTACTCATGTTGTTATGAAACACATGCTGAGTTTGTGTGTAACGAGCAC 5220  
Qy 5221 TGAATATTTTCTAGGAATTTGCGGAGGAAATGGGTAGTTAGCTATTTCTGGGTGACCC 5280  
Db 5221 TGAATATTTTCTAGGAATTTGCGGAGGAAATGGGTAGTTAGCTATTTCTGGGTGACCC 5280  
Qy 5281 AGTCTATTTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCCAGAGGAGTGG 5340  
Db 5281 AGTCTATTTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCCAGAGGAGTGG 5340  
Qy 5341 TCAATGGAAGAAACCAAGTCCAAAGCCAGCAAGATCCCAAGGACAGAAAGTCT 5400  
Db 5341 TCAATGGAAGAAACCAAGTCCAAAGCCAGCAAGATCCCAAGGACAGAAAGTCT 5400  
Qy 5401 TCAGGGGCTTAGAAATCTGTTGCTATGGGCCCTTCCAAACATGCCACAGATCAACTGG 5460  
Db 5401 TCAGGGGCTTAGAAATCTGTTGCTATGGGCCCTTCCAAACATGCCACAGATCAACTGG 5460  
Qy 5461 AATGGATGTTACAGTCTGTTGCTCTTCTGTTGGTGAAGGAGCTTTTCAATTCACCCCTG 5520  
Db 5461 AATGGATGTTACAGTCTGTTGCTCTTCTGTTGGTGAAGGAGCTTTTCAATTCACCCCTG 5520  
Qy 5521 GCACAGGTGTCACCCCAATTTGTTGTTGTGAGCCAGATGCTTGCACAGGACCAATGGCT 5580  
Db 5521 GCACAGGTGTCACCCCAATTTGTTGTTGTGAGCCAGATGCTTGCACAGGACCAATGGCT 5580



```

Qy 5581 TCCATGCAATTGGGCGAGATGTGTGAGGCACCTGTGGTGCACCGGAGAGTGGGTGTGGACA 5640
Db 5581 TCCATGCAATTGGGCGAGATGTGTGAGGCACCTGTGGTGCACCGGAGAGTGGGTGTGGACA 5640
Qy 5641 GTGTAGCACTCTACCAAGTCCAGGAGCTGGACACCTACCTGATACCCCGAGATCCCCCACA 5700
Db 5641 GTGTAGCACTCTACCAAGTCCAGGAGCTGGACACCTACCTGATACCCCGAGATCCCCCACA 5700
Qy 5701 GCCACTACTGA 5711
Db 5701 GCCACTACTGA 5711

RESULT 13
AAV46450
ID AAV46450 standard; cDNA; 5711 BP.
XX
XX AAV46450;
XX
DT 18-NOV-1998 (first entry)
DE Human BRCA1 omi3 cDNA.
XX
XX BRCA1; omi3; human; breast and ovarian cancer predisposing gene;
KW polymorphism; susceptibility; anti-oncogene; tumour suppressor;
KW chromosome 17q; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 120..5711
XX FT /*tag= a
XX FT /product= "BRCA1 omi3 protein"
XX
XX US5750400-A.
XX
XX PD 12-MAY-1998.
XX
XX PF 12-FEB-1997; 97US-0798691.
XX
XX PR 12-FEB-1996; 96US-0598591.
XX
XX PR 12-FEB-1997; 97US-0798691.
XX
XX (ONCO-) ONCORMED INC.
XX
XX PI Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ;
XX PI Schelter DB, Zeng B;
XX
XX DR WPI; 1998-296774/26.
XX
XX P-ESDB; AAW76100.
XX
XX BRCA1 omi gene coding sequences - useful for distinguishing between
XX polymorphisms and mutation(s) in the screening for disposition to
XX breast or ovarian cancer
XX
XX Claim 2e; Column 55-62; 54pp; English.
XX
XX PS This sequence encodes the human BRCA1 (breast and ovarian cancer
XX CC predisposing gene) omi3 gene. This sequence and polymorphic variations of
XX CC this sequence are useful for the identification of an individual who may
XX CC or may not have an increased susceptibility to breast or ovarian cancer.
XX CC The sequences used identify gene changes which are due to polymorphisms,
XX CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
XX CC suppressor) which is involved in genetic inheritance of cancers,
XX CC especially breast and ovarian cancer. It is found at human chromosome 17q
XX CC which is known to be linked to cancer susceptibility, especially breast
XX CC cancer. Cells containing a mutation in this gene lose the wild-type
XX CC function of BRCA1 and are more susceptible to cancers.
XX
XX SQ Sequence 5711 BP; 1953 A; 1098 C; 1277 G; 1383 T; 0 other;

Query Match 100.0%; Score 5709.4; DB 19; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;

```

```

Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 AGCTCGCTGAGACTTCCTGGACCCCGACACAGGCTGTGGGGTCTTCTCAGATAAAGTGGGCC 60
Db 1 AGCTCGCTGAGACTTCCTGGACCCCGACACAGGCTGTGGGGTCTTCTCAGATAAAGTGGGCC 60
Qy 61 CCTCGCTCAGGAGGCGCTTCAACCTCTGCTCTGGGTAAAGTTTCAATTGGAACAGAAAGAAA 120
Db 61 CCTCGCTCAGGAGGCGCTTCAACCTCTGCTCTGGGTAAAGTTTCAATTGGAACAGAAAGAAA 120
Qy 121 TGGATTTATCTGCTCTTGGGTTGAAGAAGTACAAAATGTCAATTAATCTATGCAAGAAA 180
Db 121 TGGATTTATCTGCTCTTGGGTTGAAGAAGTACAAAATGTCAATTAATCTATGCAAGAAA 180
Qy 181 TCTTAGAGTGTCCCATCTGTCTGGAGTTGATCAAGGAACCTGTCTCCACAAGTGTGACC 240
Db 181 TCTTAGAGTGTCCCATCTGTCTGGAGTTGATCAAGGAACCTGTCTCCACAAGTGTGACC 240
Qy 241 ACATATTTTGC AAAATTTTGCATGTGAAAATCTTCAACCAAGAAAGGGCTTCCACAGT 300
Db 241 ACATATTTTGC AAAATTTTGCATGTGAAAATCTTCAACCAAGAAAGGGCTTCCACAGT 300
Qy 301 GTCCCTTTATGTAAGATGATATAACCAAGAGAGCCCTACAAGAAAGTACGAGATTTAGTC 360
Db 301 GTCCCTTTATGTAAGATGATATAACCAAGAGAGCCCTACAAGAAAGTACGAGATTTAGTC 360
Qy 361 AACTTTGTTGAAGAGCTATTGAAAATCAATTTGTGCTTTTTCAGCTTGACACAGTTTGGAGT 420
Db 361 AACTTTGTTGAAGAGCTATTGAAAATCAATTTGTGCTTTTTCAGCTTGACACAGTTTGGAGT 420
Qy 421 ATGCAAAACAGCTATAATTTTGC AAAAAGGAAAATACTCTCTCTGAAACATCTAAAAGATG 480
Db 421 ATGCAAAACAGCTATAATTTTGC AAAAAGGAAAATACTCTCTCTGAAACATCTAAAAGATG 480
Qy 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAAGACTTCTACAGAGTG 540
Db 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAAGACTTCTACAGAGTG 540
Qy 541 AACCAGAAATCCCTTCCTTGAGGAAACCACTCTCAGTGTCCAACTCTCTAACCTTGGAA 600
Db 541 AACCAGAAATCCCTTCCTTGAGGAAACCACTCTCAGTGTCCAACTCTCTAACCTTGGAA 600
Qy 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCTCAAAAGACGCTCTCTACATTG 660
Db 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCTCAAAAGACGCTCTCTACATTG 660
Qy 661 AATTGGGATCTGATTTCTTGAAGATACCGTTTAATAGGCAACTTATTCAGTGTGGAG 720
Db 661 AATTGGGATCTGATTTCTTGAAGATACCGTTTAATAGGCAACTTATTCAGTGTGGAG 720
Qy 721 ATCAAGAAATGTTTACAATCACCCCTCAAGGAACCGGATGAAATCAAGTTTGGATTCTG 780
Db 721 ATCAAGAAATGTTTACAATCACCCCTCAAGGAACCGGATGAAATCAAGTTTGGATTCTG 780
Qy 781 CAAAAAAGGCTGCTTGTGAATTTTCTGAGAGCGGATGTAACAAATATCTGAACATCATCAAC 840
Db 781 CAAAAAAGGCTGCTTGTGAATTTTCTGAGAGCGGATGTAACAAATATCTGAACATCATCAAC 840
Qy 841 CCAGTAATATGATTTGAAACCACTGAGAAAGCGTGAGCTGAGAGGATCCAGAAAGT 900
Db 841 CCAGTAATATGATTTGAAACCACTGAGAAAGCGTGAGCTGAGAGGATCCAGAAAGT 900
Qy 901 ATCAGGCTAGTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCACAATACTCATGCCA 960
Db 901 ATCAGGCTAGTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCACAATACTCATGCCA 960
Qy 961 GCTCATTACAGCATGAGAACAGCAGTATTATTACTCTACTAAAGACAGAAATGATAGAAA 1020
Db 961 GCTCATTACAGCATGAGAACAGCAGTATTATTACTCTACTAAAGACAGAAATGATAGAAA 1020
Qy 1021 AGGCTGAATTTCTGTAATTAAGCAAAACAGCCTGTGCTTAGCAAGGAGCCAAATACAGAT 1080
Db 1021 AGGCTGAATTTCTGTAATTAAGCAAAACAGCCTGTGCTTAGCAAGGAGCCAAATACAGAT 1080

```

1081 GGGCTGGAAGTAAGGAAACATGTATATAGTATGCGGACTCCAGACAGAAAAAAGGTAG 1140  
1081 GGGCTGGAAGTAAGGAAACATGTATATAGTATGCGGACTCCAGACAGAAAAAAGGTAG 1140  
1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGGAATPAAGCAGAAACTGCCATGCT 1200  
1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGGAATPAAGCAGAAACTGCCATGCT 1200  
1201 CAGAGAACTCTAGAGATCTGAAGATGTTCTTGATTAACACTAAATAGCAGCATTCAGA 1260  
1201 CAGAGAACTCTAGAGATCTGAAGATGTTCTTGATTAACACTAAATAGCAGCATTCAGA 1260  
1261 AAGTTAATGAGTGGTGTTCAGAGAGTGAATGAATGTTAGGTTCTGATGACTCAATGATG 1320  
1261 AAGTTAATGAGTGGTGTTCAGAGAGTGAATGAATGTTAGGTTCTGATGACTCAATGATG 1320  
1321 GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGTTAGGACGTTCTAAATGAGGTAGATG 1380  
1381 AATATCTGTTCTTCAGAGAAATAGACTTACTGGCCAGTGAATCCTCATGAGGCTTTAA 1440  
1381 AATATCTGTTCTTCAGAGAAATAGACTTACTGGCCAGTGAATCCTCATGAGGCTTTAA 1440  
1441 TATGTAAAGTGAAGAGAGTTCACCTCCAAATCAGTAGAGAGTAATATTGAAGACAAAATAT 1500  
1441 TATGTAAAGTGAAGAGAGTTCACCTCCAAATCAGTAGAGAGTAATATTGAAGACAAAATAT 1500  
1501 TTGGGAAACCTATCGGAAGAGCAAGCCCTCCCACTTAAGCCATGTAACTGAAATC 1560  
1501 TTGGGAAACCTATCGGAAGAGCAAGCCCTCCCACTTAAGCCATGTAACTGAAATC 1560  
1561 TAATTTAGGAGCATTTGTTACTCAGCCACAGATAATACAGAGCGTCCCTCACAATA 1620  
1561 TAATTTAGGAGCATTTGTTACTCAGCCACAGATAATACAGAGCGTCCCTCACAATA 1620  
1621 AATTTAAAGCGTAAAGAGAGACTACATCAGCGCTTCATCTGAGGATTTTATCAAGAAAG 1680  
1621 AATTTAAAGCGTAAAGAGAGACTACATCAGCGCTTCATCTGAGGATTTTATCAAGAAAG 1680  
1681 CAGATTTGGGAGTTCAAAAGACTCCTGAAATGATAATACAGGAACTTAACAAACGGAGC 1740  
1681 CAGATTTGGGAGTTCAAAAGACTCCTGAAATGATAATACAGGAACTTAACAAACGGAGC 1740  
1741 AGAATGTCAGTGATCAATTAATTAATAGTGTGATGAGATTAAGGAGTGAAT 1800  
1741 AGAATGTCAGTGATCAATTAATTAATAGTGTGATGAGATTAAGGAGTGAAT 1800  
1801 CTATTCAGAATGAGAAAAATCCTAACCAATAGAAATCACTCGAAAAAGAAATCTGCTTTCA 1860  
1801 CTATTCAGAATGAGAAAAATCCTAACCAATAGAAATCACTCGAAAAAGAAATCTGCTTTCA 1860  
1861 AAAGAAAGCTGAACCTATTAAGAGCAGTATAGCAATATGGAATCGAATTAATATCC 1920  
1861 AAAGAAAGCTGAACCTATTAAGAGCAGTATAGCAATATGGAATCGAATTAATATCC 1920  
1921 ACAATTCAGAACCTTAAAGAGATAGGCTGAGGAGGAGTCTTCTACGAGCATATTC 1980  
1921 ACAATTCAGAACCTTAAAGAGATAGGCTGAGGAGGAGTCTTCTACGAGCATATTC 1980  
1981 ATGGCTTTGAACCTAGTAGTCAAGTGAATTAAGCCCACTTAATTTGATCTGAATTCGAAA 2040  
1981 ATGGCTTTGAACCTAGTAGTCAAGTGAATTAAGCCCACTTAATTTGATCTGAATTCGAAA 2040  
2041 TTGATAGTGTCTAGCAGTGAAGAGATAAGAAAAAAGTACAAACAAATGCCAGTCA 2100  
2041 TTGATAGTGTCTAGCAGTGAAGAGATAAGAAAAAAGTACAAACAAATGCCAGTCA 2100  
2101 GGCACACAGAACTCACTATGAGGAGTGAAGAACTGCAACTGGAGCCCAAGAGA 2160  
2101 GGCACACAGAACTCACTATGAGGAGTGAAGAACTGCAACTGGAGCCCAAGAGA 2160

2161 GTAAACAGCCAAATGAACAGACAGTAAGTAAAGACATGACAGTGATCTTTCCAGAGCTGA 2220  
2161 GTAAACAGCCAAATGAACAGACAGTAAGTAAAGACATGACAGTGATCTTTCCAGAGCTGA 2220  
2221 AGTTAAACAAATGCACTGGTCTTTTACTAAGTGTTCAAAATACCAAGTGAACCTTAAAGAAT 2280  
2221 AGTTAAACAAATGCACTGGTCTTTTACTAAGTGTTCAAAATACCAAGTGAACCTTAAAGAAT 2280  
2281 TTGTCAATCTCTAGCTTCCAGAGAGAGAAAGAGAGAACTAGAAAAACAGTATTAAGTGT 2340  
2281 TTGTCAATCTCTAGCTTCCAAAGAGAGAAAGAGAGAACTAGAAAAACAGTATTAAGTGT 2340  
2341 CTAAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGTGAGAAAGGTTTGGCAAATCTG 2400  
2341 CTAAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGTGAGAAAGGTTTGGCAAATCTG 2400  
2401 AAAGATCTGTAGAGAGTAGCAGTATTTCACTGGTACCTGGTACTGATTTATGGCACTCAGG 2460  
2401 AAAGATCTGTAGAGAGTAGCAGTATTTCACTGGTACCTGGTACTGATTTATGGCACTCAGG 2460  
2461 AAAGTATCTGTTACTGGAAAGTTAGCACTCTAGGGAAGGCAAAAACAGAACCAATTAAT 2520  
2461 AAAGTATCTGTTACTGGAAAGTTAGCACTCTAGGGAAGGCAAAAACAGAACCAATTAAT 2520  
2521 GTGTGAGTCAAGTGTGAGAGATTTGAAAAACCCCAAGGACTTAATTCATGGTGTTCCAAAG 2580  
2521 GTGTGAGTCAAGTGTGAGAGATTTGAAAAACCCCAAGGACTTAATTCATGGTGTTCCAAAG 2580  
2581 ATAATAGAAATGACACAGAAAGGCTTTAAAGTATCCATTTGGGACATGAAGTTAAACACAGTC 2640  
2581 ATAATAGAAATGACACAGAAAGGCTTTAAAGTATCCATTTGGGACATGAAGTTAAACACAGTC 2640  
2641 GGGAAACACAGCATAGAAATGGAAGAGAGTGAATGATGCTCAGTATTTGCGAGNATACAT 2700  
2641 GGGAAACACAGCATAGAAATGGAAGAGAGTGAATGATGCTCAGTATTTGCGAGNATACAT 2700  
2701 TCAAGGTTTCAAAAGCGCAGTCAATTTGCTCTGTTTTCAAAATCCAGGAAATTCAGAAAGG 2760  
2701 TCAAGGTTTCAAAAGCGCAGTCAATTTGCTCTGTTTTCAAAATCCAGGAAATTCAGAAAGG 2760  
2761 AATGTGCAACATTTCTGTGCCACTCTGGGGTCTTTAAAGAAACAAAGTCCAAAAGTCACTT 2820  
2761 AATGTGCAACATTTCTGTGCCACTCTGGGGTCTTTAAAGAAACAAAGTCCAAAAGTCACTT 2820  
2821 TTCAATGTGAACAAAGGAGAGAAATCAAGGAAGATGATCTTAATCAAGCCTGTAC 2880  
2821 TTCAATGTGAACAAAGGAGAGAAATCAAGGAAGATGATGATCTTAATCAAGCCTGTAC 2880  
2881 AGACAGTTAATATACATGACAGGCTTTCTGTTGGTTCAGAAAGATAAGCCAGTTGATA 2940  
2881 AGACAGTTAATATACATGACAGGCTTTCTGTTGGTTCAGAAAGATAAGCCAGTTGATA 2940  
2941 ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAAGGCA 3000  
2941 ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAAGGCA 3000  
3001 ACCAAACTGCACTCATTTCTCCAAATTAACATGAGCTTTTACAAAACCCATATCGTATAC 3060  
3001 ACCAAACTGCACTCATTTCTCCAAATTAACATGAGCTTTTACAAAACCCATATCGTATAC 3060  
3061 CACCACTTTTCCCACTCAAGTCAATTTGTTAAAACTAAATGTAAGAAAAATCTGCTAGAGG 3120  
3061 CACCACTTTTCCCACTCAAGTCAATTTGTTAAAACTAAATGTAAGAAAAATCTGCTAGAGG 3120  
3121 AAAAATTGTAGGAAACATTTCAATCTCACTGAAAGAGAAATGGGAAATGAGAACATTCCAA 3180  
3121 AAAAATTGTAGGAAACATTTCAATCTCACTGAAAGAGAAATGGGAAATGAGAACATTCCAA 3180  
3181 GTACAGTGACACAAATAGCCGTAATAACATTAGAGAAATGTTTTTAAAGGAGCCAGCT 3240  
3181 GTACAGTGACACAAATAGCCGTAATAACATTAGAGAAATGTTTTTAAAGGAGCCAGCT 3240  
3241 CAAGCAATATTAATGAAGTAGGTTCCAGTAGTAATGAAGTGGGCTCCAGTATTAATGAAA 3300

3241	Db	 CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGCTCCAGTATTAATTAAGAAA	3300
3301	Qy	TAGGTTCCAGTGATGAAACCAATTCAGACGAACTAGTAGAAGAACAGAGGCCCAAAATTCGA	3360
3301	Db	TAGGTTCCAGTGATGAAACCAATTCAGACGAACTAGTAGAAGAACAGAGGCCCAAAATTCGA	3360
3361	Qy	ATGCTATGCTTAGATTAGGGGTTTGCAACTGAGGTCTATAAACAAGGCTTCTTCCTGGAA	3420
3361	Db	ATGCTATGCTTAGATTAGGGGTTTGCAACTGAGGTCTATAAACAAGGCTTCTTCCTGGAA	3420
3421	Qy	GTAATTTGTAAGCATCTGTAATTAAGCAAGCAAGATATGAAGAAGTAGTTCAGACTGTTA	3480
3421	Db	GTAATTTGTAAGCATCTGTAATTAAGCAAGCAAGATATGAAGAAGTAGTTCAGACTGTTA	3480
3481	Qy	ATACAGATTTCTCTCCCATATCTGATTTTCAGATAACTTAGAACACGCTATGGGAAGTAGTC	3540
3481	Db	ATACAGATTTCTCTCCCATATCTGATTTTCAGATAACTTAGAACACGCTATGGGAAGTAGTC	3540
3541	Qy	ATGCATCTCAGGTTTGTTCTTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGG	3600
3541	Db	ATGCATCTCAGGTTTGTTCTTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGG	3600
3601	Qy	AGATATCTAGTTTGTCTGAAAAATGCAATTAAGGAAAGTTCTGCTGTTTTTAGCAAAAGCG	3660
3601	Db	AGATATCTAGTTTGTCTGAAAAATGCAATTAAGGAAAGTTCTGCTGTTTTTAGCAAAAGCG	3660
3661	Qy	TCCAGAGAGAGAGCTTTAGCAGAGGCTCCTAGCCCTTTACCCATACACATTTGGCTCAGG	3720
3661	Db	TCCAGAGAGAGAGCTTTAGCAGAGGCTCCTAGCCCTTTACCCATACACATTTGGCTCAGG	3720
3721	Qy	GTTTACCGAAGAGGGGCCAAGAAATTAGAGTCCTCAGAAGAGAACTTATCTAGTGAAGATG	3780
3721	Db	GTTTACCGAAGAGGGGCCAAGAAATTAGAGTCCTCAGAAGAGAACTTATCTAGTGAAGATG	3780
3781	Qy	AAGAGCTTCCTGCTTCCAAACACTTGTTGTTATTTGGTAAAGTAAACAAATATACCTTCTCAGT	3840
3781	Db	AAGAGCTTCCTGCTTCCAAACACTTGTTGTTATTTGGTAAAGTAAACAAATATACCTTCTCAGT	3840
3841	Qy	CTACTAGGCATAGCACCGTTGCTACCGAGTGCTGTCTAAGAACACAGAGGAGAAATTTAT	3900
3841	Db	CTACTAGGCATAGCACCGTTGCTACCGAGTGCTGTCTAAGAACACAGAGGAGAAATTTAT	3900
3901	Qy	TATCATTTGAAGAAATAGCTTAAATGACTGCAGTAACACAGGTAATATTGGCAAAAGGCATCTC	3960
3901	Db	TATCATTTGAAGAAATAGCTTAAATGACTGCAGTAACACAGGTAATATTGGCAAAAGGCATCTC	3960
3961	Qy	AGGAACATCACTTTAGTGAGGAAACAAAATGTTCTGCTAGCTTGTTTTCTTCAAGTGCA	4020
3961	Db	AGGAACATCACTTTAGTGAGGAAACAAAATGTTCTGCTAGCTTGTTTTCTTCAAGTGCA	4020
4021	Qy	GTGNAATTTGGAAGACTTGCACTGCAATATCAACACCCAGGATCCCTTCTTGATTTGGTTCTT	4080
4021	Db	GTGNAATTTGGAAGACTTGCACTGCAATATCAACACCCAGGATCCCTTCTTGATTTGGTTCTT	4080
4081	Qy	CCAAACAAATGAGGCATCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGACAAGGAATTTGG	4140
4081	Db	CCAAACAAATGAGGCATCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGACAAGGAATTTGG	4140
4141	Qy	TTTTCAGATGATGAAGAAGAGGAACGGGCTTGGAAAGAAAAATATCAAGAAAGACCAAGCA	4200
4141	Db	TTTTCAGATGATGAAGAAGAGGAACGGGCTTGGAAAGAAAAATATCAAGAAAGACCAAGCA	4200
4201	Qy	TGGATTCAAACTTAGGTGAAGCAGCATCTGGGTGTGAGGTGAAACAGAGGTCTCTGAAG	4260
4201	Db	TGGATTCAAACTTAGGTGAAGCAGCATCTGGGTGTGAGGTGAAACAGAGGTCTCTGAAG	4260
4261	Qy	ACTGCTCAGGGCTATCTCTCAGAGTGACATTTTTTAACCATCTCAGCAGAGGATACCATGC	4320
4261	Db	ACTGCTCAGGGCTATCTCTCAGAGTGACATTTTTTAACCATCTCAGCAGAGGATACCATGC	4320
4321	Qy	AACATAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACCTAGAGGCTGTGTTAGAAACAGC	4380

Db	4321	AA	CATACCTGATAAAGCTCCAGCAGGAANAATGGCTGAAC	TAGAAGCTGTGTTAGAACACGC	4380		
Qy	4381	AT	GCGAGCCAGCCTTCTTAACAGCTACCCTTCATCATCA	TAAAGTGACTCCTCTGCCTTTGAGS	4440		
Db	4381	AT	GCGAGCCAGCCTTCTTAACAGCTACCCTTCATCATCA	TAAAGTGACTCTTCTGCGCTTTGAGS	4440		
Qy	4441	ACT	GCGGAANTCAGAAACAAGCACATCA	GAAAAAGCAGTATTAACTTCACGAAAAGTA	4500		
Db	4441	ACT	GCGGAANTCAGAAACAAGCACATCA	GAAAAAGCAGTATTAACTTCACGAAAAGTA	4500		
Qy	4501	GT	CAATACCCCTATAAGCCAGAAATCC	AAGAGGCCCTTCTGCTGACAAGTTTGAGGTGCTCTG	4560		
Db	4501	GT	CAATACCCCTATAAGCCAGAAATCC	AAGAGGCCCTTCTGCTGACAAGTTTGAGGTGCTCTG	4560		
Qy	4561	CAG	ATAGTTCTACCAAGTAAAAATAA	AGAACCCAGGAGTGGAAAGGTCATCCCCCTTCTAAAT	4620		
Db	4561	CAG	ATAGTTCTACCAAGTAAAAATAA	AGAACCCAGGAGTGGAAAGGTCATCCCCCTTCTAAAT	4620		
Qy	4621	GCC	CATCATTAGATGATAGGTGGTA	CATGCA	CAGTTGCTCTGGGAGTCTTTCAGATAGAA	4680	
Db	4621	GCC	CATCATTAGATGATAGGTGGTA	CATGCA	CAGTTGCTCTGGGAGTCTTTCAGATAGAA	4680	
Qy	4681	ACT	ACCCTCTCAAGAGGAGCTCATTA	AAGTTGTCATGTGGAGGAGCAACAGCTCGAAG	4740		
Db	4681	ACT	ACCCTCTCAAGAGGAGCTCATTA	AAGTTGTCATGTGGAGGAGCAACAGCTCGAAG	4740		
Qy	4741	AGT	CTGGGCCACACGATTTGACG	GGAAACATCTTACTTTGCCAAGGCCAAGATCTAGAGGGAA	4800		
Db	4741	AGT	CTGGGCCACACGATTTGACG	GGAAACATCTTACTTTGCCAAGGCCAAGATCTAGAGGGAA	4800		
Qy	4801	CCC	TTACTCGGAATCTGGAATCAG	CCTCTTCTGATGACCCCTGAAATCTGATCCTTCTG	4860		
Db	4801	CCC	TTACTCGGAATCTGGAATCAG	CCTCTTCTGATGACCCCTGAAATCTGATCCTTCTG	4860		
Qy	4861	AAG	CACAGCCCCCAGAGTCAGCT	CGTGTGGCAACATACCATCTTCAA	CCTCTGCATTGA	4920	
Db	4861	AAG	CACAGCCCCCAGAGTCAGCT	CGTGTGGCAACATACCATCTTCAA	CCTCTGCATTGA	4920	
Qy	4921	AAG	TTCCCCAATTGAAAGTTG	CAGAAATCTGCCCAGAGGTC	CAGCTGCTGCTCATCTACTG	4980	
Db	4921	AAG	TTCCCCAATTGAAAGTTG	CAGAAATCTGCCCAGAGGTC	CAGCTGCTGCTCATCTACTG	4980	
Qy	4981	ATA	CTGCTGGGTATAATGCAAT	GGAAAGTGTGAGCAGGGGAGAACCCAGAAATTCACAG	5040		
Db	4981	ATA	CTGCTGGGTATAATGCAAT	GGAAAGTGTGAGCAGGGGAGAACCCAGAAATTCACAG	5040		
Qy	5041	CTT	CAACAGAAAGGGTCAACAA	AGAAATGTCATGTGTGTCTGCGCTGACCCACAGAG	5100		
Db	5041	CTT	CAACAGAAAGGGTCAACAA	AGAAATGTCATGTGTGTCTGCGCTGACCCACAGAG	5100		
Qy	5101	AA	TTTTATGCTCGTGTAACAG	TTTGCACAGAAAACACACATCACTTTAACTAAATCTAAATTA	5160		
Db	5101	AA	TTTTATGCTCGTGTAACAG	TTTGCACAGAAAACACACATCACTTTAACTAAATCTAAATTA	5160		
Qy	5161	CT	GAAGAGACTACTCATGTT	TTATGAAAACAGATGCTGAGTTTGTGTGTGAACGACAC	5220		
Db	5161	CT	GAAGAGACTACTCATGTT	TTATGAAAACAGATGCTGAGTTTGTGTGTGAACGACAC	5220		
Qy	5221	TG	AAATATTTTCTAGGAAT	TTCGCGGAGGAAAATGGTATAGTATTTCTGGGTGACCC	5280		
Db	5221	TG	AAATATTTTCTAGGAAT	TTCGCGGAGGAAAATGGTATAGTATTTCTGGGTGACCC	5280		
Qy	5281	AGT	CTATTAAGAGAAAGAAAAT	CTGAAATGAGCATGATTTTGAAGTTCAGAGGAGATGTGG	5340		
Db	5281	AGT	CTATTAAGAGAAAGAAAAT	CTGAAATGAGCATGATTTTGAAGTTCAGAGGAGATGTGG	5340		
Qy	5341	TC	AATGGAAGAAACCAAGG	TCCAAGCGAGCAAGAGAAATCCCAGGACAGAAAGATCT	5400		
Db	5341	TC	AATGGAAGAAACCAAGG	TCCAAGCGAGCAAGAGAAATCCCAGGACAGAAAGATCT	5400		
Qy	5401	TC	AGGGGGCTAGAAATCTGT	TGCTATGGGCCCTTCCACAA	CATGCCCA	CAGATCAACTG	5460
Db	5401	TC	AGGGGGCTAGAAATCTGT	TGCTATGGGCCCTTCCACAA	CATGCCCA	CAGATCAACTG	5460

QY 5461 AATGATGGTACAGCTGTGTGCTCTTCTGTGGTGAAGAGCTTTCATCATCCCTTG 5520  
DB 5461 AATGATGGTACAGCTGTGTGCTCTTCTGTGGTGAAGAGCTTTCATCATCCCTTG 5520  
QY 5521 GCACAGGTGTCACCCAAATGTTGTTGTGACGACAGATGCTGTGACAGAGACAATGGCT 5580  
DB 5521 GCACAGGTGTCACCCAAATGTTGTTGTGACGACAGATGCTGTGACAGAGACAATGGCT 5580  
QY 5581 TCCATGCAATGGCAGATGTGACGACCTGTGTGACCCGAGAGTGGGTGTGACA 5640  
DB 5581 TCCATGCAATGGCAGATGTGACGACCTGTGTGACCCGAGAGTGGGTGTGACA 5640  
QY 5641 GTGTAGCACTTACCAAGTCCAGAGCTGGACACCTTACCTGATACCCAGATCCCCACA 5700  
DB 5641 GTGTAGCACTTACCAAGTCCAGAGCTGGACACCTTACCTGATACCCAGATCCCCACA 5700  
QY 5701 GCCACTACTGA 5711  
DB 5701 GCCACTACTGA 5711

## RESULT 14

AAC60794  
ID AAC60794 standard; cDNA; 5711 BP.

XX AAC60794;

XX 07-FEB-2001 (first entry)

XX Human BRCA1 (om12) nucleotide sequence SEQ ID NO:3.

XX Human; BRCA1; chromosome 17; 17q21; breast cancer; ovarian cancer;  
XX gene therapy; diagnosis; cytostatic; genetic susceptibility; mutation;  
XX polymorphism; identification; ss.

XX Homo sapiens.

XX US6130322-A.

XX 10-OCT-2000.

XX 06-MAY-1998; 98US-0074476.

XX 12-FEB-1996; 96US-0598591.

XX 12-DEC-1997; 97US-0798691.

XX (GENE-) GENE LOGIC INC.

XX Zeng B, Thurber D, Olson SJ, Alvares CP, Allen ACP, Murphy PD;  
XX Critz BS;

XX WPI; 2000-646756/62.

XX P-PSDB; AAB24218.

XX New coding sequence of the human BRCA1 gene, i.e. BRCA1 (om12), useful  
XX in gene therapy, especially for preventing or treating breast or  
XX ovarian cancer, as well as for diagnosing or monitoring breast or  
XX ovarian cancer.

XX Claim 1; Column 45-50; 56pp; English.

XX AAC60793 to AAC60795 encode the human BRCA1 (om11-3) proteins given in  
XX mapping to position 17q21. The BRCA1 (om12) coding sequence is  
XX specifically claimed in the present invention. The BRCA1 (om12) coding  
XX sequence is useful in gene therapy, especially for preventing or treating  
XX breast or ovarian cancer. It is also useful for diagnosing or monitoring  
XX breast or ovarian cancer. Furthermore, the BRCA1 (om12) coding sequence  
XX is useful for: (a) identifying individuals having BRCA1 gene mutations  
XX and having an increased genetic susceptibility to breast or ovarian  
XX cancer, or identifying a mutation that increases the genetic  
XX susceptibility to breast or ovarian cancer; (b) avoiding

CC misinterpretation of polymorphisms found in the BRCA1 gene; (c)  
CC determining the presence of a previously unknown mutation in the BRCA1  
CC gene; (d) probing a human sample of the BRCA1 gene by allele to determine  
CC the presence of either polymorphic alleles or mutations; and (e)  
CC performing diagnosis with a reagent derived from the BRCA1 (om1) cDNA  
CC sequence. AAC60796 to AAC60861 represent PCR primers for the BRCA1 gene,  
CC which are used in an example from the present invention.

XX SQ Sequence 5711 BP; 1953 A; 1098 C; 1277 G; 1383 T; 0 other;

Query Match 100.0%; Score 5709.4; DB 21; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCTCGCTGAGACTTCTCGACCCGCCACAGGCTGTGGGGTTCACAGTAAGTGGCC 60  
DB 1 AGCTCGCTGAGACTTCTCGACCCGCCACAGGCTGTGGGGTTCACAGTAAGTGGCC 60  
QY 61 CTGCGCTCAGGAGGCTTCCACCTCTGCTCTGGTAAAGTTCATTGGAACAGAGAAA 120  
DB 61 CTGCGCTCAGGAGGCTTCCACCTCTGCTCTGGTAAAGTTCATTGGAACAGAGAAA 120  
QY 121 TGGATTTATCTGCTTCTCGGTTGAGAAAGTACAAAATGCTATGATGAGAGAAA 180  
DB 121 TGGATTTATCTGCTTCTCGGTTGAGAAAGTACAAAATGCTATGATGAGAGAAA 180  
QY 181 TCTTAGAGTGTCCCATCTGCTGAGTTGATCAAGAACCTGTCTCCACAAGTGTGACC 240  
DB 181 TCTTAGAGTGTCCCATCTGCTGAGTTGATCAAGAACCTGTCTCCACAAGTGTGACC 240  
QY 241 ACATATTTTGCATATTTTGCATGCTGAAACTTCTCAACAGAGAGAGGCGCTTCACAGT 300  
DB 241 ACATATTTTGCATATTTTGCATGCTGAAACTTCTCAACAGAGAGAGGCGCTTCACAGT 300  
QY 301 GTCTTTATGTAAGATGATATAACCAAGAGGCGCTTACAGAAAGTACGAGATTTAGTC 360  
DB 301 GTCTTTATGTAAGATGATATAACCAAGAGGCGCTTACAGAAAGTACGAGATTTAGTC 360  
QY 361 AACTTGTGAGAGCTATTGAAATCATTTGCTTTTCTGCTTTCAGCTTGACACAGGTTGAGT 420  
DB 361 AACTTGTGAGAGCTATTGAAATCATTTGCTTTTCTGCTTTCAGCTTGACACAGGTTGAGT 420  
QY 421 ATGCAAAACAGCTATAATTTTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480  
DB 421 ATGCAAAACAGCTATAATTTTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480  
QY 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAAGAGCTTCTACAGAGTG 540  
DB 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAAGAGCTTCTACAGAGTG 540  
QY 541 AACCCGAAATCTCTCTTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600  
DB 541 AACCCGAAATCTCTCTTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600  
QY 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCAAAAGAGCGTCTGTCTACATTG 660  
DB 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCAAAAGAGCGTCTGTCTACATTG 660  
QY 661 AATTGGGATCTGATTCTTCTGAAAGTACCGTTAATTAAGGCAACTTATTGCAAGTGTGGAG 720  
DB 661 AATTGGGATCTGATTCTTCTGAAAGTACCGTTAATTAAGGCAACTTATTGCAAGTGTGGAG 720  
QY 721 ATCAAGATTTGTTACAAATCACCCCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780  
DB 721 ATCAAGATTTGTTACAAATCACCCCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780  
QY 781 CAAAAGAGGCTGCTGTGAAATTTCTGAGACGAGGATGAACAAATCTGAACATCATCAAC 840  
DB 781 CAAAAGAGGCTGCTGTGAAATTTCTGAGACGAGGATGAACAAATCTGAACATCATCAAC 840  
QY 841 CCAGTAAATGATTTGAACACCACTGAGAGGCGTGCAGCTGAGAGGCGATCCAGAGAAAGT 900  
DB 841 CCAGTAAATGATTTGAACACCACTGAGAGGCGTGCAGCTGAGAGGCGATCCAGAGAAAGT 900

Qy 901 ATCAGGAGTGTCTGTTTCAAACCTTGCATGTGGAGCCATGTGGACAAATACTCATGCCA 960  
Db 901 ATCAGGAGTGTCTGTTTCAAACCTTGCATGTGGAGCCATGTGGACAAATACTCATGCCA 960  
Qy 961 GCTCATTTACAGATGAGAACAGCAGTGTATTTACTCATTAAGACAGATGAATGTAGAAA 1020  
Db 961 GCTCATTTACAGATGAGAACAGCAGTGTATTTACTCATTAAGACAGATGAATGTAGAAA 1020  
Qy 1021 AGGCTGAATCTGTAAATAAAGCAAAACAGCTGGCTTAGCAAGGAGCCAAACATACAGAT 1080  
Db 1021 AGGCTGAATCTGTAAATAAAGCAAAACAGCTGGCTTAGCAAGGAGCCAAACATACAGAT 1080  
Qy 1081 GGGCTGGAAGTAAGGAAACATGTAAATGATAGCGGACTCCAGCAGACAGAAAAAGGTAG 1140  
Db 1081 GGGCTGGAAGTAAGGAAACATGTAAATGATAGCGGACTCCAGCAGACAGAAAAAGGTAG 1140  
Qy 1141 ATCTGAATGCTGATCCCTGTGTAGAGAAAGAAATGGAATAAGCAGAACTGCCATGCT 1200  
Db 1141 ATCTGAATGCTGATCCCTGTGTAGAGAAAGAAATGGAATAAGCAGAACTGCCATGCT 1200  
Qy 1201 CAGAGAACTCTAGAGATACTGAAGATGTTCCCTTGGATAACACTAAATAGCAGCAATTGAGA 1260  
Db 1201 CAGAGAACTCTAGAGATACTGAAGATGTTCCCTTGGATAACACTAAATAGCAGCAATTGAGA 1260  
Qy 1261 AAGTTAATGAGTGGTGTTCAGAAAGTGAATGATGTTAGGTTCTGTAGTACTCAGATGATG 1320  
Db 1261 AAGTTAATGAGTGGTGTTCAGAAAGTGAATGATGTTAGGTTCTGTAGTACTCAGATGATG 1320  
Qy 1321 GGGAGTCTGAATCAAAATGCCAAAGTGAATGATGTTAGGTTCTGTAGTACTCAGATGATG 1380  
Db 1321 GGGAGTCTGAATCAAAATGCCAAAGTGAATGATGTTAGGTTCTGTAGTACTCAGATGATG 1380  
Qy 1381 AATATCTGCTGTTCTCAGAGAAATAGACTTACTTGGCCAGTGATCCTCATGAGGCTTTAA 1440  
Db 1381 AATATCTGCTGTTCTCAGAGAAATAGACTTACTTGGCCAGTGATCCTCATGAGGCTTTAA 1440  
Qy 1441 TATGTAAAGTGAAAGAGTTCACCTCCAATCAGTAGAGAGTAATATTGAAGACAAATAT 1500  
Db 1441 TATGTAAAGTGAAAGAGTTCACCTCCAATCAGTAGAGAGTAATATTGAAGACAAATAT 1500  
Qy 1501 TTGGGAAAACTATCGGAAGAGGCAAGCCTCCCAACTTAAGCCATGTAATCAAGAAAG 1560  
Db 1501 TTGGGAAAACTATCGGAAGAGGCAAGCCTCCCAACTTAAGCCATGTAATCAAGAAAG 1560  
Qy 1561 TAAATATAGGAGCATTTGTTACTGAGCCACAGATAATACAGAGCGTCCCTCACAATA 1620  
Db 1561 TAAATATAGGAGCATTTGTTACTGAGCCACAGATAATACAGAGCGTCCCTCACAATA 1620  
Qy 1621 AATTAAGCGTAAAGGAGACCTACATCAGGCGCTTCATCTGAGGATTTTATCAAGAAAG 1680  
Db 1621 AATTAAGCGTAAAGGAGACCTACATCAGGCGCTTCATCTGAGGATTTTATCAAGAAAG 1680  
Qy 1681 CAGATTTGGCAGTTCAAAAGACTCCTGAAATGATAAATCAGGGAACCTAACCAAGCGAGC 1740  
Db 1681 CAGATTTGGCAGTTCAAAAGACTCCTGAAATGATAAATCAGGGAACCTAACCAAGCGAGC 1740  
Qy 1741 AGAATGTCAGTGAATGATTAATTAATGATGTCATGAGAAATAAACAAGAGGTGATT 1800  
Db 1741 AGAATGTCAGTGAATGATTAATTAATGATGTCATGAGAAATAAACAAGAGGTGATT 1800  
Qy 1801 CTATTTCAAGATGAGAAATCCTTAACCAATAGATCACTCGAAAGAAAGATCTGCTTTCA 1860  
Db 1801 CTATTTCAAGATGAGAAATCCTTAACCAATAGATCACTCGAAAGAAAGATCTGCTTTCA 1860  
Qy 1861 AAACGAAAGCTGAACCTATAAGCAGCAGTAAAGCAATATGGAATCGAAATTAATATCC 1920  
Db 1861 AAACGAAAGCTGAACCTATAAGCAGCAGTAAAGCAATATGGAATCGAAATTAATATCC 1920  
Qy 1921 ACAATTCAGAGCACTTAAAGAAATAGGCTGAGAGGAGTCTTCTACAGGCAATATTC 1980  
Db 1921 ACAATTCAGAGCACTTAAAGAAATAGGCTGAGAGGAGTCTTCTACAGGCAATATTC 1980

Qy 1981 ATGCGCTTGAACCTAGTAGTCAGTAGAATACTAAGCCCACTTAATTTGTACTGAATTCGAAA 2040  
Db 1981 ATGCGCTTGAACCTAGTAGTCAGTAGAATACTAAGCCCACTTAATTTGTACTGAATTCGAAA 2040  
Qy 2041 TTGATAGTGTCTTAGCAGTGAAGAGATAAAGAAAAAAGTACAAACCAATGCCAGTCA 2100  
Db 2041 TTGATAGTGTCTTAGCAGTGAAGAGATAAAGAAAAAAGTACAAACCAATGCCAGTCA 2100  
Qy 2101 GGACACAGCAAAACCTCAACTCATGGAAGGTAAAGAAACCTGCAACTGGAGCCCAAGAGA 2160  
Db 2101 GGACACAGCAAAACCTCAACTCATGGAAGGTAAAGAAACCTGCAACTGGAGCCCAAGAGA 2160  
Qy 2161 GTAAACAAGCCAAATGAACAGACAAAGTAAAGACATGACAGTGTAAAGAGTGT 2220  
Db 2161 GTAAACAAGCCAAATGAACAGACAAAGTAAAGACATGACAGTGTAAAGAGTGT 2220  
Qy 2221 AGTTAAACAATGCACCTGGTCTTTTACTAAGTGTTCAAATACCAGTGAATTAAGAAAT 2280  
Db 2221 AGTTAAACAATGCACCTGGTCTTTTACTAAGTGTTCAAATACCAGTGAATTAAGAAAT 2280  
Qy 2281 TTGTCAATCTTAGCTTCCAAAGAGAAAGAAAGAGAACTAGAAACAGTAAAGAGTGT 2340  
Db 2281 TTGTCAATCTTAGCTTCCAAAGAGAAAGAAAGAGAACTAGAAACAGTAAAGAGTGT 2340  
Qy 2341 CTAAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGGTTTTGCAAACTG 2400  
Db 2341 CTAAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGGTTTTGCAAACTG 2400  
Qy 2401 AAAGATCTGTAGAGATGACAGATATTTCACTGGTACCTGGTACCTGATTTATGGCACTCAGG 2460  
Db 2401 AAAGATCTGTAGAGATGACAGATATTTCACTGGTACCTGGTACCTGATTTATGGCACTCAGG 2460  
Qy 2461 AAAGTATCTCGTTACTGGAAAGTTAGCACTCTAGGGAAGGCAAAACAGAACCAATTAAT 2520  
Db 2461 AAAGTATCTCGTTACTGGAAAGTTAGCACTCTAGGGAAGGCAAAACAGAACCAATTAAT 2520  
Qy 2521 GTGTGAGTCAGTGTGACGATTTGAAAAACCCCAAGGCACTTAATTCATGGTTGTTCCAAAG 2580  
Db 2521 GTGTGAGTCAGTGTGACGATTTGAAAAACCCCAAGGCACTTAATTCATGGTTGTTCCAAAG 2580  
Qy 2581 ATAAATAGAAATGACACAGAAAGGCTTTAAGTATCCATTTGGGACATGAAGTTAAACACAGTC 2640  
Db 2581 ATAAATAGAAATGACACAGAAAGGCTTTAAGTATCCATTTGGGACATGAAGTTAAACACAGTC 2640  
Qy 2641 GGGAAAAACAACATAGAAATGGAAGAAAGTGAAGTGAATTTGATGCTTGGTGTGAGATACAT 2700  
Db 2641 GGGAAAAACAACATAGAAATGGAAGAAAGTGAAGTGAATTTGATGCTTGGTGTGAGATACAT 2700  
Qy 2701 TCAAGGTTTTCAAGCGCCAGTCATTTGCTCTGTTTTCAAAATCCAGGAAATGCAGAAAGG 2760  
Db 2701 TCAAGGTTTTCAAGCGCCAGTCATTTGCTCTGTTTTCAAAATCCAGGAAATGCAGAAAGG 2760  
Qy 2761 AATGTGCAACATTTCTGCCCCACTCTGGGTCTTTAAAGAAACAAAGTCCAAAAGTCACTT 2820  
Db 2761 AATGTGCAACATTTCTGCCCCACTCTGGGTCTTTAAAGAAACAAAGTCCAAAAGTCACTT 2820  
Qy 2821 TTGAAATGTGAACAAAAGGAGAAATCAAGAAAGAAATGAGTCTAATATCAAGGCTGTAC 2880  
Db 2821 TTGAAATGTGAACAAAAGGAGAAATCAAGAAAGAAATGAGTCTAATATCAAGGCTGTAC 2880  
Qy 2881 AGACAGTTTAATATACATCTGACGCTTTCTGTTGGTGGTCAGAAAGATAAGCCAGTTGATA 2940  
Db 2881 AGACAGTTTAATATACATCTGACGCTTTCTGTTGGTGGTTCAGAAAGATAAGCCAGTTGATA 2940  
Qy 2941 ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTTGCTCTATCATCTCAGTTCCAGAGCA 3000  
Db 2941 ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTTGCTCTATCATCTCAGTTCCAGAGCA 3000  
Qy 3001 ACGAAATCTGACCTATTACTCCAAATAAACAATGAGCTTTTACAAACCCATATCGTATAC 3060  
Db 3001 ACGAAATCTGACCTATTACTCCAAATAAACAATGAGCTTTTACAAACCCATATCGTATAC 3060  
Qy 3061 CACCACTTTTTCCCATCAAGTCATTTGTTAAACCTAAATGTAAGAAAAATCTGCTAGAGG 3120





QY 5281 AGTCTATTAAAGAAAGAAATGCTGAATGAGCATGATTGTAAGTCAGAGGAGATGTGG 5340  
 DB 5281 AGTCTATTAAAGAAAGAAATGCTGAATGAGCATGATTGTAAGTCAGAGGAGATGTGG 5340  
 QY 5341 TCAATGGAAGAAACCAACCAAGGTCCTCAAGCGAGCAAGAGAAATCCACAGACAGAAAGATCT 5400  
 DB 5341 TCAATGGAAGAAACCAACCAAGGTCCTCAAGCGAGCAAGAGAAATCCACAGACAGAAAGATCT 5400  
 QY 5401 TCAGGGGGCTAGAAATCTGTTGCTATGCGGCCCTTCCACCAATGCCACACAGATCAACTGG 5460  
 DB 5401 TCAGGGGGCTAGAAATCTGTTGCTATGCGGCCCTTCCACCAATGCCACACAGATCAACTGG 5460  
 QY 5461 AATGATGGTACAGCTGTGTGCTCTTCTGTGGTGAAGGAGCTTTCATCAATCAACCTTG 5520  
 DB 5461 AATGATGGTACAGCTGTGTGCTCTTCTGTGGTGAAGGAGCTTTCATCAATCAACCTTG 5520  
 QY 5521 GCACAGGTGTCACCCCAATTTGTGCTGTGAGCCAGATGCTGACAGAGACAAATGGCT 5580  
 DB 5521 GCACAGGTGTCACCCCAATTTGTGCTGTGAGCCAGATGCTGACAGAGACAAATGGCT 5580  
 QY 5581 TCCATGCAATTTGGGCAGATGTGTGAGCCAGCTGTGCTGAGCCAGAGTGGGTGTGGACA 5640  
 DB 5581 TCCATGCAATTTGGGCAGATGTGTGAGCCAGCTGTGCTGAGCCAGAGTGGGTGTGGACA 5640  
 QY 5641 GTGTAGCACTTACAGTGCAGGAGCTGGACACCTTACCTGATACCCAGATCCCCCACA 5700  
 DB 5641 GTGTAGCACTTACAGTGCAGGAGCTGGACACCTTACCTGATACCCAGATCCCCCACA 5700  
 QY 5701 GCCACTACTGA 5711  
 DB 5701 GCCACTACTGA 5711

## RESULT 15

ID AAV46465 standard; cDNA; 5711 BP.  
 AC AAV46465;  
 XX 18-NOV-1998 (first entry)  
 XX Human BRCA1 omi3 polymorphism #1 cDNA.  
 DE BRCA1; omi3; human; breast and ovarian cancer predisposing gene;  
 KW polymorphism; susceptibility; anti-oncogene; tumour suppressor;  
 KW Chromosome 17q; ss.  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 PH CDS 120..5711  
 FT /\*tag= a  
 FT /product= "BRCA1 omi3 protein"  
 FT 2201  
 FT variation  
 FT /\*tag= b  
 FT /note= "This polymorphic variation can be a C or T nucleotide"

US5750400-A.

XX 12-MAY-1998.

XX 12-FEB-1997; 97US-0798691.

XX 12-FEB-1996; 96US-0598591.

XX 12-FEB-1997; 97US-0798691.

XX (ONCO-) ONCORMED INC.

XX Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ;

XX Scheller DB, Zeng B;

XX

WPI; 1998-296774/26.

XX BRCA1 omi gene coding sequences - useful for distinguishing between  
 PT polymorphisms and mutation(s) in the screening for disposition to  
 PT breast or ovarian cancer

XX Claim 2e; Page -; 54pp; English.

XX This sequence encodes a human BRCA1 (breast and ovarian cancer  
 CC predisposing gene) omi3 gene in which a polymorphic variation occurs at  
 CC nucleotide 2201. This sequence and other polymorphic variations of this  
 CC sequence are useful for the identification of an individual who may or  
 CC may not have an increased susceptibility to breast or ovarian cancer.  
 CC The sequences used identify gene changes which are due to polymorphisms,  
 CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour  
 CC suppressor) which is involved in genetic inheritance of cancers,  
 CC especially breast and ovarian cancer. It is found at human chromosome  
 CC 17q which is known to be linked to cancer susceptibility, especially  
 CC breast cancer. Cells containing a mutation in this gene lose the  
 CC wild-type function of BRCA1 and are more susceptible to cancers.  
 CC NOTE: This sequence does not appear in the specification but has been  
 CC created from the wild type BRCA1 omi3 gene represented in AAV46450.

XX Sequence 5711 BP; 1953 A; 1098 C; 1277 G; 1382 T; 1 other;

Query Match 100.0%; Score 5709; DB 19; Length 5711;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 5709; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCTCGCTGAGACTTCTGACACCCCGCACAGGCTGTGGGTTTCTCAGATAACTGGGCC 60  
 DB 1 AGCTCGCTGAGACTTCTGACACCCCGCACAGGCTGTGGGTTTCTCAGATAACTGGGCC 60  
 QY 61 CTTGCGCTCAGGAGGCTTCCACCTCTGCTCTGGTAAAGTTTCAATTCGAAACAGAAAGAAA 120  
 DB 61 CTTGCGCTCAGGAGGCTTCCACCTCTGCTCTGGTAAAGTTTCAATTCGAAACAGAAAGAAA 120  
 QY 121 TGGATTTATCTGCTCTTCGGGTTTGAAGAAGTACAAAAATGTCTATTAATGCTATGCGAGAAA 180  
 DB 121 TGGATTTATCTGCTCTTCGGGTTTGAAGAAGTACAAAAATGTCTATTAATGCTATGCGAGAAA 180  
 QY 181 TCTTAGAGTGCCCATCTGCTGAGTTGATCAAGAACCTGTCTCCACAAGTGTGACC 240  
 DB 181 TCTTAGAGTGCCCATCTGCTGAGTTGATCAAGAACCTGTCTCCACAAGTGTGACC 240  
 QY 241 ACATATTTTGCAAATTTTGCATGCTGAACTTCTCAACAGAGAAAGGGCTTTCACAGT 300  
 DB 241 ACATATTTTGCAAATTTTGCATGCTGAACTTCTCAACAGAGAAAGGGCTTTCACAGT 300  
 QY 301 GTCCTTTTATGTAAGATGATATAACCAAAAGGAGCCTACAGAAAGTACGAGATTTAGTTC 360  
 DB 301 GTCCTTTTATGTAAGATGATATAACCAAAAGGAGCCTACAGAAAGTACGAGATTTAGTTC 360  
 QY 361 AACTTTTGAAGAGCTATTGAAATCATTTGTGCTTTTACGCTTGACACAGTTGGAGT 420  
 DB 361 AACTTTTGAAGAGCTATTGAAATCATTTGTGCTTTTACGCTTGACACAGTTGGAGT 420  
 QY 421 ATGCACACAGCTATAATTTTGCACAAAGGAGAAATTAATCTCTCCGAAACATCTAAAGATG 480  
 DB 421 ATGCACACAGCTATAATTTTGCACAAAGGAGAAATTAATCTCTCCGAAACATCTAAAGATG 480  
 QY 481 AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCACAAAGACTTCTACAGAGTG 540  
 DB 481 AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCACAAAGACTTCTACAGAGTG 540  
 QY 541 AACCCGAAAATCTCTTCTGAGGAAACCAAGTCTCAGTGTCCAACTCTCTAACCTTGGAA 600  
 DB 541 AACCCGAAAATCTCTTCTGAGGAAACCAAGTCTCAGTGTCCAACTCTCTAACCTTGGAA 600  
 QY 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATAGAACTCTCAAAAGACGCTCTGTCTACATTG 660  
 DB 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATAGAACTCTCAAAAGACGCTCTGTCTACATTG 660



Db 2821 TTGAATGTGAACAAAAGGAAGAAAATCAAGGAAGAATAGTCTAATATCAAGCCTGTAC 2880  
Qy 2881 AGACAGTAAATATATCACTGCAGGCTTTCTCTGTGGTGTGTCAGAAAGATAAGCCAGTTGATA 2940  
Db 2881 AGACAGTAAATATCACTGCAGGCTTTCTCTGTGGTGTGTCAGAAAGATAAGCCAGTTGATA 2940  
Qy 2941 ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTTCAGAGGCA 3000  
Db 2941 ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTTCAGAGGCA 3000  
Qy 3001 ACAGAACTGGACTCATTTACTTCCAAATAAATGAATGACATTTTACAAAAACCATATCGTATAC 3060  
Db 3001 ACAGAACTGGACTCATTTACTTCCAAATAAATGACATTTTACAAAAACCATATCGTATAC 3060  
Qy 3061 CACCACATTTTCCCATCAAGTCATTTGTAACTAAATGTAAGAAAAATCTGCTAGAGG 3120  
Db 3061 CACCACATTTTCCCATCAAGTCATTTGTAACTAAATGTAAGAAAAATCTGCTAGAGG 3120  
Qy 3121 AAAAATTTGAGGAACATTTCAATGTCACTGAAAGAGAAAATGGGAAAATGAGAACATTTCCAA 3180  
Db 3121 AAAAATTTGAGGAACATTTCAATGTCACTGAAAGAGAAAATGGGAAAATGAGAACATTTCCAA 3180  
Qy 3181 GTACAGTGAGCACAAATAGCGGTAAATACATTAAGAGAAAATGTTTTTAAAGGAGCCAGCT 3240  
Db 3181 GTACAGTGAGCACAAATAGCGGTAAATACATTAAGAGAAAATGTTTTTAAAGGAGCCAGCT 3240  
Qy 3241 CAAGCAATTAATTAAGTAGGTTCAGTAGTCTAATGAATGAGTGGGCTCCAGTATTAATGAAA 3300  
Db 3241 CAAGCAATTAATTAAGTAGGTTCAGTAGTCTAATGAATGAGTGGGCTCCAGTATTAATGAAA 3300  
Qy 3301 TAGGTTCCAGTGATGAAAACATTCAGCAGAACATAGGTAGAAAACAGAGGGCCAAAATGGA 3360  
Db 3301 TAGGTTCCAGTGATGAAAACATTCAGCAGAACATAGGTAGAAAACAGAGGGCCAAAATGGA 3360  
Qy 3361 ATGCTATGCTTAGATTAGGGTTTTGCAACCTGAGGTCTATAAACAAGTCTTCTCTGGA 3420  
Db 3361 ATGCTATGCTTAGATTAGGGTTTTGCAACCTGAGGTCTATAAACAAGTCTTCTCTGGA 3420  
Qy 3421 GTAATGTGAAGTCTCGAAATAAAGAAAGCAAGATATGAAGAGTAGTTCAGACTGTGA 3480  
Db 3421 GTAATGTGAAGTCTCGAAATAAAGAAAGCAAGATATGAAGAGTAGTTCAGACTGTGA 3480  
Qy 3481 ATACAGATTTCTCTCCATATCTGATTTTCAGATACTTAGAACACGCTATGGGAAGTAGTC 3540  
Db 3481 ATACAGATTTCTCTCCATATCTGATTTTCAGATACTTAGAACACGCTATGGGAAGTAGTC 3540  
Qy 3541 ATGCATCTCAGGTTGTTCTGAGACACCTGATGACCTGTAGATGATGTTGAATAAAGG 3600  
Db 3541 ATGCATCTCAGGTTGTTCTGAGACACCTGATGACCTGTAGATGATGTTGAATAAAGG 3600  
Qy 3601 AAGTACTAGTTTGTGAAATGACATTAAGGAAAGTTCTGCTGTTTTTAAAGCAAAAGCG 3660  
Db 3601 AAGTACTAGTTTGTGAAATGACATTAAGGAAAGTTCTGCTGTTTTTAAAGCAAAAGCG 3660  
Qy 3661 TCCAGAGAGGAGAGCTTAGCAGGAGTCTAGCCCTTTCCACCACACACATTTGCTCAGG 3720  
Db 3661 TCCAGAGAGGAGAGCTTAGCAGGAGTCTAGCCCTTTCCACCACACACATTTGCTCAGG 3720  
Qy 3721 GTTACCGAAGAGGGGCCAAGAAAATAGAGTCTCTAGAAAGAGAACTTATCTAGTGAGGATG 3780  
Db 3721 GTTACCGAAGAGGGGCCAAGAAAATAGAGTCTCTAGAAAGAGAACTTATCTAGTGAGGATG 3780  
Qy 3781 AAGAGCTTCCCTGTTTCCAAACACTGTTATTTGTTAAAGTAAACAATATCTCTCAGT 3840  
Db 3781 AAGAGCTTCCCTGTTTCCAAACACTGTTATTTGTTAAAGTAAACAATATCTCTCAGT 3840  
Qy 3841 CTACTAGGCATAGCACCCCTGCTACCGAGTGTCTGCTTAAGAACACAGAGGAGAAATTTAT 3900  
Db 3841 CTACTAGGCATAGCACCCCTGCTACCGAGTGTCTGCTTAAGAACACAGAGGAGAAATTTAT 3900  
Qy 3901 TATCATTGAAGAAATAGCTTAAATGATCGAGTAACCGAGTAAATTTGCAAAAGGATCTC 3960  
Db 3901 TATCATTGAAGAAATAGCTTAAATGATCGAGTAACCGAGTAAATTTGCAAAAGGATCTC 3960

Qy 3961 AGGAAACATCACTTAGTGAGGAAACAAAATGTTTCTGCTAGCTTGTCTTTCACAGTGCA 4020  
Db 3961 AGGAAACATCACTTAGTGAGGAAACAAAATGTTTCTGCTAGCTTGTCTTTCACAGTGCA 4020  
Qy 4021 GTGAAATTTGGAGACTTGACATGCAAAATACAAACCCAGGATCCTTCTGATTTGGTTCTT 4080  
Db 4021 GTGAAATTTGGAGACTTGACATGCAAAATACAAACCCAGGATCCTTCTGATTTGGTTCTT 4080  
Qy 4081 CCAAAACAAATGAGGCACTCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGACAAGGAAATGG 4140  
Db 4081 CCAAAACAAATGAGGCACTCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGACAAGGAAATGG 4140  
Qy 4141 TTTTCAGATGATGAAGAAAGAGGAAACGGGCTTTGGAGAAAATAATCAAGAGAGCAAGCA 4200  
Db 4141 TTTTCAGATGATGAAGAAAGAGGAAACGGGCTTTGGAGAAAATAATCAAGAGAGCAAGCA 4200  
Qy 4201 TGGATTTCAAACTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAAACAAGCGCTCTCTGAAG 4260  
Db 4201 TGGATTTCAAACTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAAACAAGCGCTCTCTGAAG 4260  
Qy 4261 ACTGCTCAGGGCTATCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGATACCATGC 4320  
Db 4261 ACTGCTCAGGGCTATCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGATACCATGC 4320  
Qy 4321 AACATAA CCTGATAAAGCTCCAGCAGGAAATGGCTGAAGTAGAAGTGTGTTAGAAACAGC 4380  
Db 4321 AACATAA CCTGATAAAGCTCCAGCAGGAAATGGCTGAAGTAGAAGTGTGTTAGAAACAGC 4380  
Qy 4381 ATGGGAGCCAGCCTTTTAAACAGCTACCTTTCCATCATAGTGACTCTCTGCCCTTGAGG 4440  
Db 4381 ATGGGAGCCAGCCTTTTAAACAGCTACCTTTCCATCATAGTGACTCTCTGCCCTTGAGG 4440  
Qy 4441 ACCTGCCAAATCCAGAACAAAGCACATCAGAAAAAGCAGTATTAACTTTCACAGAAAAGTA 4500  
Db 4441 ACCTGCCAAATCCAGAACAAAGCACATCAGAAAAAGCAGTATTAACTTTCACAGAAAAGTA 4500  
Qy 4501 GTGAATACCTTATAAGCCAGAAATCCAGAAAGCCCTTTCTGCTGACAAGTTTGAGGTGCTG 4560  
Db 4501 GTGAATACCTTATAAGCCAGAAATCCAGAAAGCCCTTTCTGCTGACAAGTTTGAGGTGCTG 4560  
Qy 4561 CAGTAGTTCTACAGTAAATAAAGAACAGAGGTGGAAGGTCTATCCCTTCTTAAT 4620  
Db 4561 CAGTAGTTCTACAGTAAATAAAGAACAGAGGTGGAAGGTCTATCCCTTCTTAAT 4620  
Qy 4621 GCCCATCATTAGATGATAGTGTGACATGACAGTGTCTGCGAGTCTTTCAGAAATAGAA 4680  
Db 4621 GCCCATCATTAGATGATAGTGTGACATGACAGTGTCTGCGAGTCTTTCAGAAATAGAA 4680  
Qy 4681 ACTACCCATCTCAAGAGGAGCTCAATTAAGGTGTTGATGTGGAGGAGCAACAGCTGGAAG 4740  
Db 4681 ACTACCCATCTCAAGAGGAGCTCAATTAAGGTGTTGATGTGGAGGAGCAACAGCTGGAAG 4740  
Qy 4741 AGTCTGGGCCACAGATTTGACGGAACATCTTACTTGCAGAGGCAAGATCTAGAGGAA 4800  
Db 4741 AGTCTGGGCCACAGATTTGACGGAACATCTTACTTGCAGAGGCAAGATCTAGAGGAA 4800  
Qy 4801 CCCCTTACCTGGAATCTGGAATCAGCTCTTCTGATGACCCCTGAATCTCATCTCTG 4860  
Db 4801 CCCCTTACCTGGAATCTGGAATCAGCTCTTCTGATGACCCCTGAATCTCATCTCTG 4860  
Qy 4861 AAGACAGAGCCCAAGAGTCACTGCTGTGGCAACATACCACTTCAACCTCTGCATTGA 4920  
Db 4861 AAGACAGAGCCCAAGAGTCACTGCTGTGGCAACATACCACTTCAACCTCTGCATTGA 4920  
Qy 4921 AAGTTCCTCCAAATGAAAGTTGAGAAATCTGCCAGGGTCCAGTGTCTCATACTCTG 4980  
Db 4921 AAGTTCCTCCAAATGAAAGTTGAGAAATCTGCCAGGGTCCAGTGTCTCATACTCTG 4980  
Qy 4981 ATACTGTGGGTAAATGCAATGGAAGAAAGTGTGAGCAGGAGAGCCAGAAATGACAG 5040  
Db 4981 ATACTGTGGGTAAATGCAATGGAAGAAAGTGTGAGCAGGAGAGCCAGAAATGACAG 5040

QY 5041 CTTCAACAGAAAGGTCACAAAAGAAATGTCCATGGTGGTGTCTGGCTGACCCAGAAAG 5100  
Db |||||  
QY 5041 CTTCAACAGAAAGGTCACAAAAGAAATGTCCATGGTGGTGTCTGGCTGACCCAGAAAG 5100  
Db |||||  
QY 5101 AATTATGCTCGTGTAAGTTTGGCAGAAAACACCATCATCACTTTAACTAATCTAATTA 5160  
Db |||||  
QY 5101 AATTATGCTCGTGTAAGTTTGGCAGAAAACACCATCATCACTTTAACTAATCTAATTA 5160  
Db |||||  
QY 5161 CTGAAGAGACTACTCATGCTGTATGAAAACAGATGCTGAGTTTGTGTGAACGGACAC 5220  
Db |||||  
QY 5161 CTGAAGAGACTACTCATGCTGTATGAAAACAGATGCTGAGTTTGTGTGAACGGACAC 5220  
Db |||||  
QY 5221 TGAATAATTTTCTAGGAATTCGGGAGGAAAATGGTAGTTAGCTATTTCTTGGGTGACCC 5280  
Db |||||  
QY 5221 TGAATAATTTTCTAGGAATTCGGGAGGAAAATGGTAGTTAGCTATTTCTTGGGTGACCC 5280  
Db |||||  
QY 5281 AGTCTATTAAAGAAAGAAAATGCTGAATGAGCATGATTTTGAAGTCAGAGGAGATGTGG 5340  
Db |||||  
QY 5281 AGTCTATTAAAGAAAGAAAATGCTGAATGAGCATGATTTTGAAGTCAGAGGAGATGTGG 5340  
Db |||||  
QY 5341 TCAATGAAGAAACACCAAGGTCCTAAAGCGAGCAAGAGATCCAGGACAGAAAGATCT 5400  
Db |||||  
QY 5341 TCAATGAAGAAACACCAAGGTCCTAAAGCGAGCAAGAGATCCAGGACAGAAAGATCT 5400  
Db |||||  
QY 5401 TCAGGGGCTAGAAAATCTGTTGCTATGAGGCGCTTTCACCAACATGCCACAGATCAACTGG 5460  
Db |||||  
QY 5401 TCAGGGGCTAGAAAATCTGTTGCTATGAGGCGCTTTCACCAACATGCCACAGATCAACTGG 5460  
Db |||||  
QY 5461 AATGGATGGTACAGCTGTGTGGTCTGTGTGGTGAAGGAGCTTTTCATCACTCCCTTG 5520  
Db |||||  
QY 5461 AATGGATGGTACAGCTGTGTGGTCTGTGTGGTGAAGGAGCTTTTCATCACTCCCTTG 5520  
Db |||||  
QY 5521 GCACAGGTGTCACCCCAATTTGTTGTTGTCAGCCAGATGCTGGACAGAGGACAAATGGCT 5580  
Db |||||  
QY 5521 GCACAGGTGTCACCCCAATTTGTTGTTGTCAGCCAGATGCTGGACAGAGGACAAATGGCT 5580  
Db |||||  
QY 5581 TCCATGCAATTTGGCAGATGTGAGGACCTGTGGTGACCCGAGAGTGGGTGTTGGACA 5640  
Db |||||  
QY 5581 TCCATGCAATTTGGCAGATGTGAGGACCTGTGGTGACCCGAGAGTGGGTGTTGGACA 5640  
Db |||||  
QY 5641 GTGTAGCACTTACAGTCCAGAGCTGGACACCTTACCTGATACCCAGATCCCCCACA 5700  
Db |||||  
QY 5641 GTGTAGCACTTACAGTCCAGAGCTGGACACCTTACCTGATACCCAGATCCCCCACA 5700  
Db |||||  
QY 5701 GCCACTACTGA 5711  
Db |||||  
QY 5701 GCCACTACTGA 5711  
Db |||||

Search completed: December 14, 2003, 12:03:24  
Job time : 1347 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 14, 2003, 09:36:27 ; Search time 10204 Seconds  
(without alignments)  
13602.789 Million cell updates/sec

Title: US-09-923-327A-263  
Perfect score: 5711  
Sequence: 1 agcgcgtgcgactctctcg.....tccccacagccactactga 5711

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 1215238056 residues  
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
EST:  
1: em\_eacba:\*  
2: em\_eacba:\*  
3: em\_eacba:\*  
4: em\_eacba:\*  
5: em\_eacba:\*  
6: em\_eacba:\*  
7: em\_eacba:\*  
8: em\_eacba:\*  
9: gb\_eacba:\*  
10: gb\_eacba:\*  
11: gb\_eacba:\*  
12: gb\_eacba:\*  
13: gb\_eacba:\*  
14: gb\_eacba:\*  
15: em\_eacba:\*  
16: em\_eacba:\*  
17: em\_gsa\_hum:\*  
18: em\_gsa\_hum:\*  
19: em\_gsa\_hum:\*  
20: em\_gsa\_hum:\*  
21: em\_gsa\_hum:\*  
22: em\_gsa\_hum:\*  
23: em\_gsa\_hum:\*  
24: em\_gsa\_hum:\*  
25: em\_gsa\_hum:\*  
26: em\_gsa\_hum:\*  
27: em\_gsa\_hum:\*  
28: gb\_gsa2:\*  
29: gb\_gsa2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2061.4	36.1	2101	11	BC012577 Homo sapi
2	2055.6	36.0	2090	11	BC030969 Homo sapi
3	1416.4	24.8	1578	11	BC038947 Homo sapi
4	968.8	17.0	1919	11	AK086173 Mus muscu

5	863	15.1	962	13	BQ068830
6	841.4	14.7	1089	12	BM452288
7	810.2	14.2	845	9	AU122476
8	760.2	13.3	783	9	AU142729
9	746.4	13.1	933	10	BQ171200
10	738.8	12.9	899	13	BQ422380
11	734.6	12.4	878	13	BQ215100
12	706.2	12.0	856	13	BQ147444
13	698	12.0	747	12	BQ777447
14	687.6	12.0	739	10	BF508987
15	686.6	12.0	702	9	AU125312
16	686.4	12.0	987	12	BM800251
17	658.6	11.5	900	10	BF791668
18	651.6	11.4	938	10	BQ257190
19	651.6	11.2	675	9	AL704228
20	639	11.0	631	14	CB155501
21	631	10.8	921	10	BQ178466
22	617.6	10.6	630	9	A1992040
23	603.8	10.4	906	13	BQ878445
24	593	10.4	909	13	BQ676829
25	593	10.4	922	13	BQ194336
26	593	10.4	933	13	BQ683955
27	592.6	10.4	724	9	A1589028
28	591.4	10.4	627	9	A1589028
29	591.4	10.3	800	10	BF794879
30	589.4	10.3	947	13	BQ679749
31	586	10.2	949	13	BQ155689
32	582.8	10.2	910	13	BQ677666
33	581	10.2	941	13	BQ163307
34	580.4	10.2	602	10	BE043993
35	575	9.6	638	12	BM042282
36	548.2	9.6	545	14	CB118225
37	541.8	9.5	638	10	BE264293
38	535.2	9.4	563	9	AW295197
39	530	9.3	585	10	AW968546
40	528.6	9.3	528	14	CB158976
41	528	9.0	666	10	AW968720
42	516.4	8.7	509	9	AW504244
43	498.2	8.6	894	13	BQ552955
44	493	8.6	509	10	BE018878
45	492.8	8.6			

## ALIGNMENTS

RESULT 1  
LOCUS BC012577 2101 bp mRNA  
DEFINITION Homo sapiens, clone IMAGE:3996658, mRNA.  
ACCESSION BC012577.1 GI:15214876  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (baes 1 to 2101)  
AUTHORS Strausberg, R.  
TITLE Direct Submission  
JOURNAL Submitted (15-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK  
COMMENT  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgapba-remail.nih.gov](mailto:cgapba-remail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLT)  
DNA Sequencing by: Institute for Systems Biology  
<http://www.systemsbio.org>  
Contact: [amadan@systemsbio.org](mailto:amadan@systemsbio.org)

Anup Madan, Jessica Fahay, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLM at: <http://image.llnl.gov>

Series: IRAL Plate: 19 Row: a Column: 18

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6552298

This clone has the following problem: retained intron.

## FEATURES

## Source

Location/Qualifiers

1..2101  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:399658"  
/issue\_type="Bladder, Carcinoma"  
/clone\_id="NH MGC\_53"  
/lab\_host="DH10B"  
/note="Vector: pDNR-LIB"  
BASE COUNT 756 a 385 c 452 g 508 t  
ORIGIN

Query Match 36.1%; Score 2061.4; DB 11; Length 2101;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 2079; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

```

Oy 1 AGCTGCTGAGACTTCTGAGACCCCGACGAGGCTGTGGGTTCTCGATTAAGTGGGCC 60
Db 6 AGCTGCTGAGACTTCTGAGACCCCGACGAGGCTGTGGGTTCTCGATTAAGTGGGCC 64
Oy 61 CCTGCGCTCAGAGGCTTCAACCTCTGCTGTGTAAGTTCATTTGAGAGAGAGAA 120
Db 65 CTTGGGCTCAGAGGCTTCAACCTCTGCTGTGTAAGTTCATTTGAGAGAGAGAA 124
Oy 121 TGAATTTATCTGCTCTTGGCGTTGAGAGATCAAAATGTCAATTAATCTATGCAAAA 180
Db 125 TGAATTTATCTGCTCTTGGCGTTGAGAGATCAAAATGTCAATTAATCTATGCAAAA 184
Oy 181 TCTTAGAGTGTCCATCTGTCTGAGTGTATCAAGGAAGTGTCTCCCAAGAGTGGACC 240
Db 185 TCTTAGAGTGTCCATCTGTCTGAGTGTATCAAGGAAGTGTCTCCCAAGAGTGGACC 244
Oy 241 ACATATTTTGGCAATTTTGCATGCTGAACTTCTCAACAGAGAGAGGCTTCAACAGT 300
Db 245 ACATATTTTGGCAATTTTGCATGCTGAACTTCTCAACAGAGAGAGGCTTCAACAGT 304
Oy 301 GTCTTTATGTAAGATGATTAACCAAAAGAGGCTTCAAGAGATGAGATTAGTC 360
Db 305 GTCTTTATGTAAGATGATTAACCAAAAGAGGCTTCAAGAGATGAGATTAGTC 364
Oy 361 AACTGTGTGAGAGCTATGAAATCATTTGGCTTTCAAGTGTGACAGAGTTTGGAGT 420
Db 365 AACTGTGTGAGAGCTATGAAATCATTTGGCTTTCAAGTGTGACAGAGTTTGGAGT 424
Oy 421 ATGCAACAGCTATTAATTTTCAAAAAAGAAATTAATCTCTGCAATCTTAAAGATG 480
Db 425 ATGCAACAGCTATTAATTTTCAAAAAAGAAATTAATCTCTGCAATCTTAAAGATG 484
Oy 481 AAGTTTCTATCATCAAAAGTATGGCTTACAGAAACCGTGCCAAAGACTTTTACAGATG 540
Db 485 AAGTTTCTATCATCAAAAGTATGGCTTACAGAAACCGTGCCAAAGACTTTTACAGATG 544
Oy 541 AACCCGAAATTCCTTCTGAGAGAAACCAAGTCTCAAGTCTCAACTCTTAAAGTAA 600
Db 545 AACCCGAAATTCCTTCTGAGAGAAACCAAGTCTCAAGTCTCAACTCTTAAAGTAA 604
Oy 601 CTGTGAGAACTCTGAGAGCAAGAGCGGATACAACTCAAAAGAGCTGTCTTCAATG 660
Db 605 CTGTGAGAACTCTGAGAGCAAGAGCGGATACAACTCAAAAGAGCTGTCTTCAATG 664
Oy 661 AATTGGAGTGTGATTTCTTGAAGATACCGTTAATTAAGGCAACTTATTTGAGTGGAG 720
Db 665 AATTGGAGTGTGATTTCTTGAAGATACCGTTAATTAAGGCAACTTATTTGAGTGGAG 724

```

```

Oy 721 ATCAAGATTGTACAATACACCCCTCAAGGACCAAGGATGAATACAGTTTGGATCTG 780
Db 725 ATCAAGATTGTACAATACACCCCTCAAGGACCAAGGATGAATACAGTTTGGATCTG 784
Oy 781 CAAAAAGAGCTCTTGAATTTTCTGAGAGATGTAACAATACTGACATCATCAAC 840
Db 785 CAAAAAGAGCTCTTGAATTTTCTGAGAGATGTAACAATACTGACATCATCAAC 844
Oy 841 CCAATTAATGATTTTGAACCACTGAGAGAGCTGACGTGAGAGGATTCAGAAAAAGT 900
Db 845 CCAATTAATGATTTTGAACCACTGAGAGAGCTGACGTGAGAGGATTCAGAAAAAGT 904
Oy 901 ATCAGGAGATTTCTGTTTCAAACTTGCATGAGAGCCATGAGGACAAATCATGCGCA 960
Db 905 ATCAGGAGATTTCTGTTTCAAACTTGCATGAGAGCCATGAGGACAAATCATGCGCA 964
Oy 961 GCTCATTAACAGCATGAGAACAGAGTTTATTAATCACTAAAGACAGATGATAGAAA 1020
Db 965 GCTCATTAACAGCATGAGAACAGAGTTTATTAATCACTAAAGACAGATGATAGAAA 1024
Oy 1021 AGGCTGAATTTCTGTAATTAAGCAACAGCTGGCTTACAGAGAGCCATTAACAGAT 1080
Db 1025 AGGCTGAATTTCTGTAATTAAGCAACAGCTGGCTTACAGAGAGCCATTAACAGAT 1084
Oy 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGGCGGACCTCCAGACAGAAAAAGGTAG 1140
Db 1085 GGGCTGGAAGTAAAGAAACATGTAATGATAGGCGGACCTCCAGACAGAAAAAGGTAG 1144
Oy 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGAATTAACAGAACTGCCATGCT 1200
Db 1145 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGAATTAACAGAACTGCCATGCT 1204
Oy 1201 CAGGAATCTGAGATGATCTGAAATGTTCTTGGATTAACCTAATTAAGCAGCTTACA 1260
Db 1205 CAGGAATCTGAGATGATCTGAAATGTTCTTGGATTAACCTAATTAAGCAGCTTACA 1264
Oy 1261 AAGTTAATGAGTGTGTTTCCAGAGATGATGAAGTGAAGTTCATGATGACTCATGATG 1320
Db 1265 AAGTTAATGAGTGTGTTTCCAGAGATGATGAAGTGAAGTTCATGATGACTCATGATG 1324
Oy 1321 GGGAGTCTGAATCAAAATGCCAAAGTACGATGATTAATGAGAGTGAAGTGAAGT 1380
Db 1325 GGGAGTCTGAATCAAAATGCCAAAGTACGATGATTAATGAGAGTGAAGTGAAGT 1384
Oy 1381 AATATTTCTGTTCTTCAAGAGAAATAGACTTAATGAGAGTCTCTGATGAGCTTTAA 1440
Db 1385 AATATTTCTGTTCTTCAAGAGAAATAGACTTAATGAGAGTCTCTGATGAGCTTTAA 1444
Oy 1441 TATGTAAGAGTAAGAGTTCACCTCCAAATCAGTGAAGATTAATTAAGAGCAAAATAT 1500
Db 1445 TATGTAAGAGTAAGAGTTCACCTCCAAATCAGTGAAGATTAATTAAGAGCAAAATAT 1504
Oy 1501 TTGGAAAACTTATCGAAGAGCAAGCTCCCTCCCACTTAAGCATGTAACTGAAAAATC 1560
Db 1505 TTGGAAAACTTATCGAAGAGCAAGCTCCCTCCCACTTAAGCATGTAACTGAAAAATC 1564
Oy 1561 TAATTAATGAGCAATTTGTTATCTGAGCAAGATTAATTAAGAGAGCTTCTCAAAATA 1620
Db 1565 TAATTAATGAGCAATTTGTTATCTGAGCAAGATTAATTAAGAGAGCTTCTCAAAATA 1624
Oy 1621 AATTAAGCGTAAAGAGAGCACTACAGAGCTTCAATCCGAGAGATTTTATCAAGAAAG 1680
Db 1625 AATTAAGCGTAAAGAGAGCACTACAGAGCTTCAATCCGAGAGATTTTATCAAGAAAG 1684
Oy 1681 CAGATTTGAGAGTCAAAAGACTCTGAAATGATTAATCAAGGAACTTAACCAACGAGAGC 1740
Db 1685 CAGATTTGAGAGTCAAAAGACTCTGAAATGATTAATCAAGGAACTTAACCAACGAGAGC 1744
Oy 1741 AGAATGCTCAAGTATGATTAATTAATTAATGAGTCAATGAATTAACCAAGGATTAAT 1800
Db 1745 AGAATGCTCAAGTATGATTAATTAATTAATGAGTCAATGAATTAACCAAGGATTAAT 1804

```



QY 1801 CTATTTCAGAAATGAGAAAAATCTTAACCCATATGATCATCTGAAAAAGATCTGCTTCA 1860  
DB 1805 CTATTTCAGAAATGAGAAAAATCTTAACCCATATGATCATCTGAAAAAGATCTGCTTCA 1864  
QY 1861 AAACGAAAGCTGAACCTTAAGACAGCAGTATATGCAATATGGAATCTGCAATTAATATCC 1920  
DB 1865 AAACGAAAGCTGAACCTTAAGACAGCAGTATATGCAATATGGAATCTGCAATTAATATCC 1924  
QY 1921 ACAATTCAAAAGCCTTAAGAAATAGCTGAGAGAGAGAGCTTCTCAACGAGCATATTC 1980  
DB 1925 ACAATTCAAAAGCCTTAAGAAATAGCTGAGAGAGAGAGCTTCTCAACGAGCATATTC 1984  
QY 1981 ATGGCTTGAACCTATAGTCACTAGTAAGATCTTAAGCCCACTAATTTGATGATGCAAA 2040  
DB 1985 ATGGCTTGAACCTATAGTCACTAGTAAGATCTTAAGCCCACTAATTTGATGATGCAAA 2044  
QY 2041 TTGATAGTTGTTCTTACAGTGAAGATTAAGAAAAAAGTACCAACAAA 2091  
DB 2045 TTGATAGTTGTTCTTACAGTGAAGATTAAGAAAAAAGTACCAACAAA 2095  
RESULT 2  
BC030969 2090 bp mRNA linear HTC 13-JUN-2002  
LOCUS Homo sapiens, Similar to breast cancer 1, early onset, clone  
DEFINITION IMAGE:4804551, mRNA.  
ACCESSION BC030969 GI:21411299  
VERSION BC030969.1 GI:21411299  
KEYWORDS HTC.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 2090)  
AUTHORS Strausberg, R.  
TITLE Direct Submission  
JOURNAL Submitted (03-JUN-2002) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
COMMENT Contact: MGC help desk  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: DCTD/DRP  
cDNA Library Preparation: CLOUTech Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILML)  
DNA Sequencing by: Sequencing Group at the Stanford Human Genome  
Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www.shgc.stanford.edu>  
Contact: (Dickson, Mark) [mcdelpaxil.stanford.edu](mailto:mcdelpaxil.stanford.edu)  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,  
R. M.  
Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/ILML at: <http://image.llnl.gov>  
Series: IRAL Plate: 41 Row: P Column: 11  
This clone was selected for full length sequencing because it  
passed the following selection criteria: matched mRNA g1: 6552298  
This clone has the following problem: frame shifted.  
FEATURES  
source  
1..2090  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4804551"  
/tissue\_type="Prostate, adenocarcinoma."  
/clone\_id="NIH\_MGC\_60"  
/lab\_host="DH10B"  
/note="Vector: pDNR-LIB"  
BASE COUNT 754 a 385 c 444 g 507 t  
ORIGIN  
Query Match 36.0%; Score 2055.6; DB 11; Length 2090;

Best Local Similarity 99.3%; Pred. No. 0;  
Matches 2075; Conservative 0; Mismatches 14; Indels 1; Gaps 1;  
QY 1 AGCTGCGTGAAGATCTTCTGAGACCCCGACACAGGCTGTGGGGTTTCTCAGATATCTGGGCC 60  
DB 2 AGCTGCGTGAAGATCTTCTGAGACCCCGACACAGGCTGTGGGGTTTCTCAGATATCTGGGCC 60  
QY 61 CCTGCGCTCAGAGAGCCCTTCAACCTCTGCTGTGGGTTAAAGTTCAATGGACAGAAAGAA 120  
DB 61 CCTGCGCTCAGAGAGCCCTTCAACCTCTGCTGTGGGTTAAAGTTCAATGGACAGAAAGAA 120  
QY 121 TGGATTTATCTGCTCTTCCGCTTGAAGAGTACAAAATGTCATTAATGCTATGACAGAAA 180  
DB 121 TGGATTTATCTGCTCTTCCGCTTGAAGAGTACAAAATGTCATTAATGCTATGACAGAAA 180  
QY 181 TCTTAGAGTGTCCATCTGTCTGAGATTGACAGAAACCTGTCTCCACAAAGTGTGACC 240  
DB 181 TCTTAGAGTGTCCATCTGTCTGAGATTGACAGAAACCTGTCTCCACAAAGTGTGACC 240  
QY 241 ACATATTTTGGCAATTTTGGATGCTGAACCTTCAACCGAAGAAAGGGCTTCACAGT 300  
DB 241 ACATATTTTGGCAATTTTGGATGCTGAACCTTCAACCGAAGAAAGGGCTTCACAGT 300  
QY 301 GTCCCTTATGTGAAGATATATTAACCAAAAGAGCCTTACAAAGATACGATTTAGTC 360  
DB 301 GTCCCTTATGTGAAGATATATTAACCAAAAGAGCCTTACAAAGATACGATTTAGTC 360  
QY 361 AACTTGTGAAGAGCTATTTGAATCAATTTGTGCTTTTACGCTTGAACAGGTTGGAGT 420  
DB 361 AACTTGTGAAGAGCTATTTGAATCAATTTGTGCTTTTACGCTTGAACAGGTTGGAGT 420  
QY 421 ATGGAACAGCTATATATTTTGAAGAAATTAATCTCCCTGAAACATTAAGATG 480  
DB 421 ATGGAACAGCTATATATTTTGAAGAAATTAATCTCCCTGAAACATTAAGATG 480  
QY 481 AAGTTTCTATCATCAAAAGTATGAGCTACAGAAACCGTCCCAAAAGCTTCTACAGAGTG 540  
DB 481 AAGTTTCTATCATCAAAAGTATGAGCTACAGAAACCGTCCCAAAAGCTTCTACAGAGTG 540  
QY 541 AACCCGAAATCTCTTCTTGAAGAAACAGCTGACGATCTCAACCTTCAACCTTGGAA 600  
DB 541 AACCCGAAATCTCTTCTTGAAGAAACAGCTGACGATCTCAACCTTCAACCTTGGAA 600  
QY 601 CTGGAAGAACTCTGAGACCAAGAGCGGATACCAACCTCAAAACGCTCTTCAACATG 660  
DB 601 CTGGAAGAACTCTGAGACCAAGAGCGGATACCAACCTCAAAACGCTCTTCAACATG 660  
QY 661 AATTGGATCTGATTTCTTGAAGATACCGTTAATTAAGGCACTTATGCAAGTGGAG 720  
DB 661 AATTGGATCTGATTTCTTGAAGATACCGTTAATTAAGGCACTTATGCAAGTGGAG 720  
QY 721 ATCAAGAAATGTATCAAAATCACCCCTCAAGGACCAAGGATGAATCAGTTTGAATCTG 780  
DB 721 ATCAAGAAATGTATCAAAATCACCCCTCAAGGACCAAGGATGAATCAGTTTGAATCTG 780  
QY 781 CAAAAAGGCTGCTTGAATTTTCTGAGAGGATGTAAACAAATCTGMAATCATATCAAC 840  
DB 781 CAAAAAGGCTGCTTGAATTTTCTGAGAGGATGTAAACAAATCTGMAATCATATCAAC 840  
QY 841 CCAGTAATTAATGATTTTGAACACGACTGAGAGCGTGCAGTGAAGGATCATCAAGAAAGT 900  
DB 841 CCAGTAATTAATGATTTTGAACACGACTGAGAGCGTGCAGTGAAGGATCATCAAGAAAGT 900  
QY 901 ATCAAGGATGTTCTGTTTCAAACTTGAATGAGAGCAATGAGCAAAATCATATGCA 960  
DB 901 ATCAAGGATGTTCTGTTTCAAACTTGAATGAGAGCAATGAGCAAAATCATATGCA 960  
QY 961 GCTATTAACAGACAGAAACGAGCTTATTAATCACTAAAGACAAATGATAGAAA 1020  
DB 961 GCTATTAACAGACAGAAACGAGCTTATTAATCACTAAAGACAAATGATAGAAA 1020  
QY 1021 AGGCTGAATCTGATTAATTAAGCAACAGCTGCTTGAAGAGCAACATTAACAGAT 1080  
DB 1021 AGGCTGAATCTGATTAATTAAGCAACAGCTGCTTGAAGAGCAACATTAACAGAT 1080

```

Db 1021 AGGCTGATCTGTATATAAAGCAACAGCTGCTGCTTGAAGAGCAACATAACAGAT 1080
Qy 1081 GGGCTGGAAGTAAGAAACATGTATGTATAGCGGACCTCCAGCAACAAAAAAGTAG 1140
Db 1081 GGGCTGGAAGTAAGAAACATGTATGTATAGCGGACCTCCAGCAACAAAAAAGTAG 1140
Qy 1141 ATCTGAATGCTGATCCCTGTGTGAGAAAAAGATGAAATAGCAGAACTGCATGCT 1200
Db 1141 ATCTGAATGCTGATCCCTGTGTGAGAAAAAGATGAAATAGCAGAACTGCATGCT 1200
Qy 1201 CAGAGATCTTGAAGATCTGAAGATGTTCTTGGATTAACCTAATAGCAGCATTCGA 1260
Db 1201 CAGAGATCTTGAAGATCTGAAGATGTTCTTGGATTAACCTAATAGCAGCATTCGA 1260
Qy 1261 AAGTTAATGAGTGGTTTCCAGAGTGAATGTAAGTGTGAGTTCGATGATCCTCAGATG 1320
Db 1261 AAGTTAATGAGTGGTTTCCAGAGTGAATGTAAGTGTGAGTTCGATGATCCTCAGATG 1320
Qy 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGTGTATTTGAGAGCTTCTAATAGAGTAGATG 1380
Db 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGTGTATTTGAGAGCTTCTAATAGAGTAGATG 1380
Qy 1381 AATATCTGTTCTTCAAGAGAAATAGACTTACCTGCGCAGTATCTCATAGAGCTTTAA 1440
Db 1381 AATATCTGTTCTTCAAGAGAAATAGACTTACCTGCGCAGTATCTCATAGAGCTTTAA 1440
Qy 1441 TATGTAAGAGTAAGAGATTCATCTCAATAGATGATGATTAATTAAGCAAAATAT 1500
Db 1441 TATGTAAGAGTAAGAGATTCATCTCAATAGATGATGATTAATTAAGCAAAATAT 1500
Qy 1501 TTGGAAAAACCTATCGAAGAGAGGAGCCTCCCACTTAAGCAGATTAACCTGAAATC 1560
Db 1501 TTGGAAAAACCTATCGAAGAGAGGAGCCTCCCACTTAAGCAGATTAACCTGAAATC 1560
Qy 1561 TAAATATGAGGCAATTTTACTGAGCAAGATTAATCAAGAGGCTCCCTCAAAATA 1620
Db 1561 TAAATATGAGGCAATTTTACTGAGCAAGATTAATCAAGAGGCTCCCTCAAAATA 1620
Qy 1621 AATTAAGCCTTAAGAGAGCCTCATGAGGCTTCATCTGAGGATTTTATCAAGAAAG 1680
Db 1621 AATTAAGCCTTAAGAGAGCCTCATGAGGCTTCATCTGAGGATTTTATCAAGAAAG 1680
Qy 1681 CAGATTTGGCAGTTCAAAAAGACTCCTGAAATGATTAATCAGGAACTAACCAACGAGC 1740
Db 1681 CAGATTTGGCAGTTCAAAAAGACTCCTGAAATGATTAATCAGGAACTAACCAACGAGC 1740
Qy 1741 AGATGCTCAAGTATGATTAATTAATAGTGTATGATGAGATTAACCAAAAGGTGATT 1800
Db 1741 AGATGCTCAAGTATGATTAATTAATAGTGTATGATGAGATTAACCAAAAGGTGATT 1800
Qy 1801 CTATTCAGATGAGAAAAATCTTAACCAATAGATCACTGAAAAAAGATCTGCTTCA 1860
Db 1801 CTATTCAGATGAGAAAAATCTTAACCAATAGATCACTGAAAAAAGATCTGCTTCA 1860
Qy 1861 AAACGAAAGCTGAACCTTAAGCAGCAGTATTAAGCAATATGAACTGCAATTAATATCC 1920
Db 1861 AAACGAAAGCTGAACCTTAAGCAGCAGTATTAAGCAATATGAACTGCAATTAATATCC 1920
Qy 1921 ACATTCGAAAGCCTTAAGAAAGATAGGCTGAGAGAAAGTCTTTCACCGGCAATATTC 1980
Db 1921 ACATTCGAAAGCCTTAAGAAAGATAGGCTGAGAGAAAGTCTTTCACCGGCAATATTC 1980
Qy 1981 ATGGCTTGAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2040
Db 1981 ATGGCTTGAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2040
Qy 2041 TTGATAGTTGTTCTTACAGTGAAGATTAAGAAAAAAGTACACACCA 2090
Db 2041 TTGATAGTTGTTCTTACAGTGAAGTAAAAAAGAAAAAAGAAAAA 2090

```

RESULT 3  
BC038947

```

LOCUS      BC038947                1578 bp    mRNA    linear    HTC 04-MAR-2003
DEFINITION Homo sapiens, similar to breast cancer 1, early onset, clone
ACCESSION  IMAGE:5531286, mRNA.
VERSION    BC038947.1  GI:25058570
KEYWORDS   HTC.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 1578)
AUTHORS   Strausberg, R.
TITLE      Direct Submission
JOURNAL    Submitted (01-NOV-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK     NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT    Contact: MGC help desk
            Email: gcgaps-remail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland.
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nigr.nih.gov
            Akter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
            Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
            Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
            Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaspi, R.,
            Maduro, O.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
            McDowell, J., Pearson, R., Stantirpop, S., Thomas, P.J., Touchman, J.W.,
            Turgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggin, L.,
            Young, A., Zhang, L.-H. and Green, E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 82 Row: g Column: 3
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 6552304
            This clone has the following problem: retained intron.

FEATURES             location/qualifiers
     source           1..1578
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5531286"
                     /tissue_type="Uterus, leiomyosarcoma"
                     /clone_id="NIH MGC_71"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
BASE COUNT          586 a      290 c      330 g      372 t
ORIGIN
Query Match      24.8%; Score 1416.4; DB 11; Length 1578;
Best Local Similarity 92.5%; Pred. No. 3e-273;
Matches 1563; Conservative 0; Mismatches 1; Indels 126; Gaps 2;
Qy 391 GTGCTTTTCAGCTTGACACAGGTTTGGAGTATGCAAAACAGTATATTTTGCACAAAAGG 450
Db 12 GTGCTTTTCAGCTTGACACAGGTTTGGAGTATGCAAAACAGTATATTTTGCACAAAAGG 71
Qy 451 AAAATACTCTCTGAACATCTAAAGATGAAGTGTCTATCATCAAAAGTATGGCTTACA 510
Db 72 AAAATACTCTCTGAACATCTAAAGATGAAGTGTCTATCATCAAAAGTATGGCTTACA 131
Qy 511 GAAACCGTCCAAAAGCTTCTACAGGTGAACCCGAAATCTCTTCTTGACAGAAACCA 570
Db 132 GAAACCGTCCAAAAGCTTCTACAGGTGAACCCGAAATCTCTTCTT---GGAAACCA 188
Qy 571 GTCTCAGTTCACAACCTCTTAACCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 630

```

Db 189 GTCTCAATGTCCTCACTCTTAACCTTGAACTGTGAGAACTCTGAGGCAAAAGCAGCGGA 248  
 Qy 631 TACAACCTCAAAAGACGCTGTCTACATTTGAATTTGGGATCTGATTTCTTCTGAAGATACCG 690  
 Db 249 TACAACCTCAAAAGACGCTGTCTACATTTGAATTTGGGATCTGATTTCTTCTGAAGATACCG 690  
 Qy 691 TTATATAGGCAATTATTCAGTGTGGAGATCAAGATTGTTCAAATCAACCCCTCAAG 750  
 Db 283 ----- 282  
 Qy 751 GAACCAAGGATGAATATCATTTGATTTCTGCAAAAAAGCTGTCTTGTGAATTTTCTGAGA 810  
 Db 283 ----- GGCTGCTGTGGAATTTTCTGAGA 305  
 Qy 811 CGGATGTAAACAATATCTGAATCATCATCAACCACTTAATATGATTTGAAGCCACTGAGA 870  
 Db 306 CGGATGTAAACAATATCTGAATCATCATCAACCACTTAATATGATTTGAAGCCACTGAGA 365  
 Qy 871 AGCGTGAAGTGAAGGCAATCCAGAAAAGTATCAGGGATGTTCTGTTCAAACTTGACATG 930  
 Db 366 AGCGTGAAGTGAAGGCAATCCAGAAAAGTATCAGGGATGTTCTGTTCAAACTTGACATG 425  
 Qy 931 TGAAGCATGTGGCAAAATATCTATGCCAGCTCATTAACAGCATGAGAAACAGAGTTTAT 990  
 Db 426 TGAAGCATGTGGCAAAATATCTATGCCAGCTCATTAACAGCATGAGAAACAGAGTTTAT 485  
 Qy 991 TACTCATTAAGAAGAAATGATATGTAAGAAAAGCTGGAATTTCTGTAATTAAGCAAAACAGC 1050  
 Db 486 TACTCATTAAGAAGAAATGATATGTAAGAAAAGCTGGAATTTCTGTAATTAAGCAAAACAGC 545  
 Qy 1051 CTGGCTTAGCAAGAGGCAACATATACAGATGGGCTGGAAGTAAGAAAACATGTAATGATA 1110  
 Db 546 CTGGCTTAGCAAGAGGCAACATATACAGATGGGCTGGAAGTAAGAAAACATGTAATGATA 605  
 Qy 1111 GCGGCACTCCAGCAGCAAAAAAAGTGAATCTGAATGCTGATCCCTGTGTGAGAGAA 1170  
 Db 606 GCGGCACTCCAGCAGCAAAAAAAGTGAATCTGAATGCTGATCCCTGTGTGAGAGAA 665  
 Qy 1171 AAGAATGGAATTAACAGAAAATGCGCATCTGAGAAATCTCTAGAGATCTGAAGATGTTT 1230  
 Db 666 AAGAATGGAATTAACAGAAAATGCGCATCTGAGAAATCTCTAGAGATCTGAAGATGTTT 725  
 Qy 1231 CTTCGATTAACAATAATAGCAGATTCAGAAAAGTTAATGATGGTTTCCAGAAATGATG 1290  
 Db 726 CTTCGATTAACAATAATAGCAGATTCAGAAAAGTTAATGATGGTTTCCAGAAATGATG 785  
 Qy 1291 AACTGTAGGTTCTGATGACTCAGATGATGGGAGTCTGAATCAAAATGCCAAAGTACGTG 1350  
 Db 786 AACTGTAGGTTCTGATGACTCAGATGATGGGAGTCTGAATCAAAATGCCAAAGTACGTG 845  
 Qy 1351 ATGATTTAGGAGCTTCTAATATAGTGAATATTTCTGTTCTTCAGAGAAAATAGACT 1410  
 Db 846 ATGATTTAGGAGCTTCTAATATAGTGAATATTTCTGTTCTTCAGAGAAAATAGACT 905  
 Qy 1411 TACTGGCAGATGCTCATGAGGCTTAATATGTAAGAAAAGGAGTTTACTCCCAAT 1470  
 Db 906 TACTGGCAGATGCTCATGAGGCTTAATATGTAAGAAAAGGAGTTTACTCCCAAT 965  
 Qy 1471 CAGTAGAGATTAATTAATGAACAATAATTTGGGAAAACCTATCGAAGAGCAAGCC 1530  
 Db 966 CAGTAGAGATTAATTAATGAACAATAATTTGGGAAAACCTATCGAAGAGCAAGCC 1025  
 Qy 1531 TCCCAACTTAAGCATGTAACTGAAAATCTAATTAATAGAGCATTTGTTACTGAGCAC 1590  
 Db 1026 TCCCAACTTAAGCATGTAACTGAAAATCTAATTAATAGAGCATTTGTTACTGAGCAC 1085  
 Qy 1591 AGATAATTAACAAGACGCTCCCTCAAAATTAATTAAGCCGTAAGAGGACCTACATCAG 1650  
 Db 1086 AGATAATTAACAAGACGCTCCCTCAAAATTAATTAAGCCGTAAGAGGACCTACATCAG 1145  
 Qy 1651 GCCTTCACTCTGAGATTTTATCAAGAAAGAGATTTGGAGTTCAAAAGACCTCTGAAA 1710

Db 1146 GCCTTCACTCTGAGATTTTATCAAGAAAGCAGATTTGGCAGTTCAAAAGACTCTCGAAA 1205  
 Qy 1711 TGATAAATCAAGGAACTAACCAACGAGCAGAAATGCTCAAGTATGATTAATTAATA 1770  
 Db 1206 TGATAAATCAAGGAACTAACCAACGAGCAGAAATGCTCAAGTATGATTAATTAATA 1265  
 Qy 1771 GTGGTCATGAGAAATTAACAAAGAGTATCTATTCAGAAATGAGAAAATCTTAACCCAA 1830  
 Db 1266 GTGGTCATGAGAAATTAACAAAGAGTATCTATTCAGAAATGAGAAAATCTTAACCCAA 1325  
 Qy 1831 TAGAATCACTCGAAAAGAAATCTGCTTTCAAAACGAAAGCTGAACCTTAAGCAGCGATA 1890  
 Db 1326 TAGAATCACTCGAAAAGAAATCTGCTTTCAAAACGAAAGCTGAACCTTAAGCAGCGATA 1385  
 Qy 1891 TAAACAATATGAGAACTGAAATTAATATTCACAAATTCAGAAAAGCAGCTTAAGAAATAGGC 1950  
 Db 1386 TAAACAATATGAGAACTGAAATTAATATTCACAAATTCAGAAAAGCAGCTTAAGAAATAGGC 1445  
 Qy 1951 TGAAGAGAAAGTCTTTCACAGGCAATTCATGCGCTTGAACCTAGTAGTCAAGTGAATC 2010  
 Db 1446 TGAAGAGAAAGTCTTTCACAGGCAATTCATGCGCTTGAACCTAGTAGTCAAGTGAATC 1505  
 Qy 2011 TAAAGCCCACTTAATGATGTAATTCGAATTCGAATTCGATTTCTTACAGATGAAGATTA 2070  
 Db 1506 TAAAGCCCACTTAATGATGTAATTCGAATTCGAATTCGATTTCTTACAGATGAAGATTA 1565  
 Qy 2071 AGAAAAAAA 2080  
 Db 1566 AAAAAAAAAA 1575  
 RESULT 4  
 AK086173  
 LOCUS 1919 bp mRNA linear HTC 05-DEC-2002  
 DEFINITION Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched library, clone: D93010H15 product: breast cancer 1, full insert sequence.  
 ACCESSION AK086173  
 VERSION AK086173.1 GI:26103274  
 KEYWORDS HTC; CAP trapper.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 REFERENCE 1  
 Carninci, P. and Hayashizaki, Y.  
 High-efficiency full-length cDNA cloning  
 Meth. Enzymol. 303, 19-44 (1999)  
 MEDLINE 99279253  
 PUBMED 10349636  
 REFERENCE 2  
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
 Genome Res. 10 (10), 1617-1630 (2000)  
 MEDLINE 20499374  
 PUBMED 11042159  
 REFERENCE 3  
 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitanai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Watsunoto, H., Sakaguchi, S., Ilegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuzaki, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
 Genome Res. 10 (11), 1757-1771 (2000)  
 MEDLINE 20530913  
 PUBMED 11076861  
 REFERENCE 4  
 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,

Arakawa, T., Hara, A., Fukunishi, Y., Komoto, H., Adachi, J., Fukuda, S.,  
Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I.,  
Saito, T., Okazaki, Y., Goshiori, T., Bono, H., Kanekawa, T., Saito, R.,  
Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,  
Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,  
Knehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G.,  
Quackenbush, J., Schriml, L. M., Staib, F., Suzuki, R., Tomita, M.,  
Wagner, L., Mashio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,  
Baldarelli, R., Baren, G., Blake, J., Boffelli, D., Bojunga, N.,  
Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C.,  
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,  
Hochmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P.,  
Machinomi, L., Mashima, J., Mazzarelli, T., Mombaerts, P., Nordone, P.,  
Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,  
Sato, K., Schonbach, C., Seta, T., Shibata, Y., Storch, K. F., Suzuki, H.,  
Toyokawa, K., Wang, K. H., Weitz, C., Whitaker, C., Wilming, L.,  
Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohetsuki, S.,  
and Hayashizaki, Y.

Functional annotation of a full-length mouse cDNA collection  
Nature 409 (6821), 685-690 (2001)

21085660  
11217851

5

The FANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)

6 (bases 1 to 1919)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M.,  
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraka, T., Hirokane, T.,  
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,  
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Komoto, H., Kouda, M.,  
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,  
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,  
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,  
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,  
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,  
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
Muramatsu, M., and Hayashizaki, Y.

Direct Submission

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute, 1-7-22 Suenho-cho, Tsukuba, Ibaraki, 305-8565,  
Japan (E-mail: genome-res@gsc.riken.go.jp,  
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216)

Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in Riken.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.

Please visit our web site for further details.  
URL: http://genome.gsc.riken.go.jp/  
URL: http://fantom.gsc.riken.go.jp/  
Location/Qualifiers

1. 1919

/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="FANTOM,DB:0930010H15"  
/db\_xref="taxon:10090"  
/clone="ID930010H15"  
/issue\_type="head"  
/clone\_lib="RIKEN full-length enriched mouse cDNA library"  
/dev\_stage="15 days embryo"  
209. 51915  
/note="Breast cancer 1 (MGI:104537, GB|U36475,  
evidence: B1AS1N, 99%, match=1499)  
putative"

misc\_feature

BASE COUNT 616 a 401 c 462 g 440 t

ORIGIN	Query Match	17.0%	Score 968.8	DB 11	Length 1919
	Best Local Similarity	73.5%	Pred. No. 1.8e-183		
	Matches 1384	Conservative 0	Mismatches 387	Indels 113	Gaps 7
Qy	57	GGCCCCGCGCTGAGAGGCGCTTACCCCTGCTGCTGGGTAAATTCATTGGAACAGAAA	116		
Db	146	GTCCTCGGCGCTGGAAGTACGAGATCTTTTCTCGAGAAAATTCATCTGGAATCTGAA	205		
Qy	117	GAATGGAATTTATCTGCTCTTGGGTTGAAGAACTACAAATGCTATTAATGCTATGACG	176		
Db	206	GAATGGAATTTATCTGCGCGTCAATTCAGAAATGCAAAATGCTTCAATGATGACG	265		
Qy	177	AAATCTTAAGTGTCCCATCTGCTGAGATTATCAAGAAACCTGTCTCCCAAAAGTGT	236		
Db	266	AAATCTTAAGTGTCCCATCTGCTGAGATTATCAAGAAACCTGTCTCCCAAAAGTGT	325		
Qy	237	GACCACTATTTTGAATTTTGCATGCTGAACTTCTCAACGAAAGAGGCGCTTCA	296		
Db	326	GACCACTATTTTGAATTTTGCATGCTGAACTTCTTACGAAAGAGGCGCTTCA	385		
Qy	297	CAGTGTCTTATGTAAGATGATATACCAAAAGAGCGCTTACAAAGATGATTT	356		
Db	386	CAATGCTCTTGTGTAAGATGATATACCAAAAG	420		
Qy	357	AGTCACTGTGTAAGATGATATCAATTTGCTTTCAGCTTGACACAGGTTTG	416		
Db	421	-----	420		
Qy	417	GAGTATGCAACAGCTATTAATTTTGAAGAAAGAAATATCTCCGAAATCTTAAA	476		
Db	421	-----TTCAAAATGCTTTTATGTTTTCACAAAGAAATATTTCTTGAGCGTTGAAAT	476		
Qy	477	GATGAATTTCTATCATCAAAAGATGAGGCTACAGAAACGCTGCCAAAGATCTTACG	536		
Db	477	GAGAGGCGTGCATCATCAAGAGCGTGGCTACCGGAACGCTGCAGAAAGCTTCCCGAG	536		
Qy	537	AGTGAACCCGAAATCTCTTCTTGACAGAAACAGTCTCACTGTCCAACTCTTAACTT	596		
Db	537	GTCAACCTGGAATGACACCTTGAAAGAA---CAGCTTGTGTCAGCTGTCTTAACTT	593		
Qy	597	GGAAGTGTGAACCTGAGAGCAAGAGCGGATACACCTCAAAAGAGCTGTCTAC	656		
Db	594	GGAATCGTGAATGATGTAAGAAACAGCAGACCCAACTTCAAAAGAAATCTGTCTAC	653		
Qy	657	ATTGAATGGATCTGATTTCTTGAAGATACCGTTAATAGGCACTTATTCAGTGTG	716		
Db	654	ATTGAATGATCTGATTTCTTGAAGATACCGTTAATAGGCACTTATTCAGTGTG	713		
Qy	717	GGAATCAAGATTTGTTACCAATACCCCTCAAGAAACAGGATGAATATCATGTTGAT	776		
Db	714	AGAAACAGGAATTTGTTACCAAGACCGCCCTCAAAAGATGTAAGGCAAGCTGAC	773		
Qy	777	TCGCAAAAAAGCTGCTGTGAAATTTTTCGAGCGATGTAACAAATATCATGAACTCAT	836		
Db	774	TCGCAAAAAAGCTGCTGTGAAATTTTTCGAGCGATGTAACAAATATCATGAACTCAT	830		
Qy	837	CAACCAAGTATTAATGATTTGAACACCACTGAGAGGCTGACGCTGAGAGCTCAGAA	896		
Db	831	CAATGAG---TGATGATTTTAAACCTACTGAGAAATCATGAAATGAAAGCTCAGAA	887		
Qy	897	AAGTATCAGGCTGCTGCTTTCAACTTGCATGTGAGGCACTGCAAAATCTCAT	956		
Db	888	AAATGTCAGATTTTCTATTTCAAAATGCTGTGAGGCACTGCAAAATCTCAT	947		
Qy	957	GCCAGCTCATTAAGCATGAGAAAGAGGCTTATTAATCACTAAGCAGAAATGATA	1016		
Db	948	GCCAGCTCATTAAGCATGAGAAAGAGGCTTATTAATCACTAAGCAGAAATGATA	1007		
Qy	1017	GAAGAGCTGAATTTCTAATTAAGCAACAGCTGCTTACGAGAGGCAATATAC	1076		
Db	1008	GAAGAGCTGAATTTCTAATTAAGCAACAGCTGCTTACGAGAGGCAATATAC	1067		

```

Qy 1077 AGATGGCTGAGAGTAAGAAACATGTATGATAGCGGACTCCGACGACAGAAAAAAG 1136
Db 1068 AGATGGCTGAGTAAGAAACATGTATGATAGCGGAGGAGTCCGACGACTGGGAAAAAG 1127
Qy 1137 GTAGATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGGAATAGCAGAACTGCCA 1196
Db 1128 GTAGATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGGAATAGCAGAACTGCCA 1187
Qy 1197 TGTCTCAGAGATCTCAGAGATCTGAGATGTTCTTGATTAACCTAAATAGCAGCTT 1256
Db 1188 TGCCCTGGAATCTGAGAGTACCAACCATATGTTCTTGATTAACCTAAATAGCAGCTT 1247
Qy 1257 CAGAAAGTAAATGAGTGTGTTTCCAGAGTGAATCTGTAGTGTCTGATGACTCAAT 1316
Db 1248 CAGAAAGTAAATGAGTGTGTTTCCAGAGTGAATCTGTAGTGTCTGATGACTCAAT 1307
Qy 1317 GATGGGAGTCTGATCAATGCCAAAGTACGTATGATGAGCGTTCTAAATAGGTA 1376
Db 1308 GCGAGAGGACAGATCAATGCTGAGAGCTGTGTGTGAAAGTTTCAAGCAAGTG 1367
Qy 1377 GATGAATTTCTGTTCTTCCAGAAATAGACTTACGCGCAGTATCTCTATGAGGT 1436
Db 1368 GATGGGAGTGTGATCTTCAAGGAAACAGACTTATGACCCCGACCCCATCATCT 1427
Qy 1437 TTAATATGTAAGAGTAAGAGTTCATCCAAATCAGTATGAGATATATGAGACAA 1496
Db 1428 TTAATATGTAAGAGTAAGAGTTCATCCAAATCAGTATGAGATATATGAGATATA 1487
Qy 1497 ATATTTGGGAAACCTATCGAGAGAGCAAGCCCTCCCACTTAAGCATGTAATGTA 1556
Db 1488 ATATTTGGGAAACCTATCGAGAGAGCAAGCCCTCCCACTTAAGCATGTAATGTA 1546
Qy 1557 AATCTAATTAAGAGCAATTTGTTACTGAGCCACAGATTAATCAAGAGCTCCCTCA 1616
Db 1547 -----AATTAAGAGCAATTTAATCAAGACCAAGATTAACAGAGAGCTCCCTCA 1601
Qy 1617 AATAAATTAAGAGCAATTTGTTACTGAGCCACAGATTAATCAAGAGCTCCCTCA 1676
Db 1602 AATAAATTAAGAGCAATTTGTTACTGAGCCACAGATTAATCAAGAGCTCCCTCA 1655
Qy 1677 AAGAGAGTTCGCA---GTTCAAAAGACTCTGTAATGATTAATCAGGAACTAACCA 1733
Db 1656 AAGAGAGTTCGCAAGTTCGCAAGGACTCTGTAATGATTAATCAGGAACTAACCA 1715
Qy 1734 ACGAGAGCAATGCTCAAGTGAATTAATTAATGATGCTCATGAGATTAACAAA 1793
Db 1716 ATGAGAGCAATGAGCAAGTGAATTAATTAATGATGCTCATGAGATTAACAAA 1775
Qy 1794 GGTATTTCTATTCGAATGAGAAATATCTTAACCAATGATTAATCAGGAAAGAACT 1853
Db 1776 GGTATTTCTATTCGAATGAGAAATATCTTAACCAATGATTAATCAGGAAAGAACT 1835
Qy 1854 GCTTTCAAAAGCAAGTGAATCTTAATGAGAGCAATTAAGCAATGAACTCAATTA 1913
Db 1836 GCTTTCAAAAGCAAGTGAATCTTAATGAGAGCAATTAAGCAATGAACTCAATTA 1895
Qy 1914 AATATCCAAATTCAAAGCACT 1937
Db 1896 AACGTCCAGTTCAAAGCACT 1919

```

```

RESULT 5
LOCUS B0068830
DEFINITION AGNCOURT 6740238 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5802685
5' mRNA sequence.
ACCESSION B0068830
VERSION B0068830.1 GI:19897888
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

REFERENCE
1 (bases 1 to 962)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.lnl.gov
Plate: L1CM2037 row: h column: 14
High quality sequence stop: 700.
FEATURES
source
1. .962
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5802685"
/tissue_type="neuroblastoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH MGC 47"
/note="Organ: brain; Vector: pOT81; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 302 a 195 c 235 g 229 t 1 others
ORIGIN
Query Match 15.1% Score 863; DB 13; Length 962;
Best local Similarity 96.3%; Pred. No. 2.4e-16;
Matches 891; Conservative 0; Mismatches 32; Indels 2; Gaps 1;
Qy 4451 TCAGAGCAAGATCAGAGCAAGAGCAAGATTAATCAAGAGCAAGAGCAAGAGCAAG 4510
Db 15 TTGGGCAAGAGCAAGATCAGAGCAAGAGCAAGATTAATCAAGAGCAAGAGCAAGAGCA 74
Qy 4511 TATAAGCCAGATCAGAGCAAGAGCAAGATTAATCAAGAGCAAGAGCAAGAGCAAG 4570
Db 75 TATAAGCCAGATCAGAGCAAGAGCAAGATTAATCAAGAGCAAGAGCAAGAGCAAG 134
Qy 4571 TACAGATTAATTAAGAGCAAGAGCAAGAGCAAGAGCAAGAGCAAGAGCAAGAGCA 4630
Db 135 TACAGATTAATTAAGAGCAAGAGCAAGAGCAAGAGCAAGAGCAAGAGCAAGAGCA 194
Qy 4631 AGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4690
Db 195 AGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 254
Qy 4691 TCAAGAGAGCTCATTAAGTTGTTGATGAGAGCAAGAGCAAGAGCAAGAGCAAGAG 4750
Db 255 TCAAGAGAGCTCATTAAGTTGTTGATGAGAGCAAGAGCAAGAGCAAGAGCAAGAG 314
Qy 4751 ACAGATTTGACGAGAAACATCTTACCTGCAAGCAAGATTAAGAGGAAACCCCTTACT 4810
Db 315 ACAGATTTGACGAGAAACATCTTACCTGCAAGCAAGATTAAGAGGAAACCCCTTACT 374
Qy 4811 GGAATCTGATTCAGAGCTCTCTCTGATGATGATGATGATGATGATGATGATGATGAT 4870
Db 375 GGAATCTGATTCAGAGCTCTCTCTGATGATGATGATGATGATGATGATGATGATGAT 434
Qy 4871 CCCAGAGTCAAGCTGTTGGCAACATACATCTTCAACCTCTGATGATGATGATGATGAT 4930
Db 435 CCCAGAGTCAAGCTGTTGGCAACATACATCTTCAACCTCTGATGATGATGATGATGAT 494

```

QY	4931	ATTGAAATGCGAAGATCTGGCCAGAGGCTCAGCTGCTCTCATATCTACTGATCTGCTGG	4931	ATTGAAATGCGAAGATCTGGCCAGAGGCTCAGCTGCTCTCATATCTACTGATCTGCTGG	4931	ATTGAAATGCGAAGATCTGGCCAGAGGCTCAGCTGCTCTCATATCTACTGATCTGCTGG	4931	ATTGAAATGCGAAGATCTGGCCAGAGGCTCAGCTGCTCTCATATCTACTGATCTGCTGG	4931	ATTGAAATGCGAAGATCTGGCCAGAGGCTCAGCTGCTCTCATATCTACTGATCTGCTGG	4931	ATTGAAATGCGAAGATCTGGCCAGAGGCTCAGCTGCTCTCATATCTACTGATCTGCTGG
Db	495	ATTGAAATGCGAAGATCTGGCCAGAGGCTCAGCTGCTCTCATATCTACTGATCTGCTGG	495	ATTGAAATGCGAAGATCTGGCCAGAGGCTCAGCTGCTCTCATATCTACTGATCTGCTGG	495	ATTGAAATGCGAAGATCTGGCCAGAGGCTCAGCTGCTCTCATATCTACTGATCTGCTGG	495	ATTGAAATGCGAAGATCTGGCCAGAGGCTCAGCTGCTCTCATATCTACTGATCTGCTGG	495	ATTGAAATGCGAAGATCTGGCCAGAGGCTCAGCTGCTCTCATATCTACTGATCTGCTGG	495	ATTGAAATGCGAAGATCTGGCCAGAGGCTCAGCTGCTCTCATATCTACTGATCTGCTGG
QY	4991	GTATATATGCATATGGAAGAAGTGTGAGCAGGAGGAGGAAGCCAGAAATTCAGCTTCAACAGA	4991	GTATATATGCATATGGAAGAAGTGTGAGCAGGAGGAGGAAGCCAGAAATTCAGCTTCAACAGA	4991	GTATATATGCATATGGAAGAAGTGTGAGCAGGAGGAGGAAGCCAGAAATTCAGCTTCAACAGA	4991	GTATATATGCATATGGAAGAAGTGTGAGCAGGAGGAGGAAGCCAGAAATTCAGCTTCAACAGA	4991	GTATATATGCATATGGAAGAAGTGTGAGCAGGAGGAGGAAGCCAGAAATTCAGCTTCAACAGA	4991	GTATATATGCATATGGAAGAAGTGTGAGCAGGAGGAGGAAGCCAGAAATTCAGCTTCAACAGA
Db	5051	AAGGTCACACAAAGAAATGCTCAGTGTGTCTGCTGCTGACCCCAAGAAATTTATGCT	5051	AAGGTCACACAAAGAAATGCTCAGTGTGTCTGCTGCTGACCCCAAGAAATTTATGCT	5051	AAGGTCACACAAAGAAATGCTCAGTGTGTCTGCTGCTGACCCCAAGAAATTTATGCT	5051	AAGGTCACACAAAGAAATGCTCAGTGTGTCTGCTGCTGACCCCAAGAAATTTATGCT	5051	AAGGTCACACAAAGAAATGCTCAGTGTGTCTGCTGCTGACCCCAAGAAATTTATGCT	5051	AAGGTCACACAAAGAAATGCTCAGTGTGTCTGCTGCTGACCCCAAGAAATTTATGCT
QY	5111	CGTGACAAAGTTGGCCAGAAAACACACATATCACTTTAATCTAATCTGAAGAAGAC	5111	CGTGACAAAGTTGGCCAGAAAACACACATATCACTTTAATCTAATCTGAAGAAGAC	5111	CGTGACAAAGTTGGCCAGAAAACACACATATCACTTTAATCTAATCTGAAGAAGAC	5111	CGTGACAAAGTTGGCCAGAAAACACACATATCACTTTAATCTAATCTGAAGAAGAC	5111	CGTGACAAAGTTGGCCAGAAAACACACATATCACTTTAATCTAATCTGAAGAAGAC	5111	CGTGACAAAGTTGGCCAGAAAACACACATATCACTTTAATCTAATCTGAAGAAGAC
Db	675	CGTGACAAAGTTGGCCAGAAAACACACATATCACTTTAATCTAATCTGAAGAAGAC	675	CGTGACAAAGTTGGCCAGAAAACACACATATCACTTTAATCTAATCTGAAGAAGAC	675	CGTGACAAAGTTGGCCAGAAAACACACATATCACTTTAATCTAATCTGAAGAAGAC	675	CGTGACAAAGTTGGCCAGAAAACACACATATCACTTTAATCTAATCTGAAGAAGAC	675	CGTGACAAAGTTGGCCAGAAAACACACATATCACTTTAATCTAATCTGAAGAAGAC	675	CGTGACAAAGTTGGCCAGAAAACACACATATCACTTTAATCTAATCTGAAGAAGAC
QY	5171	TACTCATGTTGTTATGAAGAAGATGCTGATGTTGTGTGTAACGCACTGAATATTT	5171	TACTCATGTTGTTATGAAGAAGATGCTGATGTTGTGTGTAACGCACTGAATATTT	5171	TACTCATGTTGTTATGAAGAAGATGCTGATGTTGTGTGTAACGCACTGAATATTT	5171	TACTCATGTTGTTATGAAGAAGATGCTGATGTTGTGTGTAACGCACTGAATATTT	5171	TACTCATGTTGTTATGAAGAAGATGCTGATGTTGTGTGTAACGCACTGAATATTT	5171	TACTCATGTTGTTATGAAGAAGATGCTGATGTTGTGTGTAACGCACTGAATATTT
Db	735	TACTCATGTTGTTATGAAGAAGATGCTGATGTTGTGTGTAACGCACTGAATATTT	735	TACTCATGTTGTTATGAAGAAGATGCTGATGTTGTGTGTAACGCACTGAATATTT	735	TACTCATGTTGTTATGAAGAAGATGCTGATGTTGTGTGTAACGCACTGAATATTT	735	TACTCATGTTGTTATGAAGAAGATGCTGATGTTGTGTGTAACGCACTGAATATTT	735	TACTCATGTTGTTATGAAGAAGATGCTGATGTTGTGTGTAACGCACTGAATATTT	735	TACTCATGTTGTTATGAAGAAGATGCTGATGTTGTGTGTAACGCACTGAATATTT
QY	5231	TCATGAATTCGGGAGGAGAAAATGGGTAAGTATTTCTGGGTGACCCAGTCTATTAA	5231	TCATGAATTCGGGAGGAGAAAATGGGTAAGTATTTCTGGGTGACCCAGTCTATTAA	5231	TCATGAATTCGGGAGGAGAAAATGGGTAAGTATTTCTGGGTGACCCAGTCTATTAA	5231	TCATGAATTCGGGAGGAGAAAATGGGTAAGTATTTCTGGGTGACCCAGTCTATTAA	5231	TCATGAATTCGGGAGGAGAAAATGGGTAAGTATTTCTGGGTGACCCAGTCTATTAA	5231	TCATGAATTCGGGAGGAGAAAATGGGTAAGTATTTCTGGGTGACCCAGTCTATTAA
Db	795	TCATGAATTCGGGAGGAGAAAATGGGTAAGTATTTCTGGGTGACCCAGTCTATTAA	795	TCATGAATTCGGGAGGAGAAAATGGGTAAGTATTTCTGGGTGACCCAGTCTATTAA	795	TCATGAATTCGGGAGGAGAAAATGGGTAAGTATTTCTGGGTGACCCAGTCTATTAA	795	TCATGAATTCGGGAGGAGAAAATGGGTAAGTATTTCTGGGTGACCCAGTCTATTAA	795	TCATGAATTCGGGAGGAGAAAATGGGTAAGTATTTCTGGGTGACCCAGTCTATTAA	795	TCATGAATTCGGGAGGAGAAAATGGGTAAGTATTTCTGGGTGACCCAGTCTATTAA
QY	5291	AGAAAGAAAATGCTGATGAGCAGATTTTGAATCTAGAGAGATGTGG--TCAATGA	5291	AGAAAGAAAATGCTGATGAGCAGATTTTGAATCTAGAGAGATGTGG--TCAATGA	5291	AGAAAGAAAATGCTGATGAGCAGATTTTGAATCTAGAGAGATGTGG--TCAATGA	5291	AGAAAGAAAATGCTGATGAGCAGATTTTGAATCTAGAGAGATGTGG--TCAATGA	5291	AGAAAGAAAATGCTGATGAGCAGATTTTGAATCTAGAGAGATGTGG--TCAATGA	5291	AGAAAGAAAATGCTGATGAGCAGATTTTGAATCTAGAGAGATGTGG--TCAATGA
Db	855	AGAAAGAAAATGCTGATGAGCAGATTTTGAATCTAGAGAGATGTGGTCAATGGA	855	AGAAAGAAAATGCTGATGAGCAGATTTTGAATCTAGAGAGATGTGGTCAATGGA	855	AGAAAGAAAATGCTGATGAGCAGATTTTGAATCTAGAGAGATGTGGTCAATGGA	855	AGAAAGAAAATGCTGATGAGCAGATTTTGAATCTAGAGAGATGTGGTCAATGGA	855	AGAAAGAAAATGCTGATGAGCAGATTTTGAATCTAGAGAGATGTGGTCAATGGA	855	AGAAAGAAAATGCTGATGAGCAGATTTTGAATCTAGAGAGATGTGGTCAATGGA
QY	5349	AGAAACCAACCAAGGCTCCAAAGCGAG	5349	AGAAACCAACCAAGGCTCCAAAGCGAG	5349	AGAAACCAACCAAGGCTCCAAAGCGAG	5349	AGAAACCAACCAAGGCTCCAAAGCGAG	5349	AGAAACCAACCAAGGCTCCAAAGCGAG	5349	AGAAACCAACCAAGGCTCCAAAGCGAG
Db	915	AGAAACCAACCAAGGCTCCAAAGCGAG	915	AGAAACCAACCAAGGCTCCAAAGCGAG	915	AGAAACCAACCAAGGCTCCAAAGCGAG	915	AGAAACCAACCAAGGCTCCAAAGCGAG	915	AGAAACCAACCAAGGCTCCAAAGCGAG	915	AGAAACCAACCAAGGCTCCAAAGCGAG
RESULT 6	BM452288	1089 bp	mRNA	linear	EST 05-FEB-2002							
LOCUS	BM452288	5', mRNA sequence.										
DEFINITION	AGENCOURT_6386302 NIH_MGC_72	Homo sapiens	cdna	clone	IMAGE:5526666							
ACCESSION	BM452288											
VERSION	BM452288.1	GI:18501328										
KEYWORDS	EST.											
SOURCE	Homo sapiens											
ORGANISM	Homo sapiens (human)											
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;											
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.											
TITLE	1 (bases 1 to 1089)											
JOURNAL	NIH-MGC <a href="http://mgs.nci.nih.gov/">http://mgs.nci.nih.gov/</a> .											
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished											
	Contact: Robert Strausberg, Ph.D.											
	Email: <a href="mailto:cgapbs-rc@mail.nih.gov">cgapbs-rc@mail.nih.gov</a>											
	Tissue Procurement: ATCC/DCTP											
	CDNA Library Preparation: Life Technologies, Inc.											
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)											
	DNA Sequencing by: Agencourt Bioscience Corporation											
	Clone distribution: MGC clone distribution information can be											
	found through the I.M.A.G.E. Consortium/LNLN at:											
	<a href="http://image.lnl.gov">http://image.lnl.gov</a>											
	Plate: LILAM12200 row: k column: 19											
	High quality sequence stop: 667.											
FEATURES	Location/Qualifiers											
Source	1. 1089											
	/organism="Homo sapiens"											
	/mol_type="mRNA"											
	/db_xref="taxon:9606"											
	/clone="IMAGE:5526666"											
	/lab_host="melanotic melanoma"											
	/lab_host="DH10B (phage-resistant)"											
	/clone_id="NIH MGC 72"											
	/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;											
	Site 2: SalI; Cloned unidirectionally. primer: oligo dT.											
	Average insert size 2 kb. Library constructed by Life											
	Technologies."											

BASE COUNT	389 a	212 c	248 g	240 t	ORIGIN
Query Match	14.7%	Score 841.4;	DB 12;	Length 1089;	
Best Local Similarity	96.0%;	Pred. No. 5.4e-158;			
Matches 928;	Conservative	0;	Mismatches 31;	Indels 8;	Gaps 6;
QY	1925	TTCAAAAGCCTTAAAAAAGATTAGGCTGAGAGGAAGTCTTCTACAGGCAATATTATGC	1988		
DB	13	TTCAAAACACCTTAAAAAAGATTAGGCTGAGAGGAAGTCTTCTACAGGCAATATTATGC	72		
QY	1985	GCTTGAATAGTAGTCAGTAGAAATCTAAGCCCACTAATTGTACTGAATTGGCAAAATTGA	2044		
DB	73	GCTTGAATAGTAGTCAGTAGAAATCTAAGCCCACTAATTGTACTGAATTGGCAAAATTGA	132		
QY	2045	TAGTTGTTCTAGCAGTGAAGATTAAGAAAAAAAGTACAAACCAATAGCCAGTCAGCA	2104		
DB	133	TAGTTGTTCTAGCAGTGAAGATTAAGAAAAAAAGTACAAACCAATAGCCAGTCAGCA	192		
QY	2105	CAGCGAAACCTACACATCATGGAAGGTAAAGAACTGCAACTGAGCCAAAGAGATTA	2166		
DB	193	CAGCGAAACCTACACATCATGGAAGGTAAAGAACTGCAACTGAGCCAAAGAGATTA	252		
QY	2165	CAAGCGAAATGAACGACAAAGTAAAGCATGACAGTATCTTTCCAGAGCTGAAGTT	2222		
DB	253	CAAGCGAAATGAACGACAAAGTAAAGCATGACAGTATCTTTCCAGAGCTGAAGTT	312		
QY	2225	AACAAATGCACCTGGTCTTTTACTAATGTTCAAATACAGTGAACCTTAAAGATTGT	2284		
DB	313	AACAAATGCACCTGGTCTTTTACTAATGTTCAAATACAGTGAACCTTAAAGATTGT	372		
QY	2285	CAATCTTAGCTTCCAGAGAAAGAAAGAAAGAACTAGAAACGTTAAAGTGTCTAA	2344		
DB	373	CAATCTTAGCTTCCAGAGAAAGAAAGAAAGAAAGAACTAGAAACGTTAAAGTGTCTAA	432		
QY	2345	TAAATGCTGAACCCCAAGATCTCATGTTAAGTGGAAGGGTTTGGCAAATGTAAG	2404		
DB	433	TAAATGCTGAACCCCAAGATCTCATGTTAAGTGGAAGGGTTTGGCAAATGTAAG	492		
QY	2405	ATCTGTAGAGTAGTAGCAGTATTTTCACTGCTGTACTGATTAATGCACTCAGAAAG	2464		
DB	493	ATCTGTAGAGTAGTAGCAGTATTTTCACTGCTGTACTGATTAATGCACTCAGAAAG	552		
QY	2465	TATCTCGTTACTGGAAGTTAGCACTTAGGGAAGGCAAAAACAGAACCAATTAATGTGT	2522		
DB	553	TATCTCGTTACTGGAAGTTAGCACTTAGGGAAGGCAAAAACAGAACCAATTAATGTGT	612		
QY	2525	GAGTCAGTGCACAGATTTTGAAAACCCCAAGGACTAATTAATGTTTCCAAAGATTA	2588		
DB	613	GAGTCAGTGCACAGATTTTGAAAACCCCAAGGACTAATTAATGTTTCCAAAGATTA	672		
QY	2585	TAGAATGACACAGAGGCTTTAAGTATCCATTGGGACATGAAGTTAACCAACAGTCGGA	2644		
DB	673	TAGAATGACACAGAGGCTTTAAGTATCCATTGGGACATGAAGTTAACCAACAGTCGGA	732		
QY	2645	AACAAGCATAGAAAT-GGAAGAAAAGTAACTTGATGCTCAGTATTTGGAGAATACATTCA	2703		
DB	733	AACAAGCATAGAAATGGGAAGAAAGTAACTTGATGCTCAGTATTTGGAGAATACATTCA	792		
QY	2704	AGCTTTCAAACCGCAGTCAATTTGCTCTGTTTTCAAATCCAGGAATGCAAGAGAAAT	2766		
DB	793	A-GTTTCAAAACGGCAGTCAATTTGCTCTGTTTTCAAATCC-GGAATGCAAAAGAGAT	850		
QY	2764	GTGCAACATTTCTGCGCCACTCTGGGCTTTTAAAGAAACAAAGTCCAAAGTCCCTTTT	2822		
DB	851	GTGCAACATTTCTGCGCCACTCTGGGCTTTTAAAGAAACAAAGTCCAAAGTCCCTTTT	910		
QY	2823	GAATGTGACAAAA--GGAAGAAATCAAGAAAGATGATCTAA-TATCAAGCCTGT	2878		
DB	911	GAATGTGACAAAAAGGAAGAAAAATCAGGAAAGATGATGATTAATCAAGCCTTT	970		
QY	2879	AACAGACA 2885			



Db	971 AACGAA 977
RESULT 7	
LOCUS	AUI22476 845 bp mRNA linear EST 01-AUG-2002
DEFINITION	AUI22476 MAMMAL Homo sapiens CDNA clone MAMMAL002447 5', mRNA
ACCESSION	AUI22476
VERSION	AUI22476.1
KEYWORDS	GI:10937746
SOURCE	EST.
ORGANISM	Homo sapiens (human)
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakematsu, A., Nakamura, Y., Nagai, T., Sugano, S. and Iwagaki, T.
TITLE	HRI human CDNA project
JOURNAL	Unpublished
COMMENT	Contact: Takao Isogai Genomics Laboratory Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel: 81-438-52-3975 Fax: 81-438-52-3986 Email: genomics@hri.co.jp HRI human CDNA project; 5'- & 3'-end one pass sequencing; Helix Research Institute; CDNA library construction; Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute. Location/Qualifiers 1. 845 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="MAMMAL002447" /tissue_type="mammary gland" /clone_id="MAMMAL1" /note="Vector: pME18SFL3"
FEATURES	
source	1. 845 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="MAMMAL002447" /tissue_type="mammary gland" /clone_id="MAMMAL1" /note="Vector: pME18SFL3"
BASE COUNT	279 a 172 c 191 g 200 t 3 others
ORIGIN	
Query Match	14.2%; Score 810.2; DB 9; Length 845;
Best Local Similarity	98.9%; Pred. No. 9, 1e-152;
Matches 835; Conservative	0; Mismatches 6; Indels 3; Gaps 2;
QY	3819 GTAAACATATACCTTCTCAGCTCTAGGCACTAGACCCGTTGTCACCGAGTGTGTCT
Db	1 GTAAACATATACCTTCTCAGCTCTAGGCACTAGACCCGTTGTCACCGAGTGTGTCT
QY	3879 AAGAACACAGAGAGAAATTTATTCATTCATTGAAGAAATAGCTTAATGATCGAGTAACCG
Db	61 AAGAACACAGAGAGAAATTTATTCATTCATTGAAGAAATAGCTTAATGATCGAGTAACCG
QY	3939 GTAATATTGGCAAGGCACTTCAGAGACATCACTTAAGTGAAGAAACAAATGTTCTGCT
Db	121 GTAATATTGGCAAGGCACTTCAGAGACATCACTTAAGTGAAGAAACAAATGTTCTGCT
QY	3999 AGCTTGTTTTCTTCAAGTGCAGTGAATTGGAAGCTTGAATGATCAATATCAACACCCAG
Db	181 AGCTTGTTTTCTTCAAGTGCAGTGAATTGGAAGCTTGAATGATCAATATCAACACCCAG
QY	4059 GATCCTTCTTGATGTGTTCTTCCAAACAAATGAGGCACTGCTGAAGCCAGGAGATT
Db	241 GATCCTTCTTGATGTGTTCTTCCAAACAAATGAGGCACTGCTGAAGCCAGGAGATT
QY	4119 GGTCTGAGTCAAGAAATGGTTTCAATGATGAAGAAAGAGAACGGGCTTGGAGAAG
Db	301 GGTCTGAGTCAAGAAATGGTTTCAATGATGAAGAAAGAGAACGGGCTTGGAGAAG
QY	4179 AATAATCAAGAGAGCAAGCATGGAATTCAACTTAAGTGAAGCAGCATCTGGGTGTGAG
Db	4233

Df		361	AATATATCAGAAAGGCGAAGAAGTATGGATTCTTAACCTTAGTGAAAGCATCTGGGTGAG	420
OY		4239	AGTGAACAACACCGTCTCTGAAGACTGCTCAGAGGCTATCTCTCAGAGTGACATTTTAACC	4298
Df		421	AGTGAACAACACCGTCTCTGAAGACTGCTCAGAGGCTATCTCTCAGAGTGACATTTTAACC	480
OY		4239	ACTCAGCAGAGGGATGCCATGCACATTAAGCTTCAGAGCAAAAATGGCTGAA	4358
Df		481	ACTCAGCAGAGGGATGCCATGCACATTAAGCTTCAGAGCAAAAATGGCTGAA	540
OY		4359	CTAGAAGCTGTGTGTGAAGAACAGCATGGGAGCCAGGCTTCTAACAGCTACCTTCATCATATA	4418
Df		541	CTAGAAGCTGTGTGTGAAGAACAGCATGGGAGCCAGGCTTCTAACAGCTACCTTCATCATATA	600
OY		4419	AGTGAAGCTCTCTGCCCCCTTGAAGAACCTTGGAATCCAGAACCAACCATCAGAAAAAGCA	4478
Df		601	AGTGAAGCTCTCTGCCCCCTTGAAGAACCTTGGAATCCAGAACCAACCATCAGAAAAAGCA	660
OY		4479	GTAATTAACCTTACACGAAAAAGTAGTAATACCTTATAAGCCAGAAATCCAGAAAGGCTTTCT	4538
Df		661	GTAATTAACCTTACACGAAAAAGTAGTAATACCTTATAAGCCAGAAATCCAGAAAGGCTTTCT	720
OY		4539	GCTGCAAGAGTTGAGGTGTCTGCAGATAGTTCTACAGTAATAAATPAAGAACACAGAA--G	4596
Df		721	GCTGCAAGAGTTGAGGTGTCTGCAGATAGTTCTACAGTAATAAATPAAGAACACAGAAAGT	780
OY		4597	TGGAAGAGTCA-TCGCCCTTCTTAATGCCCACATTAAGTAGTAGTGGTGATCATGCACAGT	4655
Df		781	TGGAAGAGTCAATCCCTTCTTAATGCCCACATTAAGTAGTAGTGGTGATCATGCACAGT	840
OY		4656	TGCT 4659     	
Df		841	TGCT 844	
RESULT 8				
LOCUS	AU142729			
DEFINITION	AU142729 Y79AA1 Homo sapiens cDNA clone Y79AA1000792 5', mRNA sequence.	783 bp	mRNA	linear EST 05-AUG-2002
ACCESSION	AU142729			
VERSION	AU142729.1	GI:11004250		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 783)			
AUTHORS	Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T. HRI human cDNA project			
TITLE	Unpublished			
JOURNAL	Contact: Takeo Isogai			
COMMENT	Genomics Laboratory Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel.: 81-438-52-3975 Fax: 81-438-52-3986 Email: genomics@hri.co.jp HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.  Location/Qualifiers 1..783 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="Y79AA1000792" /cell_type="retinoblastoma" /cell_line="Y79"			
FEATURES	Source			

BASE COUNT 255 a 146 c 185 g 194 t 3 others  
 ORIGIN

Query Match 13.3%; Score 760.2; DB 9; Length 783;  
 Best Local Similarity 99.1%; Pred. No. 9,5e-142;  
 Matches 773; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 3579 TTAAGTATGTTGTAATAAGAGATCTAGTTTGTGCTGAAAATGACATTAGAGAACT 3638  
 Db 1 TTAGTATGTTGTAATAAGAGATCTAGTTTGTGCTGAAAATGACATTAGAGAACT 60  
 QY 3639 TCTGCTGTTTTAGCAAAAGCGTCCAGAGAGAGAGCTTAGCAGAGAGTCCAGCCCTTC 3698  
 Db 61 TCTGCTGTTTTAGCAAAAGCGTCCAGAGAGAGAGCTTAGCAGAGAGTCCAGCCCTTC 120  
 QY 3699 ACCCATACACATTTGGCTCAGGGTTACCGAAGAGGGGCGAAGAAATTAGAGTCTCAGAA 3758  
 Db 121 ACCCATACACATTTGGCTCAGGGTTACCGAAGAGGGGCGAAGAAATTAGAGTCTCAGAA 180  
 QY 3759 GAGAACTTATCTAGAGAGATGAAAGCTTCCCTGCTTCCAACTTTGTATTGGTAAA 3818  
 Db 181 GAGAACTTATCTAGAGAGATGAAAGCTTCCCTGCTTCCAACTTTGTATTGGTAAA 240  
 QY 3819 GTAAACATATATACCTTCTCAGTCTCTAGAGAGATGACACGTTGTACCGAGTGTCTCT 3878  
 Db 241 GTAAACATATATACCTTCTCAGTCTCTAGAGAGATGACACGTTGTGTCTCT 300  
 QY 3879 AAGAACACAGAGAGAAATTTATTCATTGAAAGAAATAGCTTAATGACTGACGTAACCG 3938  
 Db 301 AAGAACACAGAGAGAAATTTATTCATTGAAAGAAATAGCTTAATGACCGGATACCG 360  
 QY 3939 GTAATATTGGCAAAAGGATCTCAGAGAAATCACCCTTAGTGAAGAAACAAATGTTCTCT 3998  
 Db 361 GTAATATTGGCAAAAGGATCTCAGAGAAATCACCCTTAGTGAAGAAACAAATGTTCTCT 420  
 QY 3999 AGCTGTTTCTTCCAGTGCAGTGAATTTGGAAAGCTTGAACGCAATATACAAACACCCAG 4058  
 Db 421 AGCTGTTTCTTCCAGTGCAGTGAATTTGGAAAGCTTGAACGCAATATACAAACACCCAG 480  
 QY 4059 GATCCTTTCTTGATTTGTTCTTCCAAACAAATGAGGATCAGTCTGAAAGCCAGGAGTT 4118  
 Db 481 GATCCTTTCTTGATTTGTTCTTCCAAACAAATGAGGATCAGTCTGAAAGCCAGGAGTT 540  
 QY 4119 GGTCTGAGTGAACAAGATTTGGTTTCAGATGATGAAAGAAAGGAAACGGGCTTGGAAAG 4178  
 Db 541 GGTCTGAGTGAACAAGATTTGGTTTCAGATGATGAAAGAAAGGAAACGGGCTTGGAAAG 600  
 QY 4179 AATATCAAGAAGAGCAAGCATGATTCAAACTTAGTGAAGAGCATCTGGGTGTGAG 4238  
 Db 601 AATATCAAGAAGAGCAAGCATGATTCAAACTTAGTGAAGAGCATCTGGGTGTGAG 660  
 QY 4239 AGTGAACAAGCGTCTTGAAAGATGCTCAGGGCTATCTCTCAGAGTGAACATTTAA-C 4297  
 Db 661 AGTGAACAAGCGTCTTGAAAGATGCTCAGGGCTATCTCTCAGAGTGAACATTTAA-C 720  
 QY 4298 CACTCAGAGAGAGGATACATGACAACTAACCTGTAAGCTCCAGCGAGAAATGGCTGGA 4357  
 Db 721 CACTCAGAGAGAGGATACATGACAACTAACCTGTAAGCTCCAGCGAGAAATGGCTGGA 780

RESULT 9  
 BUI71200 933 bp mRNA linear EST 04-SEP-2002  
 LOCUS  
 DEFINITION AGNCOURT\_7956206 NIH\_MGC\_72 Homo sapiens cDNA clone IMAGE:6161612  
 5', mRNA sequence.  
 ACCESSION BUI71200  
 VERSION BUI71200.1 GI:22685184  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 933)  
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgsbbs-romail.nih.gov  
 Tissue Procurement: ATCC/DCTD/DRP  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:  
 http://image.liml.gov  
 plate: LIML3514 row: c column: 21  
 High quality sequence stop: 672.

FEATURES  
 source  
 1..933  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6161612"  
 /issue\_type="melanotic melanoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC 72"  
 /note="Organ: skin; Vector: pcMV-SPORT6; Site 1: NciI; Site 2: SalI; Cloned unidirectionally. primer: oligo dT. Average insert size 2 kb. Library constructed by Life Technologies."

BASE COUNT 264 a 197 c 246 g 221 t 5 others  
 ORIGIN

Query Match 13.1%; Score 746.4; DB 13; Length 933;  
 Best Local Similarity 98.3%; Pred. No. 5.8e-139;  
 Matches 765; Conservative 0; Mismatches 11; Indels 2; Gaps 1;

QY 4709 GGTGTTGATGTGAGAGGACAACAGCTGGAAGATCTGGGCGACACGATTTGACGAAAC 4768  
 Db 12 GGTGTTGATGTGAGAGGACAACAGCTGGAAGATCTGGGCGACACGATTTGACGAAAC 71  
 QY 4769 ATCTTACTTGGCAAGGCAAGATCTGAGAGGAAACCTTACTGGAATCTGGAATCAGCT 4828  
 Db 72 ATCTTACTTGGCAAGGCAAGATCTGAGAGGAAACCTTACTGGAATCTGGAATCAGCT 131  
 QY 4829 CTTCCTGATGACCTCGTAATCTGATCTCTGAGAGAGAGCCCGACAGTCACTCGCT 4888  
 Db 132 CTTCCTGATGACCTCGTAATCTGATCTCTGAGAGAGAGCCCGACAGTCACTCGCT 191  
 QY 4889 TGGCAACATACCATCTTCAACCTCTGATGAAAGTTCCCAATTGAAAGTTGAGAAATC 4948  
 Db 192 TGGCAACATACCATCTTCAACCTCTGATGAAAGTTCCCAATTGAAAGTTGAGAAATC 251  
 QY 4949 TGCCAGGGTCCAGCTGCTGCTCATCTACTGATCTGCTGCGGTATTAATGCAATGAAAG 5008  
 Db 252 TGCCAGGGTCCAGCTGCTGCTCATCTACTGATCTGCTGCGGTATTAATGCAATGAAAG 311  
 QY 5009 AAGTGTAGCAGGAGGAAGCCAGAAATTGACAGCTTCAACAGAAAGGTCACAAAGGAT 5068  
 Db 312 AAGTGTAGCAGGAGGAAGCCAGAAATTGACAGCTTCAACAGAAAGGTCACAAAGGAT 371  
 QY 5069 GTCCATGTTGTTCTGCGCTGACCCCGAAGAAATTTATGCTGCTGTAACAATTTGGCAG 5128  
 Db 372 GTCCATGTTGTTCTGCGCTGACCCCGAAGAAATTTATGCTGCTGTAACAATTTGGCAG 431  
 QY 5129 AAAACACCAATCACTTTAACTAATCTAATTAATCTGAAGAGACTAATGTTGTTATGAA 5188  
 Db 432 AAAACACCAATCACTTTAACTAATCTAATTAATCTGAAGAGACTAATGTTGTTATGAA 491  
 QY 5189 AACAGATGCTGAAGTTGTGTGTAACGAGACATGAAATATTTTCTAGAAATTTGGGAGG 5248  
 Db 492 AACAGATGCTGAAGTTGTGTGTAACGAGACATGAAATATTTTCTAGAAATTTGGGAGG 551  
 QY 5249 AAATGAGTAGTATGATATTCTGGGTGACCCAGCTATTTAAAGAAAGAAATGCTGAA 5308

Db 552 AAAATGGGTAGTACTATTTCTGGGTGACCCAGCTATTAAGAAAGAAAATGCTGAA 611  
Qy 5309 TGACACATGATTTTAAAGTCAGAGAGATGTGTCAATGGAAGAAACCAAGGTCCAA 5368  
Db 612 TGACACATGATTTTAAAGTCAGAGAGATGTGTCAATGGAAGAAACCAAGGTCCAA 671  
Qy 5369 GCGAGCAGAGAAATCCCGAGACAGAAAGATCTTCAGGGGGCTAGAAATCTGTGTATAG 5428  
Db 672 GCGAGCAGAGAAATCCCGAGACAGAAAGATCTTCAGGGGGCTAGAAATCTGTGTATAG 731  
Qy 5429 GCCCTTCACCAACATGCCCACAG-ATCAACTGGAATGATGTACAGCTGTGTG 5484  
Db 732 GCCCTTCACCAACATGCCCACAGNATCATCTGGGAATGATGTGGGTGAGCTGTGTG 789  
RESULT 10  
Bg681276 743 bp mRNA linear EST 01-MAY-2001  
LOCUS 602627125F1 NCI\_CGAP\_Skn4 Homo sapiens cDNA clone IMAGE:4751887 5',  
DEFINITION mRNA sequence.  
ACCESSION Bg681276 GI:13912673  
VERSION Bg681276.1 GI:13912673  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 743)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strusberg, Ph.D.  
Email: cga@bbs-remail.nih.gov  
Tissue Procurement: James Cleaver, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
Plate: LLM10609 row: a column: 08  
High quality sequence stop: 741.  
location/Qualifiers  
1..743  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4751887"  
/tissue\_type="squamous cell carcinoma"  
/lab\_host="DH10B (TI phage-resistant)"  
/clone\_11b="NCI\_CGAP\_Skn4"  
/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NCI;  
Site 2: Sail; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.5kb. Library constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."  
BASE COUNT 233 a 156 c 182 g 172 t  
ORIGIN  
Query Match 12.9%; Score 738.8; DB 10; Length 743;  
Best Local Similarity 99.7%; Pred. No. 1.8e-137; Indels 0; Gaps 0;  
Matches 740; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 121 TGAATCTGATCTCTCTGAGACAGAGCCCGAGCTGAGCTGTGTGGCAATATCCATC 180  
Qy 4904 TTCAACCTCTGATTTGAAGTTCCCAATTGAAAGTTGACAGATCTGCCAGGGTCCAGC 4963  
Db 181 TTCAACCTCTGATTTGAAGTTCCCAATTGAAAGTTGACAGATCTGCCAGGGTCCAGC 240  
Qy 4964 TGTCTCTATCTACTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 5023  
Db 241 TGTCTCTATCTACTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 300  
Qy 5024 GAAGCCAGAAATTGACAGCTTCAACAGAAAGGTTCAACAAAGATGTCTAGTGTGTCTC 5083  
Db 301 GAAGCCAGAAATTGACAGCTTCAACAGAAAGGTTCAACAAAGATGTCTAGTGTGTCTC 360  
Qy 5084 TGCGCTGACCCCGAAGAAATTATGCTGTGTACAGTTTCCGAAACCAATCATC 5143  
Db 361 TGCGCTGACCCCGAAGAAATTATGCTGTGTACAGTTTCCGAAACCAATCATC 420  
Qy 5144 TTTAATCTATCTAATTTAATCTGAGAGACTCATGTTGTATGAAACAGATGCTAGTT 5203  
Db 421 TTTAATCTATCTAATTTAATCTGAGAGACTCATGTTGTATGAAACAGATGCTAGTT 480  
Qy 5204 TGTGTGTGAACGACACTGAATATTTTCTAGAAATTCGGAGAGAAATGGGTAGT 5263  
Db 481 TGTGTGTGAACGACACTGAATATTTTCTAGAAATTCGGAGAGAAATGGGTAGT 540  
Qy 5264 CTATTTTCTGGGTGACCCGCTTATTTAAGAAAGAAATGCTGAATGACATGATTTTGA 5323  
Db 541 CTATTTTCTGGGTGACCCGCTTATTTAAGAAAGAAATGCTGAATGACATGATTTTGA 600  
Qy 5324 AGTCAGAGAGATGTGTGTCATATGGAAGAAACCAAGAGTCCAAAGCAGAGAGAGATC 5383  
Db 601 AGTCAGAGAGATGTGTGTCATATGGAAGAAACCAAGAGTCCAAAGCAGAGAGATC 660  
Qy 5384 CCAGACAGAAAGATCTTCAAGGAGCTAGAAATCTGTTGATGGCCCTTCAACCAAT 5443  
Db 661 CCAGACAGAAAGATCTTCAAGGAGCTAGAAATCTGTTGATGGCCCTTCAACCAAT 720  
Qy 5444 GCCCAGATCACTGGAATG 5465  
Db 721 GCCCAGATCACTGGAATG 742  
RESULT 11  
B0422380 899 bp mRNA linear EST 23-MAY-2002  
LOCUS B0422380  
DEFINITION AGENCOURT 7802085 NIH\_MGC\_92 Homo sapiens cDNA clone IMAGE:6042052  
5', mRNA sequence.  
ACCESSION B0422380 GI:21117695  
VERSION B0422380.1 GI:21117695  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 899)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strusberg, Ph.D.  
Email: cga@bbs-remail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
Plate: LLM13280 row: n column: 05  
High quality sequence stop: 897.  
location/Qualifiers  
1..899  
/organism="Homo sapiens"

```

/mol type="mRNA"
/db xref="taxon:9606"
/clone="IMAGE:6042052"
/tissue_type="embryonal carcinoma, cell line"
/lab host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_92"
/note="Organ: testis; Vector: pCMV-Sport6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT      291 a 182 c 192 g 230 t 4 others
ORIGIN
Query Match      12.9%; Score 734.6; DB 13; Length 899;
Best Local Similarity 97.1%; Pred. No. 1.3e-136;
Matches 824; Conservative 0; Mismatches 11; Indels 14; Gaps 7;
QY 30 CAGGCTGTGGGTTCTCAGATACTGGGCCCTGCGCTCAGAGAGCCTTCAACCTCTGC 89
DB 16 CAGGCTGTGGGTTCTCAGATACTGGGCCCTGCGCTCAGAGAGCCTTCAACCTCTGC 75
QY 90 TCTGGGTAAAGTTCAATGTAAGAGAAATGATTTATCTGCTCTTCCGCTGAAGAA 149
DB 76 TCTG-----GTTCAATGTAAGAGAAATGATTTATCTGCTCTTCCGCTGAAGAA 129
QY 150 GTACAAATGTCAATATGCTATGAGAAATCTTAGAGTCCCATCTGCTGAGTTG 209
DB 130 GTACAAATGTCAATATGCTATGAGAAATCTTAGAGTCCCATCTGCTGAGTTG 189
QY 210 ATCAAGAACTGTCTCCACAAGAGTACCAACATATTTTGCATTTTGCAGTGA 269
DB 190 ATCAAGAACTGTCTCCACAAGAGTACCAACATATTTTGCATTTTGCAGTGA 249
QY 270 CTTCTCAACGAGAAAGGGCTTCAAGTGTCTTATGTATGATATATACCA 329
DB 250 CTTCTCAACGAGAAAGGGCTTCAAGTGTCTTATGTATGATATATACCA 309
QY 330 AGGAGCCTCAAGAAAGTACAGATTTAGTCACTGTGTGAAGAGCTATGAAATCTT 389
DB 310 AGGAGCCTCAAGAAAGTACAGATTTAGTCACTGTGTGAAGAGCTATGAAATCTT 369
QY 390 TGTGCTTTTCACTTGAACAGAGTTTGAATGCAACAGCTATATTTTGCAGAA 449
DB 370 TGTGCTTTTCACTTGAACAGAGTTTGAATGCAACAGCTATATTTTGCAGAA 429
QY 450 GAAATTAATCTCTCTGAACATCTAAAGATGAAGTTTCTATCTCAATCAAGATG 509
DB 430 GAAATTAATCTCTCTGAACATCTAAAGATGAAGTTTCTATCTCAATCAAGATG 489
QY 510 AGAAACCTGCAAAAGACTTCTACAGAGTGAACCCGAAATCTTCTTGCAGAA 569
DB 490 AGAAACCTGCAAAAGACTTCTACAGAGTGAACCCGAAATCTTCTTGCAGAA 546
QY 570 AGTCTAGTGTCAACTCTTCAACCTTGAACCTGGAACCTGGAAGCAAGAGAG 629
DB 547 AGTCTAGTGTCAACTCTTCAACCTTGAACCTGGAACCTGGAAGCAAGAGAG 606
QY 630 ATCAACCTCAAAAGAGCTGTGTCTCACTTAATGAATGGATCTGATTTCTTGA 689
DB 607 ATCAACCTCAAAAGAGCTGTGTCTCACTTAATGAATGGATCTGATTTCTTGA 666
QY 690 GTTATATAGGCACTTATTTGAGGTGGAGATCAAGATTTGTAACAATCAACCTT 749
DB 667 GTTATATAGGCACTTATTTGAGGTGGAGATCAAGATTTGTAACAATCAACCTT 726
QY 750 GGAACCA-GGAGTGAATCAGTTTGAATTTGCAAAAAGGCTGC-TTGTGAATTTT 807
DB 727 GGAACCAAGGATGAATCAGTTTGAATTTGCAAAAAGGCTGTTTGTGAATTTT 786
QY 808 AGACGAGTGAACA-ATACTGAATC-ATCAACCAAGTATATGA-TTTGAACCA 864
DB 787 AGACGAGTGAACAATATCTGAACATCAACCAAGTATATATGATTTTGAACCA 846

```

```

QY 865 CTGAGAGC 873
DB 847 CTGAGAAC 855

RESULT 12
LOCUS      BQ215100
DEFINITION BQ215100      878 bp      mRNA      linear      EST 02-MAY-2002
AGENCY     AGENCOURT_7591049 NIH_MGC_72 Homo sapiens cdna clone IMAGE:6065516
5', mRNA sequence.
ACCESSION  BQ215100
VERSION    BQ215100.1 GI:20396500
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 878)
            NIH-MGC http://mgi.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            JOURNAL
            COMMENT
            Unpublished
            Contact: Robert Strausberg, Ph.D.
            Email: cga@bbs.femail.nih.gov
            Tissue Procurement: ATCC/DCTP/DRP
            CDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            http://image.llnl.gov
            Plate: LLM1341 row: 0 column: 21
            High quality sequence stop: 669.

FEATURES
    source
        1..878
        /organism="Homo sapiens"
        /mol type="mRNA"
        /db xref="taxon:9606"
        /clone="IMAGE:6065516"
        /tissue_type="melanotic melanoma"
        /lab host="DH10B (phage-resistant)"
        /clone_id="NIH_MGC_72"
        /note="Organ: skin; Vector: pCMV-Sport6; Site 1: NotI;
        Site 2: SalI; Cloned unidirectionally. Primer: oligo dT.
        Average insert size 2 kb. Library constructed by Life
        Technologies."
BASE COUNT      281 a 180 c 190 g 227 t
ORIGIN
Query Match      12.4%; Score 706.2; DB 13; Length 878;
Best Local Similarity 98.8%; Pred. No. 6.6e-131;
Matches 754; Conservative 0; Mismatches 3; Indels 6; Gaps 4;
QY 30 CAGGCTGTGGGTTCTCAGATACTGGGCCCTGCGCTCAGAGAGCCTTCAACCTCTGC 89
DB 13 CAGGCTGTGGGTTCTCAGATACTGGGCCCTGCGCTCAGAGAGCCTTCAACCTCTGC 72
QY 90 TCTGGGTAAAGTTCAATGTAAGAGAAATGATTTATCTGCTCTTCCGCTGAAGAA 149
DB 73 TCTGGGTAAAGTTCAATGTAAGAGAAATGATTTATCTGCTCTTCCGCTGAAGAA 132
QY 150 GTACAAATGTCAATATGCTATGAGAAATCTTAGAGTCCCATCTGCTGAGTTG 209
DB 133 GTACAAATGTCAATATGCTATGAGAAATCTTAGAGTCCCATCTGCTGAGTTG 192
QY 210 ATCAAGAACTGTCTCCACAAGAGTGAACACATATTTTGCATTTTGCATGCTGAAA 269
DB 193 ATCAAGAACTGTCTCCACAAGAGTGAACACATATTTTGCATTTTGCATGCTGAAA 252
QY 270 CTTCTCAACGAGAAAGGGCTTCAAGTGTCTTATGTATGAATGATATACCAAA 329
DB 253 CTTCTCAACGAGAAAGGGCTTCAAGTGTCTTATGTATGAATGATATACCAAA 312

```

QY 330 AGGAGCTACAGAAAGTACGAGATTAGTCACTTTGTGAGAGACTATTGAAATCATTT 389  
 DB 313 AGGAGCTACAGAAAGTACGAGATTAGTCACTTTGTGAGAGACTATTGAAATCATTT 372  
 QY 390 TGTGCTTTTCACTTGTGACACAGTTTGGAGTATGCAACAGCTTAAATTTTGCAGAAAAG 449  
 DB 373 TGTGCTTTTCACTTGTGACACAGTTTGGAGTATGCAACAGCTTAAATTTTGCAGAAAAG 432  
 QY 450 GAAATTAATCTCTCTGAAACATCTAAAGATGAGTTTCTATCAATCCAAAGTATGGGCTAC 509  
 DB 433 GAAATTAATCTCTCTGAAACATCTAAAGATGAGTTTCTATCAATCCAAAGTATGGGCTAC 492  
 QY 510 AGAAGCGTGCAGAAAGACTTTCTACAGAGTGAACCCGAAATCTCTTGCAGAGAAACC 569  
 DB 493 AGAAGCGTGCAGAAAGACTTTCTACAGAGTGAACCCGAAATCTCTTGCAGAGAAACC 549  
 QY 570 AGTCTCAGTGTCCAACTCTCTTACACCTTGAACCTGTGAGAACTGTGAGACCAAGACGCG 629  
 DB 550 AGTCTCAGTGTCCAACTCTCTTACACCTTGAACCTGTGAGAACTGTGAGACCAAGACGCG 609  
 QY 630 ATTCAGCTCAAAAGAGTGTCTGTCTACATTTGAATTTGGATCTGATTTCTTGAAGATACC 689  
 DB 610 ATTCAGCTCAAAAGAGTGTCTGTCTACATTTGAATTTGGATCTGATTTCTTGAAGATACC 669  
 QY 690 GTTAAATAGGCACTTATTTGAGT-GTGGAGATCAAGATTGTACAAATCACCCCTCA 748  
 DB 670 GTTAAATAGGCACTTATTTGAGTGTGGAGATCAAGATTGTACAAATCACCCCTCA 729  
 QY 749 AGGAACA-GGATGAATCAG-TTTGATTTTGCAGAAAAG 789  
 DB 730 AGGACACGAGGAGTGAATCAGTTTGGATTCTGCACAAAAG 772  
 RESULT 13  
 BU147444  
 LOCUS 856 bp mRNA linear EST 03-SEP-2002  
 DEFINITION AGENCOURT 8122208 Lupski dorsal root ganglion Homo sapiens cDNA  
 clone IMAGE:6181860 5', mRNA sequence.  
 BU147444  
 BU147444.1 GI:22660976  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 856)  
 NIH-MGC http://mgi.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished  
 Contact: Robert Strausberg, Ph.D.  
 Email: gsa@db-remail.nih.gov  
 Tissue Procurement: Dr. James R. Lupski  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNLN at:  
 http://image.lnl.gov  
 Plate: LLM13566 row: 0 column: 13  
 High quality sequence stop: 695.  
 location/qualifiers  
 1. 856  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6181860"  
 /sex="male"  
 /tissue\_type="dorsal root ganglia"  
 /dev\_stage="adult, 36 yr"  
 /lab\_host="DH10B"  
 /clone\_lib="Lupski dorsal root ganglion"  
 /note="Vector: pCMV-SPORT6 (Life Technologies); Site\_1:  
 Not; Site\_2: SalI; cDNA made by oligo-dT priming.

BASE COUNT 266 a 177 c 192 g 219 t 2 others  
 ORIGIN  
 Query Match 12.2%; Score 698; DB 13; Length 856;  
 Best Local Similarity 97.9%; Pred. No. 2.9e-129;  
 Matches 762; Conservative 0; Mismatches 5; Indels 11; Gaps 5;  
 Directionally cloned using the following adaptors:  
 5'-TCGACCCAGCGTCG-3' and  
 5'-GACTGCTTATGATCGGAGCGGCCCTT(15)-3'. Size selected >  
 1 kb for average insert length 1.7 kb. This is a primary  
 library, non-amplified. Library constructed by Life  
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor  
 College of Medicine) and is available through Life  
 Technologies."  
 1 AGCTCGCTGAGACTTCTCTGAGACCCCGACAGAGTGTGGGTTCTCAGATTAATCTGGGCC 60  
 DB 82 AGCTCGCTGAGACTTCTCTGAGACCGGGGA-CAGGCTGTGGGGTTTCTCAGATTAATCTGGGCC 140  
 QY 61 CCTGCGCTCAGAGAGCCCTTCACTCTGCTGTGGGTAAAGTTCAATTGGAACAGAAAGAA 120  
 DB 141 CCTGCGCTCAGAGAGCCCTTCACTCTGCTGTGGGTAAAGTTCAATTGGAACAGAAAGAA 194  
 QY 121 TGAATTTATCTGCTCTTGTGAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 180  
 DB 195 TGAATTTATCTGCTCTTGTGAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 254  
 QY 181 TCTTAAGAGTGTCCATCTGTGTGAGTTGATCAAGAACTGTGTCCAAAGTGTGACC 240  
 DB 255 TCTTAAGAGTGTCCATCTGTGTGAGTTGATCAAGAACTGTGTCCAAAGTGTGACC 314  
 QY 241 ACATATTTTGAATTTTGAATGCTGAACTTCAACAGAGAAAGGGGCTTCAAGT 300  
 DB 315 ACATATTTTGAATTTTGAATGCTGAACTTCAACAGAGAAAGGGGCTTCAAGT 374  
 QY 301 GTCTTTATGTAAGATATTAACCAAGAGAGCTTCAAGAAAGTACGATTTAGTC 360  
 DB 375 GTCTTTATGTAAGATATTAACCAAGAGAGCTTCAAGAAAGTACGATTTAGTC 434  
 QY 361 AACTTTGTAAGAGCTATTTGAAATCAATTGTGCTTTTCACTTGCAGACAGGTTGGAGT 420  
 DB 435 AACTTTGTAAGAGCTATTTGAAATCAATTGTGCTTTTCACTTGCAGACAGGTTGGAGT 494  
 QY 421 ATGGAACAGCTAATTTTGAAGAAAGAAATTAATCTCTGGAACATTAAGATG 480  
 DB 495 ATGGAACAGCTAATTTTGAAGAAAGAAATTAATCTCTGGAACATTAAGATG 554  
 QY 481 AAGTTTCTATCATCAAGATATGAGCTACAGAAACCGTGCAGAAAGCTTCTACAGAGTG 540  
 DB 555 AAGTTTCTATCATCAAGATATGAGCTACAGAAACCGTGCAGAAAGCTTCTACAGAGTG 614  
 QY 541 AACCCGAAATCTTCTCTTGCAGAGAAACAGCTCTCAGTGTCAACTCTTACCTTGGAA 600  
 DB 615 AACCCGAAATCTTCTCTTGCAGAGAAACAGCTCTCAGTGTCAACTCTTACCTTGGAA 674  
 QY 601 CTGTGAAGACTCTTGAAGCAAGAGGAGTACAACTCTCAAAAGACGTTGTCTTACATG 660  
 DB 675 CTGTGAAGACTCTTGAAGCAAGAGGAGTACAACTCTCAAAAGACGTTGTCTTACATG 734  
 QY 661 AATGGGATCTGATTTCTTCTGAAGATACCGTTAATTAAGGCACTTAATGAGAGTG-AGA 719  
 DB 735 AATGGGATCTGATTTCTTCTGAAGATACCGTTAATTAAGGCACTTAATGAGAGTG-AGA 794  
 QY 720 GATCAAG-AATTTGTACAAATCACCCCTCAAGAAACAGAGG--ATGAATCAGTTTGG 774  
 DB 795 GATCAAGAAATTTGTACAAATCACCCCTCAAGAAACAGAGGAAATGAATCAGTTTGG 852  
 RESULT 14  
 BG777447  
 LOCUS 747 bp mRNA linear EST 15-MAY-2001  
 DEFINITION 60266758P1 NIH\_MGC\_60 Homo sapiens cDNA clone IMAGE:4804551 5',  
 mRNA sequence.

ACCESSION	BG777447
VERSION	BG777447.1
KEYWORDS	EST.
SOURCE	GI:14047764
ORGANISM	Homo sapiens (human)
	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS	1 (bases 1 to 747)
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgaabs-remail.nih.gov Tissue Procurement: DCTD/DRP cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <a href="http://image.lnl.gov">http://image.lnl.gov</a> Plate: LILCM1651 row: c column: 16 High quality sequence stop: 725. Location/Qualifiers
FEATURES	1..747
source	/organism="Homo sapiens" /mol_type="RNA" /db_xref="taxon:9606" /clone="IMAGE:4804551" /tissue.type="adenocarcinoma" /lab_host="DH10B (TI phage-resistant)" /clone.lib="NIH_MGC_60" /note="Organ: prostate; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccgcctcgccc); Site 2: SfiI (ggccatattgccc ); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-ATTCTAAGCGCCGAGGGGCCGATC-dT(30)-BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC library."
BASE COUNT	232 a 160 c 162 g 193 t
ORIGIN	
Query Match	12.0%; Score 687.6; DB 12; Length 747; Best Local Similarity 97.7%; Pred. No. 3,4e-127; Matches 729; Conservative 0; Mismatches 14; Indels 3; Gaps 3;
OY	1 AGCTGCTGAAGACTTCCTTGAGACC CGCACCAAGCTGTGGGTTTCTCAGATACTGGGCC 60
DB	3 AGCTGCTGAAGACTTCCTTGAGAGGGGGA-CAGGCTGTGGGGTTTCTCAGATACTGGGCC 61
OY	61 CCTGGCTCAGAAGGCCCTTCAACCTCTGCTCTGGSTAAAGTTTCATTGGACAAGAAAGAA 120
DB	62 CCTGGCTCAGAAGGCCCTTCAACCTCTCTCTGGGGTAAGTTTCATTGGACAAGAAAGAA 121
OY	121 TGATATTATCTGCTCTTGGCGCTTGAAGAAAGTACAAAAGTCAATTAAGTCTTGACAGAAA 180
DB	122 TGATATTATCTGCTCTTGGCGCTTGAAGAAAGTCAATTAAGTCTTAATCTTAGCAGAAA 181
OY	181 TCTTAAGATGTCCTCATCTGTCTGAAGTTGATCAAGAACCTGTCCCAAAGTGTGACC 240
DB	182 TCTTAAGATGTCCTCATCTGTCTGAAGTTGATCAAGAACCTGTCCCAAAGTGTGACC 241
OY	241 ACATATTTTGCAAAATTTTGCATGCTGAAGAACTTCTAACCAGAGAAAGGGCTTCACAGT 300
DB	242 ACATATTTTGCAAAATTTTGCATGCTGAAGAACTTCTTCAACAGAGAAAGGGCTTCACAGT 301
OY	301 GTCCCTTAATGTAAGATATATTAACAAAGAGGCTCAAGAAAGTACGAGATTTATGTC 360
DB	302 GTCCCTTAATGTAAGATATATTAACAAAGAGGCTCAAGAAAGTACGAGATTTATGTC 361

QY	361	AACTGTTGAAGAGCTAATGAA	-AATCAATTTGTCCTTTTGA	CTTGA	CACAGTTTGAG	419
QY <td>362 <td>AACCTGTTGAAGAGCTAATGAA <td>CAATCTTTTGTGCTTTTCA <td>CTTGA <td>CACAGTTTGAG <td>421</td> </td></td></td></td></td>	362 <td>AACCTGTTGAAGAGCTAATGAA <td>CAATCTTTTGTGCTTTTCA <td>CTTGA <td>CACAGTTTGAG <td>421</td> </td></td></td></td>	AACCTGTTGAAGAGCTAATGAA <td>CAATCTTTTGTGCTTTTCA <td>CTTGA <td>CACAGTTTGAG <td>421</td> </td></td></td>	CAATCTTTTGTGCTTTTCA <td>CTTGA <td>CACAGTTTGAG <td>421</td> </td></td>	CTTGA <td>CACAGTTTGAG <td>421</td> </td>	CACAGTTTGAG <td>421</td>	421
QY <td>420 <td>TATGAAACACGCTAATAATTTT <td>GCAAAAAAGAAAAATAA <td>CTCTCCTGA <td>CATCTAAAAAT <td>479</td> </td></td></td></td></td>	420 <td>TATGAAACACGCTAATAATTTT <td>GCAAAAAAGAAAAATAA <td>CTCTCCTGA <td>CATCTAAAAAT <td>479</td> </td></td></td></td>	TATGAAACACGCTAATAATTTT <td>GCAAAAAAGAAAAATAA <td>CTCTCCTGA <td>CATCTAAAAAT <td>479</td> </td></td></td>	GCAAAAAAGAAAAATAA <td>CTCTCCTGA <td>CATCTAAAAAT <td>479</td> </td></td>	CTCTCCTGA <td>CATCTAAAAAT <td>479</td> </td>	CATCTAAAAAT <td>479</td>	479
QY <td>422 <td>TATGAAACACGCTAATAATTTT <td>GCAAAAAAGAAAAATAA <td>CTCTCCTGA <td>CATCTAAAAAT <td>481</td> </td></td></td></td></td>	422 <td>TATGAAACACGCTAATAATTTT <td>GCAAAAAAGAAAAATAA <td>CTCTCCTGA <td>CATCTAAAAAT <td>481</td> </td></td></td></td>	TATGAAACACGCTAATAATTTT <td>GCAAAAAAGAAAAATAA <td>CTCTCCTGA <td>CATCTAAAAAT <td>481</td> </td></td></td>	GCAAAAAAGAAAAATAA <td>CTCTCCTGA <td>CATCTAAAAAT <td>481</td> </td></td>	CTCTCCTGA <td>CATCTAAAAAT <td>481</td> </td>	CATCTAAAAAT <td>481</td>	481
QY <td>480 <td>GAACTTTTATCATCCAAAGTA <td>TGGGCTACAGAAACCGT <td>GCCAAAAGACTTTTCA <td>CAGAGT <td>539</td> </td></td></td></td></td>	480 <td>GAACTTTTATCATCCAAAGTA <td>TGGGCTACAGAAACCGT <td>GCCAAAAGACTTTTCA <td>CAGAGT <td>539</td> </td></td></td></td>	GAACTTTTATCATCCAAAGTA <td>TGGGCTACAGAAACCGT <td>GCCAAAAGACTTTTCA <td>CAGAGT <td>539</td> </td></td></td>	TGGGCTACAGAAACCGT <td>GCCAAAAGACTTTTCA <td>CAGAGT <td>539</td> </td></td>	GCCAAAAGACTTTTCA <td>CAGAGT <td>539</td> </td>	CAGAGT <td>539</td>	539
QY <td>482 <td>GAACTTTTATCATCCAAAGTA <td>TGGGCTACAGAAACCGT <td>GCCAAAAGACTTTTCA <td>CAGAGT <td>541</td> </td></td></td></td></td>	482 <td>GAACTTTTATCATCCAAAGTA <td>TGGGCTACAGAAACCGT <td>GCCAAAAGACTTTTCA <td>CAGAGT <td>541</td> </td></td></td></td>	GAACTTTTATCATCCAAAGTA <td>TGGGCTACAGAAACCGT <td>GCCAAAAGACTTTTCA <td>CAGAGT <td>541</td> </td></td></td>	TGGGCTACAGAAACCGT <td>GCCAAAAGACTTTTCA <td>CAGAGT <td>541</td> </td></td>	GCCAAAAGACTTTTCA <td>CAGAGT <td>541</td> </td>	CAGAGT <td>541</td>	541
QY <td>540 <td>GAAACCCGAAAAATCCTTCT <td>CCCTGCAAGAAACAGT <td>CTCAGTGTCCA <td>ACTCTTAACTTTGA <td>599</td> </td></td></td></td></td>	540 <td>GAAACCCGAAAAATCCTTCT <td>CCCTGCAAGAAACAGT <td>CTCAGTGTCCA <td>ACTCTTAACTTTGA <td>599</td> </td></td></td></td>	GAAACCCGAAAAATCCTTCT <td>CCCTGCAAGAAACAGT <td>CTCAGTGTCCA <td>ACTCTTAACTTTGA <td>599</td> </td></td></td>	CCCTGCAAGAAACAGT <td>CTCAGTGTCCA <td>ACTCTTAACTTTGA <td>599</td> </td></td>	CTCAGTGTCCA <td>ACTCTTAACTTTGA <td>599</td> </td>	ACTCTTAACTTTGA <td>599</td>	599
QY <td>542 <td>GAAACCCGAAAAATCCTTCT <td>CCCTGCAAGAAACAGT <td>CTCAGTGTCCA <td>ACTCTTAACTTTGA <td>601</td> </td></td></td></td></td>	542 <td>GAAACCCGAAAAATCCTTCT <td>CCCTGCAAGAAACAGT <td>CTCAGTGTCCA <td>ACTCTTAACTTTGA <td>601</td> </td></td></td></td>	GAAACCCGAAAAATCCTTCT <td>CCCTGCAAGAAACAGT <td>CTCAGTGTCCA <td>ACTCTTAACTTTGA <td>601</td> </td></td></td>	CCCTGCAAGAAACAGT <td>CTCAGTGTCCA <td>ACTCTTAACTTTGA <td>601</td> </td></td>	CTCAGTGTCCA <td>ACTCTTAACTTTGA <td>601</td> </td>	ACTCTTAACTTTGA <td>601</td>	601
QY <td>600 <td>ACTGTGAACTGTGAGGACAA <td>AGCAGCGGATACCACT <td>CTCAAAAGCGTGTCT <td>CTTCACTT <td>659</td> </td></td></td></td></td>	600 <td>ACTGTGAACTGTGAGGACAA <td>AGCAGCGGATACCACT <td>CTCAAAAGCGTGTCT <td>CTTCACTT <td>659</td> </td></td></td></td>	ACTGTGAACTGTGAGGACAA <td>AGCAGCGGATACCACT <td>CTCAAAAGCGTGTCT <td>CTTCACTT <td>659</td> </td></td></td>	AGCAGCGGATACCACT <td>CTCAAAAGCGTGTCT <td>CTTCACTT <td>659</td> </td></td>	CTCAAAAGCGTGTCT <td>CTTCACTT <td>659</td> </td>	CTTCACTT <td>659</td>	659
QY <td>602 <td>ACTGTGAACTGTGAGGACAA <td>AGCAGCGGATACCACT <td>CTCAAAAGCGTGTCT <td>CTTCACTT <td>661</td> </td></td></td></td></td>	602 <td>ACTGTGAACTGTGAGGACAA <td>AGCAGCGGATACCACT <td>CTCAAAAGCGTGTCT <td>CTTCACTT <td>661</td> </td></td></td></td>	ACTGTGAACTGTGAGGACAA <td>AGCAGCGGATACCACT <td>CTCAAAAGCGTGTCT <td>CTTCACTT <td>661</td> </td></td></td>	AGCAGCGGATACCACT <td>CTCAAAAGCGTGTCT <td>CTTCACTT <td>661</td> </td></td>	CTCAAAAGCGTGTCT <td>CTTCACTT <td>661</td> </td>	CTTCACTT <td>661</td>	661
QY <td>660 <td>GAACTTTGGATCTGATCTCT <td>CTGGAAGATACCGTTAA <td>TAAAGCACTTATTTG <td>CAGAGT <td>718</td> </td></td></td></td></td>	660 <td>GAACTTTGGATCTGATCTCT <td>CTGGAAGATACCGTTAA <td>TAAAGCACTTATTTG <td>CAGAGT <td>718</td> </td></td></td></td>	GAACTTTGGATCTGATCTCT <td>CTGGAAGATACCGTTAA <td>TAAAGCACTTATTTG <td>CAGAGT <td>718</td> </td></td></td>	CTGGAAGATACCGTTAA <td>TAAAGCACTTATTTG <td>CAGAGT <td>718</td> </td></td>	TAAAGCACTTATTTG <td>CAGAGT <td>718</td> </td>	CAGAGT <td>718</td>	718
QY <td>662 <td>GAACTTTGGATCTGATCTCT <td>CTGGAAGATACCGTTAA <td>TAAAGCACTTATTTG <td>CAGAGT <td>721</td> </td></td></td></td></td>	662 <td>GAACTTTGGATCTGATCTCT <td>CTGGAAGATACCGTTAA <td>TAAAGCACTTATTTG <td>CAGAGT <td>721</td> </td></td></td></td>	GAACTTTGGATCTGATCTCT <td>CTGGAAGATACCGTTAA <td>TAAAGCACTTATTTG <td>CAGAGT <td>721</td> </td></td></td>	CTGGAAGATACCGTTAA <td>TAAAGCACTTATTTG <td>CAGAGT <td>721</td> </td></td>	TAAAGCACTTATTTG <td>CAGAGT <td>721</td> </td>	CAGAGT <td>721</td>	721
QY <td>719 <td>AGATCAAGAAATTTGTAACA <td>ATCACC <td>744</td> <td></td> <td></td> </td></td></td>	719 <td>AGATCAAGAAATTTGTAACA <td>ATCACC <td>744</td> <td></td> <td></td> </td></td>	AGATCAAGAAATTTGTAACA <td>ATCACC <td>744</td> <td></td> <td></td> </td>	ATCACC <td>744</td> <td></td> <td></td>	744		
QY <td>722 <td>AGATCAAGAAATTTGTAACA <td>ATCACC <td>747</td> <td></td> <td></td> </td></td></td>	722 <td>AGATCAAGAAATTTGTAACA <td>ATCACC <td>747</td> <td></td> <td></td> </td></td>	AGATCAAGAAATTTGTAACA <td>ATCACC <td>747</td> <td></td> <td></td> </td>	ATCACC <td>747</td> <td></td> <td></td>	747		
RESULT 15						
BF508987/c						
LOCUS						
DEFINITION						
UI-H-B14-aot-b-06-0-UI						
IMAGE:3085787.3						
IMAGE						
BF508987						
BF508987.1						
GI:11592285						
EST.						
Homo sapiens						
Homo sapiens (human)						
Homo sapiens						
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.						
1 (bases 1 to 739)						
NCI-CCAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .						
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),						
Tumor Gene Index						
Unpublished						
Contact: Robert Strausberg, Ph.D.						
Email: <a href="mailto:cgapbs-remail.nih.gov">cgapbs-remail.nih.gov</a>						
The sequence contained an oligo-dT track that was present in the						
oligonucleotide that was used to prime the synthesis of first						
strand cDNA and therefore this may represent a bonafide poly A						
tail. cDNA library Preparation: M.B. Soares Lab clone distribution:						
NCI-CCAP clone distribution information can be found through the						
I.M.A.G.E. Consortium/ILNL at:						
<a href="http://www-bio.illn.gov/bdirp/image/image.html">www-bio.illn.gov/bdirp/image/image.html</a>						
Seq primer: M13 Forward						
POLYA=Yes.						
Location/Qualifiers						
1..739						
/organism="Homo sapiens"						
/mol_type="mRNA"						
/db_xref="taxon:9606"						
/clone="IMAGE:3085787"						
/lab_host="MDH10B (Life Technologies)"						
/clone_lib="NCI-CCAP Sub8"						
/note="Vector: pVTJ3D-Pac (Pharmacia) with a modified						
polylinker; Site 1: Not I; Site 2: Eco RI; NCI CGAP Sub8						
is a subtracted library derived from NCI CGAP Sub8. The						
NCI CGAP Sub8 library had 2.5 million recombinants. A						
single-stranded DNA preparation of NCI CGAP Sub8 was used						
as a tracer in a subtractive hybridization with a driver						
comprising: a pool of clones from NCI CGAP Sub5 (IMAGE						



clone ids 2732833-2737415, 3068040-3069191; 25% of the driver population), a pool of clones from NCI CGAP Sub4 (IMAGE clone ids 2723592-2729326; 25% of the driver population), NCI CGAP Sub6 (pool AIF-AJU IMAGE ids 2728969-2733190; 25% of the driver population), and NCI CGAP Sub7 (IMAGE ids 3069192-3072238, 3081864-3084550; 25% of the driver population). Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.

BASE COUNT 173 a 141 c 128 g 295 t 2 others  
TAG\_SEQ=None found"  
ORIGIN

Query Match 12.0%; Score 686.6; DB 10; Length 739;  
Best Local Similarity 99.1%; Pred.No. 5.3e-127;  
Matches 689; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1386 TCTGTTCTTCAGAGAAATAGACTTACTGGCCAGTGATCCCATGAGGCTTTAATATGT 1445  
DB 698 TCTGTTCTTCAGAGAAATAGACTTACTGGCCAGTGATCCCATGAGGCTTTAATATGT 639

QY 1446 AAAAGTGAAAGTCTCACTCCAAATCAGTAGAGTAAATTTGAAGACAAATATTTGGG 1505  
DB 638 AAAAGTGAAAGTCTCACTCCAAATCAGTAGAGTAAATTTGAAGACAAATATTTGGG 579

QY 1506 AAAAACCCTATCGGAAAGGCAAGCTCCCACTTAAGCCATGTAAGTAAATTAATTT 1565  
DB 578 AAAAACCCTATCGGAAAGGCAAGCTCCCACTTAAGCCATGTAAGTAAATTAATTT 519

QY 1566 ATAGAGACATTTGTTACTGAGCACAAGATTAATACAAAGCGTCCCTCAAAATTAATTA 1625  
DB 518 ATAGAGACATTTGTTACTGAGCACAAGATTAATACAAAGCGTCCCTCAAAATTAATTA 459

QY 1626 AAGCGTAAAGAGACCTACATCAGGCCCTTCATCCTGAGATTTTATCAAGAAAGCAGAT 1685  
DB 458 AAGCGTAAAGAGACCTACATCAGGCCCTTCATCCTGAGATTTTATCAAGAAAGCAGAT 399

QY 1686 TTGGCAGTTCAAAAAGACTCTCGAAATGATTAATCAGGGAATTAACCAACGAGCAGAT 1745  
DB 398 TTGGCAGTTCAAAAAGACTCTCGAAATGATTAATCAGGGAATTAACCAACGAGCAGAT 339

QY 1746 GGTCAAGTATGATTAATTAATTAATGATGATTAATTAATTAATTAATTAATTAATTA 1805  
DB 338 GGTCAAGTATGATTAATTAATTAATGATGATTAATTAATTAATTAATTAATTAATTA 279

QY 1806 CAGATGAGAAAAATCTTAACCAATAGATCACTCGAAAAAGAAATCTGCTTTCAAAACG 1865  
DB 278 CAGATGAGAAAAATCTTAACCAATAGATCACTCGAAAAAGAAATCTGCTTTCAAAACG 219

QY 1866 AAAGCTGAACCTATAGCAGAGATTAAGCAATATGAACTCGAATTAATTAATTCACAAT 1925  
DB 218 AAAGCTGAACCTATAGCAGAGATTAAGCAATATGAACTCGAATTAATTAATTCACAAT 159

QY 1926 TCAAAAGCACTTAATAAAGATTAAGGCTGAGAGAAAGTCTTCTACCAAGCATATTCATGCG 1985  
DB 158 TCAAAAGCACTTAATAAAGATTAAGGCTGAGAGAAAGTCTTCTACCAAGCATATTCATGCG 99

QY 1986 CTTGAAGTATGATCAGTAGAAATCTAAGCCCACTTAATTTGTAAGTGAATGCAATTTGAT 2045  
DB 98 CTTGAAGTATGATCAGTAGAAATCTAAGCCCACTTAATTTGTAAGTGAATGCAATTTGAT 39

QY 2046 AGTTGTTCTAGCAGTGAAGAGATTAAGAAAAAA 2080  
DB 38 AGTTGTTCTAGCAGTGAAGAGATTAAGAAAAAA 4

Search completed: December 14, 2003, 20:27:59  
Job time : 10217 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

## OM nucleic - nucleic search, using bw model

Run on: December 14, 2003, 09:58:57 ; Search time 348 Seconds  
(without alignments)  
7243.503 Million cell updates/sec

Title: US-09-923-327A-263

Perfect score: 5711  
Sequence: 1 agtcgcgtgagactctctgg.....tccccacagcactactga 5711Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:\*

- 1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*
- 2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*
- 3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*
- 4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*
- 5: /cgn2\_6/ptodata/2/ina/PCtUS\_COMB.seq:\*
- 6: /cgn2\_6/ptodata/2/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5711	100.0	5711	1	US-08-598-591-1 Sequence 1, Appli
2	5711	100.0	5711	1	US-08-798-691-1 Sequence 1, Appli
3	5711	100.0	5711	3	US-08-825-487A-1 Sequence 1, Appli
4	5711	100.0	5711	3	US-09-074-476-1 Sequence 1, Appli
5	5709.4	100.0	5711	1	US-08-798-691-5 Sequence 5, Appli
6	5709.4	100.0	5711	3	US-08-825-487A-5 Sequence 3, Appli
7	5709.4	100.0	5711	1	US-09-074-476-3 Sequence 3, Appli
8	5701.4	99.8	5711	1	US-08-798-691-3 Sequence 3, Appli
9	5701.4	99.8	5711	3	US-08-825-487A-3 Sequence 3, Appli
10	5701.4	99.8	5711	3	US-09-074-476-5 Sequence 3, Appli
11	5699.8	99.8	5711	2	US-08-658-322-1 Sequence 1, Appli
12	5699.8	99.8	5712	2	US-08-603-753D-1 Sequence 1, Appli
13	5699.8	99.8	5712	2	US-09-099-753-1 Sequence 1, Appli
14	5699.8	99.8	5712	3	US-08-966-106-1 Sequence 1, Appli
15	5699.8	99.8	5712	4	US-09-007-678B-47 Sequence 1, Appli
16	5699.8	99.8	5914	1	US-08-480-784-1 Sequence 1, Appli
17	5699.8	99.8	5914	1	US-08-483-553-1 Sequence 1, Appli
18	5699.8	99.8	5914	1	US-08-487-002-1 Sequence 1, Appli
19	5699.8	99.8	5914	1	US-08-483-554B-1 Sequence 1, Appli
20	5699.8	99.8	5914	1	US-08-488-011B-1 Sequence 1, Appli
21	5699.8	99.8	5914	3	US-08-850-727-1 Sequence 1, Appli
22	5699.8	99.8	5914	5	PCT-US95-10202-1 Sequence 1, Appli
23	5699.8	99.8	5914	5	PCT-US95-10203-1 Sequence 1, Appli
24	5699.8	99.8	5914	5	PCT-US95-10220-1 Sequence 1, Appli
25	5698.2	99.8	5711	1	US-08-425-061-4 Sequence 10, Appli
26	5698.2	99.8	5711	1	US-08-425-061-10 Sequence 4, Appli
27	5698.2	99.8	5711	1	US-08-825-886-4 Sequence 4, Appli

28	5698.2	99.8	5711	1	US-08-825-886-10 Sequence 10, Appli
29	5698.2	99.8	5711	4	US-08-989-890-4 Sequence 4, Appli
30	5698.2	99.8	5711	4	US-08-989-890-10 Sequence 10, Appli
31	5688.8	99.6	5712	1	US-08-425-061-12 Sequence 12, Appli
32	5688.8	99.6	5712	1	US-08-825-886-12 Sequence 12, Appli
33	5688.8	99.6	5712	4	US-08-989-890-12 Sequence 6, Appli
34	5687.8	99.6	5710	1	US-08-425-061-6 Sequence 6, Appli
35	5687.8	99.6	5710	4	US-08-989-890-6 Sequence 6, Appli
36	5687.8	99.6	5709	1	US-08-425-061-2 Sequence 2, Appli
37	5685.8	99.6	5709	1	US-08-425-061-7 Sequence 7, Appli
38	5685.8	99.6	5709	1	US-08-425-061-8 Sequence 8, Appli
39	5685.8	99.6	5709	1	US-08-425-061-9 Sequence 9, Appli
40	5685.8	99.6	5709	1	US-08-825-886-2 Sequence 2, Appli
41	5685.8	99.6	5709	1	US-08-825-886-7 Sequence 7, Appli
42	5685.8	99.6	5709	1	US-08-825-886-7 Sequence 8, Appli
43	5685.8	99.6	5709	1	US-08-825-886-8 Sequence 9, Appli
44	5685.8	99.6	5709	1	US-08-825-886-9 Sequence 2, Appli
45	5685.8	99.6	5709	4	US-08-989-890-2 Sequence 2, Appli

## ALIGNMENTS

RESULT 1  
US-08-598-591-1  
; Sequence 1, Application US/08598591  
; Patent No. 5654155  
; GENERAL INFORMATION:  
; APPLICANT: Allen, Antonette C.  
; APPLICANT: Alvarez, Christopher P.  
; APPLICANT: Critz, Brenda S.  
; APPLICANT: Murphy, Patricia D.  
; APPLICANT: Olson, Sheri J.  
; APPLICANT: Schelter, Denise B.  
; APPLICANT: Zeng, Bin  
; TITLE OF INVENTION: A Consensus Sequence of the Human BRCA1 Gene  
; Patent No. 5654155  
; NUMBER OF SEQUENCES: 74  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince St.  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/598,591  
; FILING DATE: herewith  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Swecker, Robert S.  
; REGISTRATION NUMBER: 19,885  
; REFERENCE/DOCKET NUMBER: 020160-282  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-836-6620  
; TELEFAX: 703-836-2021  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5711 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; STRAIN: BRCA1  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT: 17

MAP POSITION: 17q21  
US-08-598-591-1

Query Match 100.0%; Score 5711; DB 1; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 AGCTGCTGAGACTTCTGAGACCCGACACAGGCTGTGGGTTTCTCAGATTAAGTGGCC 60
DB 1 AGCTGCTGAGACTTCTGAGACCCGACACAGGCTGTGGGTTTCTCAGATTAAGTGGCC 60
QY 61 CCTGGCTCAGAGAGGCTTCAACCTCTGCTTGGTAAAGTTCAITGGACAGAAAGAAA 120
DB 61 CCTGGCTCAGAGAGGCTTCAACCTCTGCTTGGTAAAGTTCAITGGACAGAAAGAAA 120
QY 121 TGGATTATCTGCTCTTGGGTTGAAGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 180
DB 121 TGGATTATCTGCTCTTGGGTTGAAGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 180
QY 181 TCTTAGAGTGTCCATCTGTCTGAGAGTATCAAGAACTGTCTCAAAAGTGTACC 240
DB 181 TCTTAGAGTGTCCATCTGTCTGAGAGTATCAAGAACTGTCTCAAAAGTGTACC 240
QY 241 ACATATTTTGCATAATTTGCACTGCTGAACTTCTCAACCAAGAAAGAGGCTTCAAGT 300
DB 241 ACATATTTTGCATAATTTGCACTGCTGAACTTCTCAACCAAGAAAGAGGCTTCAAGT 300
QY 301 GTCCTTATGTAAAGATGATATTAACCAAGAGGCTTCAAGAAAGTAAAGTAAAGTAA 360
DB 301 GTCCTTATGTAAAGATGATATTAACCAAGAGGCTTCAAGAAAGTAAAGTAAAGTAA 360
QY 361 AACTTGTGAAGAGCTATGAAAAATCATTTGTGCTTTCAGCTTGAACAGAGTTGGAGT 420
DB 361 AACTTGTGAAGAGCTATGAAAAATCATTTGTGCTTTCAGCTTGAACAGAGTTGGAGT 420
QY 421 ATGCAAAACAGCTATTAATTTTGCAAAAAGAAAAATTAATCTCTGAAACATTAAGAATG 480
DB 421 ATGCAAAACAGCTATTAATTTTGCAAAAAGAAAAATTAATCTCTGAAACATTAAGAATG 480
QY 481 AAGTTTCATGATCCAAAGTATGGGCTACAGAAACCGGCAAAAGACTTCTTAAGAGTG 540
DB 481 AAGTTTCATGATCCAAAGTATGGGCTACAGAAACCGGCAAAAGACTTCTTAAGAGTG 540
QY 541 AACCCGAAAAATCTTCTCTGAGAGAAACAGTCTCAGTGTCAACTCTTAACCTTGGAA 600
DB 541 AACCCGAAAAATCTTCTCTGAGAGAAACAGTCTCAGTGTCAACTCTTAACCTTGGAA 600
QY 601 CTGTGAGAACTCTGAGACAAAGCAGCGATACAACTCAAAAGACGTCTGTCTTAATTTG 660
DB 601 CTGTGAGAACTCTGAGACAAAGCAGCGATACAACTCAAAAGACGTCTGTCTTAATTTG 660
QY 661 AATTGGGATCTGATTTCTTCTGAGATACCGTTAATTAAGGCAACTTAATGCAATGGAG 720
DB 661 AATTGGGATCTGATTTCTTCTGAGATACCGTTAATTAAGGCAACTTAATGCAATGGAG 720
QY 721 ATCAAGAATGTCTCAAAATCAACCTCAAGAAACAGGAGTGAATCAGTTGGATTTCTG 780
DB 721 ATCAAGAATGTCTCAAAATCAACCTCAAGAAACAGGAGTGAATCAGTTGGATTTCTG 780
QY 781 CAAAAAAGGCTGCTTGTGAATTTTCTGAGACGAGTGAACAAATTAATGAAATCATCAAC 840
DB 781 CAAAAAAGGCTGCTTGTGAATTTTCTGAGACGAGTGAACAAATTAATGAAATCATCAAC 840
QY 841 CCAATTAATTAATGATTTGAACACCTGAGAGCGTGCAGTGAAGGATTCAGAAAAAGT 900
DB 841 CCAATTAATTAATGATTTGAACACCTGAGAGCGTGCAGTGAAGGATTCAGAAAAAGT 900
QY 901 ATCAGGATAGTCTGTTTCAAACTGATGAGAGCATGAGCAAAATATCATGCA 960
DB 901 ATCAGGATAGTCTGTTTCAAACTGATGAGAGCATGAGCAAAATATCATGCA 960
QY 961 GCTCATTAACAGCATGAGAAACGAGTTTATTACTTAAGACAGATGATGTAGAA 1020
DB 961 GCTCATTAACAGCATGAGAAACGAGTTTATTACTTAAGACAGATGATGTAGAA 1020
```

```
DB 961 GCTCATTAACAGCATGAGAAACGAGTTTATTACTTAAGACAGATGATGTAGAA 1020
QY 1021 AGCTGAATCTGTATTAATAAGCAAAACAGCTGTGCTTGAAGAGGCAACATACAT 1080
DB 1021 AGCTGAATCTGTATTAATAAGCAAAACAGCTGTGCTTGAAGAGGCAACATACAT 1080
QY 1081 GGGCTGGAAGTAAAGAAACATGTATGATAGCGGACTCCACAGACAGAAAAAGGTAG 1140
DB 1081 GGGCTGGAAGTAAAGAAACATGTATGATAGCGGACTCCACAGACAGAAAAAGGTAG 1140
QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGAATTAACAGAAATGCCATGCT 1200
DB 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGAATTAACAGAAATGCCATGCT 1200
QY 1201 CAGAGATCTTGAAGATCTGAAGATGTTCTTGGATTAACCTTAATTAAGCAGATTGCA 1260
DB 1201 CAGAGATCTTGAAGATCTGAAGATGTTCTTGGATTAACCTTAATTAAGCAGATTGCA 1260
QY 1261 AAGTTAATGAGTGTCTTCCAGAAAGTATGAACCTGTTAGGTTCTGATGACTCAGATG 1320
DB 1261 AAGTTAATGAGTGTCTTCCAGAAAGTATGAACCTGTTAGGTTCTGATGACTCAGATG 1320
QY 1321 GGGAGTCTGAATCAAAATGCCAAAGTACTGATGTATGAGACGTTCTAAATGAAGTATG 1380
DB 1321 GGGAGTCTGAATCAAAATGCCAAAGTACTGATGTATGAGACGTTCTAAATGAAGTATG 1380
QY 1381 AATATCTGCTTCTGAGAGAAATAGACTTACTGAGCAGATGCTCATAGGCTTTAA 1440
DB 1381 AATATCTGCTTCTGAGAGAAATAGACTTACTGAGCAGATGCTCATAGGCTTTAA 1440
QY 1441 TATGTAAAGTGAAGAGTCTCACTCAAAATCAGTGAAGATTAATTAAGACAAAAAT 1500
DB 1441 TATGTAAAGTGAAGAGTCTCACTCAAAATCAGTGAAGATTAATTAAGACAAAAAT 1500
QY 1501 TTGGGAAAACCTATCGGAAGAGGCAAGCTCCCAACTTAAGCATGTAACTGAATATC 1560
DB 1501 TTGGGAAAACCTATCGGAAGAGGCAAGCTCCCAACTTAAGCATGTAACTGAATATC 1560
QY 1561 TAATTATGAGAGCAATTTGTTACTGAGCAAGATTAATCAAGAGCGTCCCTCAAAATA 1620
DB 1561 TAATTATGAGAGCAATTTGTTACTGAGCAAGATTAATCAAGAGCGTCCCTCAAAATA 1620
QY 1621 AATTAAGCGTAAAGAGAGACTACATCAGGCTTCACTCTGAGATTTTATCAAGAAAG 1680
DB 1621 AATTAAGCGTAAAGAGAGACTACATCAGGCTTCACTCTGAGATTTTATCAAGAAAG 1680
QY 1681 CAGATTTGGCAGTTCAAAAGACTCTCTGAATGATTAATCAGGGAATTAACCAACGAG 1740
DB 1681 CAGATTTGGCAGTTCAAAAGACTCTCTGAATGATTAATCAGGGAATTAACCAACGAG 1740
QY 1741 AGAATGCTCAAGTATGATTAATTAATGATGCTGATGAATTAACCAAGGATGATT 1800
DB 1741 AGAATGCTCAAGTATGATTAATTAATGATGCTGATGAATTAACCAAGGATGATT 1800
QY 1801 CTATTCAAGATGAGAAAAATCTTAACCAATAGATCACTCGAAAAAGATCTGCTTTCA 1860
DB 1801 CTATTCAAGATGAGAAAAATCTTAACCAATAGATCACTCGAAAAAGATCTGCTTTCA 1860
QY 1861 AAACGAAAGCTGAACTTAATAGCAGAGTATAGCAATTAAGAACTGGAATTAATATCC 1920
DB 1861 AAACGAAAGCTGAACTTAATAGCAGAGTATAGCAATTAAGAACTGGAATTAATATCC 1920
QY 1921 ACAATTAAGAAACCTTAAGAAAGATAGGCTGAGAGGAAAGTCTTCAACGAGCATATTC 1980
DB 1921 ACAATTAAGAAACCTTAAGAAAGATAGGCTGAGAGGAAAGTCTTCAACGAGCATATTC 1980
QY 1981 ATGCGCTTGAACCTAGTATGATGATGAATCTAAGCCCACTTAATTTAGTGAATTTGCAA 2040
DB 1981 ATGCGCTTGAACCTAGTATGATGATGAATCTAAGCCCACTTAATTTAGTGAATTTGCAA 2040
QY 2041 TTGATAGTGTCTTGAAGAGTAAAGAAAAAGTAAAGAAAAAGTAAAGTAAAGTAAAGTAA 2100
DB 2041 TTGATAGTGTCTTGAAGAGTAAAGAAAAAGTAAAGAAAAAGTAAAGTAAAGTAAAGTAA 2100
```

QY 2101 GGCACAGAGAACTTACAACTCATGGAAGGTAAAGAACTGCAACTGAGCCAGAAAGA 2160  
| | | | |  
Db 2101 GGCACAGAGAACTTACAACTCATGGAAGGTAAAGAACTGCAACTGAGCCAGAAAGA 2160  
QY 2161 GTAAACAAGCCCAATGAAACAAGTAAGAAAGACATGACATGATACCTTCCAGAGCTGA 2220  
2161 GTAAACAAGCCCAATGAAACAAGTAAGAAAGACATGACATGATACCTTCCAGAGCTGA 2220  
QY 2221 AGTTAACAAATGCACTGCTGTTCTTTTACTAGTGTCAAATACCAATGACCTTAAGAAAT 2280  
2221 AGTTAACAAATGCACTGCTGTTCTTTTACTAGTGTCAAATACCAATGACCTTAAGAAAT 2280  
Db 2281 AGTTAACAAATGCACTGCTGTTCTTTTACTAGTGTCAAATACCAATGACCTTAAGAAAT 2280  
2281 AGTTAACAAATGCACTGCTGTTCTTTTACTAGTGTCAAATACCAATGACCTTAAGAAAT 2280  
QY 2341 CTAAATAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGCTTTTGCAAACTG 2400  
2341 CTAAATAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGCTTTTGCAAACTG 2400  
Db 2401 CTAAATAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGCTTTTGCAAACTG 2400  
2401 CTAAATAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGCTTTTGCAAACTG 2400  
QY 2401 AAAGATCTGTAGAGATGACAGTATTTCACTGCTGTAAGTGAAGAAAGGCTTTTGCAAACTG 2460  
2401 AAAGATCTGTAGAGATGACAGTATTTCACTGCTGTAAGTGAAGAAAGGCTTTTGCAAACTG 2460  
Db 2401 AAAGATCTGTAGAGATGACAGTATTTCACTGCTGTAAGTGAAGAAAGGCTTTTGCAAACTG 2460  
2401 AAAGATCTGTAGAGATGACAGTATTTCACTGCTGTAAGTGAAGAAAGGCTTTTGCAAACTG 2460  
QY 2461 AAAGATCTGTAGAGATGACAGTATTTCACTGCTGTAAGTGAAGAAAGGCTTTTGCAAACTG 2520  
2461 AAAGATCTGTAGAGATGACAGTATTTCACTGCTGTAAGTGAAGAAAGGCTTTTGCAAACTG 2520  
Db 2461 AAAGATCTGTAGAGATGACAGTATTTCACTGCTGTAAGTGAAGAAAGGCTTTTGCAAACTG 2520  
2461 AAAGATCTGTAGAGATGACAGTATTTCACTGCTGTAAGTGAAGAAAGGCTTTTGCAAACTG 2520  
QY 2521 GTGTAGATCTGTAGAGATGACAGTATTTCACTGCTGTAAGTGAAGAAAGGCTTTTGCAAACTG 2580  
2521 GTGTAGATCTGTAGAGATGACAGTATTTCACTGCTGTAAGTGAAGAAAGGCTTTTGCAAACTG 2580  
Db 2521 GTGTAGATCTGTAGAGATGACAGTATTTCACTGCTGTAAGTGAAGAAAGGCTTTTGCAAACTG 2580  
2521 GTGTAGATCTGTAGAGATGACAGTATTTCACTGCTGTAAGTGAAGAAAGGCTTTTGCAAACTG 2580  
QY 2581 ATTAATAGAAATGACAGAGAGGCTTTTAAGTATCCATTGGGAACATGAAGTTAACCAAGCTC 2640  
2581 ATTAATAGAAATGACAGAGAGGCTTTTAAGTATCCATTGGGAACATGAAGTTAACCAAGCTC 2640  
Db 2581 ATTAATAGAAATGACAGAGAGGCTTTTAAGTATCCATTGGGAACATGAAGTTAACCAAGCTC 2640  
2581 ATTAATAGAAATGACAGAGAGGCTTTTAAGTATCCATTGGGAACATGAAGTTAACCAAGCTC 2640  
QY 2641 GGGAAACAAGCATGGAATGGAAGAAAGTGAACCTTGAATGCTCAGATTTTGAAGAAATCAT 2700  
2641 GGGAAACAAGCATGGAATGGAAGAAAGTGAACCTTGAATGCTCAGATTTTGAAGAAATCAT 2700  
Db 2641 GGGAAACAAGCATGGAATGGAAGAAAGTGAACCTTGAATGCTCAGATTTTGAAGAAATCAT 2700  
2641 GGGAAACAAGCATGGAATGGAAGAAAGTGAACCTTGAATGCTCAGATTTTGAAGAAATCAT 2700  
QY 2701 TCAAGTTCCTCAAGCGCCAGTCACTTGTCTGTTTCCAAATCCAGAAATGACAGAGAG 2760  
2701 TCAAGTTCCTCAAGCGCCAGTCACTTGTCTGTTTCCAAATCCAGAAATGACAGAGAG 2760  
Db 2701 TCAAGTTCCTCAAGCGCCAGTCACTTGTCTGTTTCCAAATCCAGAAATGACAGAGAG 2760  
2701 TCAAGTTCCTCAAGCGCCAGTCACTTGTCTGTTTCCAAATCCAGAAATGACAGAGAG 2760  
QY 2761 AATGTGCAACATCTCTGCGCCTCTGCGCTCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
2761 AATGTGCAACATCTCTGCGCCTCTGCGCTCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
Db 2761 AATGTGCAACATCTCTGCGCCTCTGCGCTCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
2761 AATGTGCAACATCTCTGCGCCTCTGCGCTCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
QY 2821 TTGAAATGTGAACAAAGAAAGAAATCAAGAAAGAAATGATCTAATCAAGCTGTATC 2880  
2821 TTGAAATGTGAACAAAGAAAGAAATCAAGAAAGAAATGATCTAATCAAGCTGTATC 2880  
Db 2821 TTGAAATGTGAACAAAGAAAGAAATCAAGAAAGAAATGATCTAATCAAGCTGTATC 2880  
2821 TTGAAATGTGAACAAAGAAAGAAATCAAGAAAGAAATGATCTAATCAAGCTGTATC 2880  
QY 2881 AGACAGTTAATATCACTGAGAGGCTTCTGCTGTTGGTCAAGAAAGATGAGCAAGTTGATA 2940  
2881 AGACAGTTAATATCACTGAGAGGCTTCTGCTGTTGGTCAAGAAAGATGAGCAAGTTGATA 2940  
Db 2881 AGACAGTTAATATCACTGAGAGGCTTCTGCTGTTGGTCAAGAAAGATGAGCAAGTTGATA 2940  
2881 AGACAGTTAATATCACTGAGAGGCTTCTGCTGTTGGTCAAGAAAGATGAGCAAGTTGATA 2940  
QY 2941 ATGCGCAATGTAGTATCAAGAGAGGCTCTAGGTTTGTCTATCACTCAGTTCAAGAGCA 3000  
2941 ATGCGCAATGTAGTATCAAGAGAGGCTCTAGGTTTGTCTATCACTCAGTTCAAGAGCA 3000  
Db 2941 ATGCGCAATGTAGTATCAAGAGAGGCTCTAGGTTTGTCTATCACTCAGTTCAAGAGCA 3000  
2941 ATGCGCAATGTAGTATCAAGAGAGGCTCTAGGTTTGTCTATCACTCAGTTCAAGAGCA 3000  
QY 3001 ACGAAATCTGACCTATCTCCAAATTAACATGACCTTTTCAAAACCCCAATATGATATC 3060  
3001 ACGAAATCTGACCTATCTCCAAATTAACATGACCTTTTCAAAACCCCAATATGATATC 3060  
Db 3001 ACGAAATCTGACCTATCTCCAAATTAACATGACCTTTTCAAAACCCCAATATGATATC 3060  
3001 ACGAAATCTGACCTATCTCCAAATTAACATGACCTTTTCAAAACCCCAATATGATATC 3060  
QY 3061 CACCACTTTTCCCATCAAGTCACTTTGTTAAACCTAAATGTAAAGAAATCTGCTAGAG 3120  
3061 CACCACTTTTCCCATCAAGTCACTTTGTTAAACCTAAATGTAAAGAAATCTGCTAGAG 3120  
Db 3061 CACCACTTTTCCCATCAAGTCACTTTGTTAAACCTAAATGTAAAGAAATCTGCTAGAG 3120  
3061 CACCACTTTTCCCATCAAGTCACTTTGTTAAACCTAAATGTAAAGAAATCTGCTAGAG 3120  
QY 3121 AAAAATTGAGGAACTTCAATGTCACTGAAAGAAATGGAATGAGAACTTCCAA 3180  
3121 AAAAATTGAGGAACTTCAATGTCACTGAAAGAAATGGAATGAGAACTTCCAA 3180  
Db 3121 AAAAATTGAGGAACTTCAATGTCACTGAAAGAAATGGAATGAGAACTTCCAA 3180  
3121 AAAAATTGAGGAACTTCAATGTCACTGAAAGAAATGGAATGAGAACTTCCAA 3180

QY 3181 GTACAGTAGACACAAATAGCCGTATATTAACATTTAGAGAAATGTTTTTAAAGACCACT 3240  
3181 GTACAGTAGACACAAATAGCCGTATATTAACATTTAGAGAAATGTTTTTAAAGACCACT 3240  
Db 3181 GTACAGTAGACACAAATAGCCGTATATTAACATTTAGAGAAATGTTTTTAAAGACCACT 3240  
3181 GTACAGTAGACACAAATAGCCGTATATTAACATTTAGAGAAATGTTTTTAAAGACCACT 3240  
QY 3241 CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGCTCCAGTATTAATGAAA 3300  
3241 CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGCTCCAGTATTAATGAAA 3300  
Db 3241 CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGCTCCAGTATTAATGAAA 3300  
3241 CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGCTCCAGTATTAATGAAA 3300  
QY 3301 TAGGTTCCAGTAGAAGAAACAATTCAAGAGAACTAAGTAGAAGAGAGGCGCAAAATTGA 3360  
3301 TAGGTTCCAGTAGAAGAAACAATTCAAGAGAACTAAGTAGAAGAGAGGCGCAAAATTGA 3360  
Db 3301 TAGGTTCCAGTAGAAGAAACAATTCAAGAGAACTAAGTAGAAGAGAGGCGCAAAATTGA 3360  
3301 TAGGTTCCAGTAGAAGAAACAATTCAAGAGAACTAAGTAGAAGAGAGGCGCAAAATTGA 3360  
QY 3361 ATGCTATGCTTAAAGTAAAGGCTTTTGAACCTGAGGCTTAATAACAAAGCTTCTCGAA 3420  
3361 ATGCTATGCTTAAAGTAAAGGCTTTTGAACCTGAGGCTTAATAACAAAGCTTCTCGAA 3420  
Db 3361 ATGCTATGCTTAAAGTAAAGGCTTTTGAACCTGAGGCTTAATAACAAAGCTTCTCGAA 3420  
3361 ATGCTATGCTTAAAGTAAAGGCTTTTGAACCTGAGGCTTAATAACAAAGCTTCTCGAA 3420  
QY 3421 GTAAATGTAGACATCTGAAATTAATAAAGCAAGAAATGAAGAAAGTGTGAGCTGTTA 3480  
3421 GTAAATGTAGACATCTGAAATTAATAAAGCAAGAAATGAAGAAAGTGTGAGCTGTTA 3480  
Db 3421 GTAAATGTAGACATCTGAAATTAATAAAGCAAGAAATGAAGAAAGTGTGAGCTGTTA 3480  
3421 GTAAATGTAGACATCTGAAATTAATAAAGCAAGAAATGAAGAAAGTGTGAGCTGTTA 3480  
QY 3481 ATACAGATTTCTCTCCATATCTGATTTCAATTAAGTAAACAGCTTATGGGAATGATC 3540  
3481 ATACAGATTTCTCTCCATATCTGATTTCAATTAAGTAAACAGCTTATGGGAATGATC 3540  
Db 3481 ATACAGATTTCTCTCCATATCTGATTTCAATTAAGTAAACAGCTTATGGGAATGATC 3540  
3481 ATACAGATTTCTCTCCATATCTGATTTCAATTAAGTAAACAGCTTATGGGAATGATC 3540  
QY 3541 ATGATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTGATGATGATGATGATGATG 3600  
3541 ATGATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTGATGATGATGATGATGATG 3600  
Db 3541 ATGATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTGATGATGATGATGATGATG 3600  
3541 ATGATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTGATGATGATGATGATGATG 3600  
QY 3601 AAGATCTAGTATTGCTGAAATGACATTAAGAAAGTCTGCTGTTTGAAGAAAGCG 3660  
3601 AAGATCTAGTATTGCTGAAATGACATTAAGAAAGTCTGCTGTTTGAAGAAAGCG 3660  
Db 3601 AAGATCTAGTATTGCTGAAATGACATTAAGAAAGTCTGCTGTTTGAAGAAAGCG 3660  
3601 AAGATCTAGTATTGCTGAAATGACATTAAGAAAGTCTGCTGTTTGAAGAAAGCG 3660  
QY 3661 TCCAGAGAGAGACTTACAGAGAGTCTGACCTTTCAACCAATACATTTGGCTCAGG 3720  
3661 TCCAGAGAGAGACTTACAGAGAGTCTGACCTTTCAACCAATACATTTGGCTCAGG 3720  
Db 3661 TCCAGAGAGAGACTTACAGAGAGTCTGACCTTTCAACCAATACATTTGGCTCAGG 3720  
3661 TCCAGAGAGAGACTTACAGAGAGTCTGACCTTTCAACCAATACATTTGGCTCAGG 3720  
QY 3721 GTTACCGAAGAGGCGCCAAAGAAATTAAGTCTCAGAGAGAACTTATCTAGTGAAGATG 3780  
3721 GTTACCGAAGAGGCGCCAAAGAAATTAAGTCTCAGAGAGAACTTATCTAGTGAAGATG 3780  
Db 3721 GTTACCGAAGAGGCGCCAAAGAAATTAAGTCTCAGAGAGAACTTATCTAGTGAAGATG 3780  
3721 GTTACCGAAGAGGCGCCAAAGAAATTAAGTCTCAGAGAGAACTTATCTAGTGAAGATG 3780  
QY 3781 AAGAGCTTCCCTGCTTCCAACTTGTATTTGTTGAAGTAAACATATATCTCAGT 3840  
3781 AAGAGCTTCCCTGCTTCCAACTTGTATTTGTTGAAGTAAACATATATCTCAGT 3840  
Db 3781 AAGAGCTTCCCTGCTTCCAACTTGTATTTGTTGAAGTAAACATATATCTCAGT 3840  
3781 AAGAGCTTCCCTGCTTCCAACTTGTATTTGTTGAAGTAAACATATATCTCAGT 3840  
QY 3841 CTACTAGGATAGACACCGTGTCTACCAAGTGTCTGTCTAAGAAACAGAGAGAAATTTAT 3900  
3841 CTACTAGGATAGACACCGTGTCTACCAAGTGTCTGTCTAAGAAACAGAGAGAAATTTAT 3900  
Db 3841 CTACTAGGATAGACACCGTGTCTACCAAGTGTCTGTCTAAGAAACAGAGAGAAATTTAT 3900  
3841 CTACTAGGATAGACACCGTGTCTACCAAGTGTCTGTCTAAGAAACAGAGAGAAATTTAT 3900  
QY 3901 TATCATTTGAAGAAATAGCTTAAATGAATGACAGTAACTAAGTAAATTTGGCAAGGATCTC 3960  
3901 TATCATTTGAAGAAATAGCTTAAATGAATGACAGTAACTAAGTAAATTTGGCAAGGATCTC 3960  
Db 3901 TATCATTTGAAGAAATAGCTTAAATGAATGACAGTAACTAAGTAAATTTGGCAAGGATCTC 3960  
3901 TATCATTTGAAGAAATAGCTTAAATGAATGACAGTAACTAAGTAAATTTGGCAAGGATCTC 3960  
QY 3961 AGAAACATCACTTATGAGAGAAACAAATTTCTGCTAGCTGTTTCTTCAAGTGA 4020  
3961 AGAAACATCACTTATGAGAGAAACAAATTTCTGCTAGCTGTTTCTTCAAGTGA 4020  
Db 3961 AGAAACATCACTTATGAGAGAAACAAATTTCTGCTAGCTGTTTCTTCAAGTGA 4020  
3961 AGAAACATCACTTATGAGAGAAACAAATTTCTGCTAGCTGTTTCTTCAAGTGA 4020  
QY 4021 GTGAATTTGAAGACTTGAATGCAATTAACAAACCCAGAGATCTTTTCTGATGCTTCT 4080  
4021 GTGAATTTGAAGACTTGAATGCAATTAACAAACCCAGAGATCTTTTCTGATGCTTCT 4080  
Db 4021 GTGAATTTGAAGACTTGAATGCAATTAACAAACCCAGAGATCTTTTCTGATGCTTCT 4080  
4021 GTGAATTTGAAGACTTGAATGCAATTAACAAACCCAGAGATCTTTTCTGATGCTTCT 4080  
QY 4081 CCAAAACAATGAGGATCACTGATGAAAGCCAGAGAGTGTGTAGTGAACAAGAAATTGG 4140  
4081 CCAAAACAATGAGGATCACTGATGAAAGCCAGAGAGTGTGTAGTGAACAAGAAATTGG 4140  
Db 4081 CCAAAACAATGAGGATCACTGATGAAAGCCAGAGAGTGTGTAGTGAACAAGAAATTGG 4140  
4081 CCAAAACAATGAGGATCACTGATGAAAGCCAGAGAGTGTGTAGTGAACAAGAAATTGG 4140  
QY 4141 TTTCAATGATGAGAGAAAGAGAGAGGCTTGAAGAAATATCAAGAAAGAGAGCA 4200  
4141 TTTCAATGATGAGAGAAAGAGAGAGGCTTGAAGAAATATCAAGAAAGAGAGCA 4200  
Db 4141 TTTCAATGATGAGAGAAAGAGAGAGGCTTGAAGAAATATCAAGAAAGAGAGCA 4200  
4141 TTTCAATGATGAGAGAAAGAGAGAGGCTTGAAGAAATATCAAGAAAGAGAGCA 4200  
QY 4201 TGAATTTCAACTTATGAGAGAGAGAGAGGCTTGAAGAAATATCAAGAAAGAGAGCA 4260  
4201 TGAATTTCAACTTATGAGAGAGAGAGAGGCTTGAAGAAATATCAAGAAAGAGAGCA 4260  
Db 4201 TGAATTTCAACTTATGAGAGAGAGAGAGGCTTGAAGAAATATCAAGAAAGAGAGCA 4260  
4201 TGAATTTCAACTTATGAGAGAGAGAGAGGCTTGAAGAAATATCAAGAAAGAGAGCA 4260  
QY 4261 ACTGCTCAGGCTATCTCTCAGAGTGAACATTTTAACCACTCAGAGAGGATACCATGC 4320  
4261 ACTGCTCAGGCTATCTCTCAGAGTGAACATTTTAACCACTCAGAGAGGATACCATGC 4320

Db 4261 ACTGCTGAGGCTATCTCTCAGAGTGACATTTTAACACTCAGCAGAGGATACCATGC 4320  
Qy 4321 AACCTAACCTTAAGCTCCAGCAGAAATGGCTGAACCTGAAGCTGTGTAAGAACGC 4380  
Db 4321 AACCTAACCTTAAGCTCCAGCAGAAATGGCTGAACCTGAAGCTGTGTAAGAACGC 4380  
Qy 4381 ATGGAGGACGACCTTCTTAACAGCTACCTTCATCATTAAGTGAATCTCTCTCCCTTGAGG 4440  
Db 4381 ATGGAGGACGACCTTCTTAACAGCTACCTTCATCATTAAGTGAATCTCTCTCCCTTGAGG 4440  
Qy 4441 ACCTGCGAAATCCAGAACAAAGCAGATGAGAAAGAGAGATTAATCTTCAAGAAAGTA 4500  
Db 4441 ACCTGCGAAATCCAGAACAAAGCAGATGAGAAAGAGAGATTAATCTTCAAGAAAGTA 4500  
Qy 4501 GTGAATACCTTAAGCCAGAAATCCAGAAAGCCTTTCTGCTGACAGAGTTGAGGTCTG 4560  
Db 4501 GTGAATACCTTAAGCCAGAAATCCAGAAAGCCTTTCTGCTGACAGAGTTGAGGTCTG 4560  
Qy 4561 CAGATAGTTCTACCAAGTAAATTAAGAACAGAGAGTGAAGGTCAATCCCTCTTAAT 4620  
Db 4561 CAGATAGTTCTACCAAGTAAATTAAGAACAGAGAGTGAAGGTCAATCCCTCTTAAT 4620  
Qy 4621 GCCCATCTTAGATGATAGTGTGATGATGACAGTGTCTGAGAGTCTTCAAGATAGAA 4680  
Db 4621 GCCCATCTTAGATGATAGTGTGATGATGACAGTGTCTGAGAGTCTTCAAGATAGAA 4680  
Qy 4681 ACTACCATCTCAGAGAGAGTCTAATTAAGTGTGATGATGAGAGAGAACAGCTGAGAG 4740  
Db 4681 ACTACCATCTCAGAGAGAGTCTAATTAAGTGTGATGATGAGAGAGAACAGCTGAGAG 4740  
Qy 4741 AGTCTGGGCGACAGATTTGACGAAACATCTTCTTCCAGAGCAAGATCTAGAGGAA 4800  
Db 4741 AGTCTGGGCGACAGATTTGACGAAACATCTTCTTCCAGAGCAAGATCTAGAGGAA 4800  
Qy 4801 CCCCTTACCTGGAATCTGGAATCAAGCTCTTCTCTGATGACCTGGAATCTGATCTTCTG 4860  
Db 4801 CCCCTTACCTGGAATCTGGAATCAAGCTCTTCTCTGATGACCTGGAATCTGATCTTCTG 4860  
Qy 4861 AAGACAGAGCCCGACAGAGTCACTGCTGTGCAACATCACTTCAACCTCTCATTTGA 4920  
Db 4861 AAGACAGAGCCCGACAGAGTCACTGCTGTGCAACATCACTTCAACCTCTCATTTGA 4920  
Qy 4921 AAGTCCCAATTTGAAGTTCAGAAATCTGCCAGAGGCTCAGCTGCTCTCATACTAG 4980  
Db 4921 AAGTCCCAATTTGAAGTTCAGAAATCTGCCAGAGGCTCAGCTGCTCTCATACTAG 4980  
Qy 4981 ATACTGCTGGGTATATGCAATGAGAAAGTGTGAGCAGAGGAGAGCAGAAATTTGACAG 5040  
Db 4981 ATACTGCTGGGTATATGCAATGAGAAAGTGTGAGCAGAGGAGAGCAGAAATTTGACAG 5040  
Qy 5041 CTTGAACAGAAAGGTCACAAAGAAATGTCATGCTGTGCTGTGCTGACCCAGAG 5100  
Db 5041 CTTGAACAGAAAGGTCACAAAGAAATGTCATGCTGTGCTGTGCTGACCCAGAG 5100  
Qy 5101 AATTATGCTGTGATGCAAGTTTGCAGAAACACCATATCACTTAATCTAATTA 5160  
Db 5101 AATTATGCTGTGATGCAAGTTTGCAGAAACACCATATCACTTAATCTAATTA 5160  
Qy 5161 CTGAAGAGACTACTGATGTTGTAAGAAACAGATGCTGAATTTGTGTGAGCAGAC 5220  
Db 5161 CTGAAGAGACTACTGATGTTGTAAGAAACAGATGCTGAATTTGTGTGAGCAGAC 5220  
Qy 5221 TGAATATTTTCTAGGAATTCGCGAGAGAAATGGGTAGTGAATTTCTGGGTGACCC 5280  
Db 5221 TGAATATTTTCTAGGAATTCGCGAGAGAAATGGGTAGTGAATTTCTGGGTGACCC 5280  
Qy 5281 AGTCTATTAAGAAAGAAATGCTGATGAGCAATGATTTGAAGTCAAGAGAGATGAG 5340  
Db 5281 AGTCTATTAAGAAAGAAATGCTGATGAGCAATGATTTGAAGTCAAGAGAGATGAG 5340  
Qy 5341 TCAATGAGAAACACCAAGGTCACAAAGCAGAGAGAGATTCAGAGAGAAAGATCT 5400  
Db 5341 TCAATGAGAAACACCAAGGTCACAAAGCAGAGAGAGATTCAGAGAGAAAGATCT 5400

Db 5341 TCAATGAGAAACACCAAGGTCACAAAGCAGAGAGAGATTCAGAGAGAAAGATCT 5400  
Qy 5401 TCAGGGGGCTAGAAATGTTGTTATAGGGCCCTTACCAACATGCGCAGATCAACTGG 5460  
Db 5401 TCAGGGGGCTAGAAATGTTGTTATAGGGCCCTTACCAACATGCGCAGATCAACTGG 5460  
Qy 5461 AATGATGATACAGCTGTGTGTGCTCTGTGTGAGAGAGCTTTCATCATTTCACTTGG 5520  
Db 5461 AATGATGATACAGCTGTGTGTGCTCTGTGTGAGAGAGCTTTCATCATTTCACTTGG 5520  
Qy 5521 GCACAGGTCTACCCCAATTTGTTGTGTGACGACCAATGCTTGAACAGAGCAATGCT 5580  
Db 5521 GCACAGGTCTACCCCAATTTGTTGTGTGACGACCAATGCTTGAACAGAGCAATGCT 5580  
Qy 5581 TCATGCAATTTGGCAGATGTGTGAGGACCTGTGTGATGCCAGAGAGTGGTGTGACA 5640  
Db 5581 TCATGCAATTTGGCAGATGTGTGAGGACCTGTGTGATGCCAGAGAGTGGTGTGACA 5640  
Qy 5641 GTTAGCACTCTACAGTGCAGAGAGCTGACACCTAATGATACCCAGATCCCCACA 5700  
Db 5641 GTTAGCACTCTACAGTGCAGAGAGCTGACACCTAATGATACCCAGATCCCCACA 5700  
Qy 5701 GCCACTACTGA 5711  
Db 5701 GCCACTACTGA 5711

RESULT 2  
US-08-798-691-1  
; Sequence 1, Application US/08798691  
; Patent No. 5750400  
; GENERAL INFORMATION:  
; APPLICANT: Murphy, Patricia D.  
; APPLICANT: Allen, Antoinette C.  
; APPLICANT: Alvarez, Christopher P.  
; APPLICANT: Crlitz, Brenda S.  
; APPLICANT: Olson, Sheri J.  
; APPLICANT: Schelter, Denise B.  
; APPLICANT: Zeng, Bin  
; TITLE OF INVENTION: Coding Sequences of the Human  
; TITLE OF INVENTION: BRCA1 Gene  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: ONCORMED  
; STREET: 200 Perry Parkway  
; CITY: Gaithersburg  
; STATE: MD  
; COUNTRY: USA  
; ZIP: 20877  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/798,691  
; FILING DATE: 12-Feb-97  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Thomas Gallegos  
; REGISTRATION NUMBER: 32,692  
; REFERENCE/DOCKET NUMBER: PA-0054CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 301-527-2051  
; TELEFAX: 301-208-6997  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5711 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; ORIGINAL SOURCE:

ORGANISM: Homo sapiens  
STRAIN: BRCA1  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17  
MAP POSITION: 17q21  
US-08-798-691-1

Query Match 100.0%; Score 5711; DB 1; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGCTGAGACTTCTGAGACCCCGCACCGAGCTGTGGGTTTCTCAGATTAAGTGGCC 60  
DB 1 AGCTGCTGAGACTTCTGAGACCCCGCACCGAGCTGTGGGTTTCTCAGATTAAGTGGCC 60  
QY 61 CCTGGCTCAGAGGCTTCACCCCTCTGCTGGGTTAAAGTCAATTTGGAAGAGAA 120  
DB 61 CCTGGCTCAGAGGCTTCACCCCTCTGCTGGGTTAAAGTCAATTTGGAAGAGAA 120  
QY 121 TGGATTATCTGCTCTTGGCGCTTGAAGATCAAAATGTCAATTAATGCTATGACAGAAA 180  
DB 121 TGGATTATCTGCTCTTGGCGCTTGAAGATCAAAATGTCAATTAATGCTATGACAGAAA 180  
QY 181 TCTTAGAGTGTCCATCTGTCTGAGATTGATCAGAGAACTGTCTCAAAAGTGTGACC 240  
DB 181 TCTTAGAGTGTCCATCTGTCTGAGATTGATCAGAGAACTGTCTCAAAAGTGTGACC 240  
QY 241 ACATTTTTCGCAAAATTTTGCATGCTGAAACTTCTCAACGAGAAAGAGGCTTCAACGT 300  
DB 241 ACATTTTTCGCAAAATTTTGCATGCTGAAACTTCTCAACGAGAAAGAGGCTTCAACGT 300  
QY 301 GTCCCTTATGTAGAAATGATATACCAAAAGGCTTCAAGAAAGTACGAGATTATGTC 360  
DB 301 GTCCCTTATGTAGAAATGATATACCAAAAGGCTTCAAGAAAGTACGAGATTATGTC 360  
QY 361 AACTGTGAGAGCTATTTGAAATCATTTTGTCTTTCACTTGAACAAGTTTGAAGT 420  
DB 361 AACTGTGAGAGCTATTTGAAATCATTTTGTCTTTCACTTGAACAAGTTTGAAGT 420  
QY 421 ATGCAACAGCTATATTTTGCAGAAAGAGAAATTAATCTCTGTAACATCTTAAAGATG 480  
DB 421 ATGCAACAGCTATATTTTGCAGAAAGAGAAATTAATCTCTGTAACATCTTAAAGATG 480  
QY 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCTTCAACAGATG 540  
DB 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCTTCAACAGATG 540  
QY 541 AACCGGAAATCTCTCTTGCAGAAACCAAGTCTCAGTGTCCAACCTCTTCACTTGA 600  
DB 541 AACCGGAAATCTCTCTTGCAGAAACCAAGTCTCAGTGTCCAACCTCTTCACTTGA 600  
QY 601 CTGTGAGAACTCTGAGCAAAAGCAGCGGATCAACCTTCAAAAGACGTGTCTACATTTG 660  
DB 601 CTGTGAGAACTCTGAGCAAAAGCAGCGGATCAACCTTCAAAAGACGTGTCTACATTTG 660  
QY 661 AATTGGATCTGATCTTCTGAGAGTACCGTTAATAAGGCACTTATGCAAGTGGAG 720  
DB 661 AATTGGATCTGATCTTCTGAGAGTACCGTTAATAAGGCACTTATGCAAGTGGAG 720  
QY 721 ATCAAGATTTGTTCAAAATCAACCCCTCAAGAGCAAGGATGAATCAGTTTGAATTCG 780  
DB 721 ATCAAGATTTGTTCAAAATCAACCCCTCAAGAGCAAGGATGAATCAGTTTGAATTCG 780  
QY 781 CAAAAAGGCTGTGTGAAATTTTCTGAGCGGATGTAACAATACTGAACATCATCAAC 840  
DB 781 CAAAAAGGCTGTGTGAAATTTTCTGAGCGGATGTAACAATACTGAACATCATCAAC 840  
QY 841 CCAAGTAATATGATTTGAAACACCACTGAGAGCGTGCAGCTGAGAGGCAATCCAGAAAAGT 900  
DB 841 CCAAGTAATATGATTTGAAACACCACTGAGAGCGTGCAGCTGAGAGGCAATCCAGAAAAGT 900  
QY 901 ATCAGGATGTTCTGTTTCAAACTTGATGTGAGGCAATGTGGCAAAATATCTCATGCA 960  
DB 901 ATCAGGATGTTCTGTTTCAAACTTGATGTGAGGCAATGTGGCAAAATATCTCATGCA 960

DB 901 ATCAGGATGTTCTGTTTCAAACTTGATGTGAGGCAATGTGGCAAAATATCTCATGCA 960  
QY 961 GCTCATACAGCATGAGAAACGACAGTTTATTAATCACTTAAAGACAGATGTAGAAA 1020  
DB 961 GCTCATACAGCATGAGAAACGACAGTTTATTAATCACTTAAAGACAGATGTAGAAA 1020  
QY 1021 AGGCTGAATTCGTATATTAAGCAACAGCCCTGCTTGAAGAGGCAATTAACAGAT 1080  
DB 1021 AGGCTGAATTCGTATATTAAGCAACAGCCCTGCTTGAAGAGGCAATTAACAGAT 1080  
QY 1081 GGGCTGGAATGAGAAACATGTATGATAGCGGACCTCCAGCAACAGAAAAAGTGG 1140  
DB 1081 GGGCTGGAATGAGAAACATGTATGATAGCGGACCTCCAGCAACAGAAAAAGTGG 1140  
QY 1141 ATCTGAATGTGATCCCTGTGTGAGAAAAAGATGAATTAAGCAAACTGCATGCT 1200  
DB 1141 ATCTGAATGTGATCCCTGTGTGAGAAAAAGATGAATTAAGCAAACTGCATGCT 1200  
QY 1201 CAGAGAAATCTAGAGATCTGAGAGTGTCTTGGATTAACATAATAGCAGCATTCAGA 1260  
DB 1201 CAGAGAAATCTAGAGATCTGAGAGTGTCTTGGATTAACATAATAGCAGCATTCAGA 1260  
QY 1261 AAGTTAATGAGTGTTCCTCAGAAAGTGAATCTGTAGTTCTGATGATCACTGATG 1320  
DB 1261 AAGTTAATGAGTGTTCCTCAGAAAGTGAATCTGTAGTTCTGATGATCACTGATG 1320  
QY 1321 GGGAGTCTGAATCAAAATCCCAAGATGATGATTTGAGAGTCTTAATGAGATGATG 1380  
DB 1321 GGGAGTCTGAATCAAAATCCCAAGATGATGATTTGAGAGTCTTAATGAGATGATG 1380  
QY 1381 AATATTTCTGTTCTTCAAGAAAAATGACTTAAGTGGCAGTATCTCATGAGGCTTTAA 1440  
DB 1381 AATATTTCTGTTCTTCAAGAAAAATGACTTAAGTGGCAGTATCTCATGAGGCTTTAA 1440  
QY 1441 TATGTAAAGTGAAGAGTTCATCTCAAAATGATGAGATTAATGAGACAAATAT 1500  
DB 1441 TATGTAAAGTGAAGAGTTCATCTCAAAATGATGAGATTAATGAGACAAATAT 1500  
QY 1501 TTGGGAAAACTATGTGGAAGAGGCAAGCTTCCCACTTAAGCATGTAATGTAATTC 1560  
DB 1501 TTGGGAAAACTATGTGGAAGAGGCAAGCTTCCCACTTAAGCATGTAATGTAATTC 1560  
QY 1561 TAAATATGAGCAATTTGTTCTGAGCAAGATTAACAAGAGGCTCCCTCAAAATA 1620  
DB 1561 TAAATATGAGCAATTTGTTCTGAGCAAGATTAACAAGAGGCTCCCTCAAAATA 1620  
QY 1621 AATTAAAGCTTAAAGAGACCTACATAGGCTTCACTCTGAGAGATTTTATCAAGAAAG 1680  
DB 1621 AATTAAAGCTTAAAGAGACCTACATAGGCTTCACTCTGAGAGATTTTATCAAGAAAG 1680  
QY 1681 CAGATTTGGCAGTTCAAAAAGCTCTGAAATGATTAACAGGAACTTAACCAAGGAGC 1740  
DB 1681 CAGATTTGGCAGTTCAAAAAGCTCTGAAATGATTAACAGGAACTTAACCAAGGAGC 1740  
QY 1741 AGAATGTCAAGTGTGAATTTACTAATAGGTCAGAGAAATAAAGTGGAT 1800  
DB 1741 AGAATGTCAAGTGTGAATTTACTAATAGGTCAGAGAAATAAAGTGGAT 1800  
QY 1801 CTATTCAGAAATGAGAAAAATCTTAACCAATAGATCACTCGAAAAAATCTGCTTCA 1860  
DB 1801 CTATTCAGAAATGAGAAAAATCTTAACCAATAGATCACTCGAAAAAATCTGCTTCA 1860  
QY 1861 AAAAGAAAGCTGAACCTTAAGCAGCAGATTAAGCAATATGGAATCTCAATTAATATCC 1920  
DB 1861 AAAAGAAAGCTGAACCTTAAGCAGCAGATTAAGCAATATGGAATCTCAATTAATATCC 1920  
QY 1921 ACAATTTCAAAAGCACTTAAAGAAATAGCTGAGAGAAAGTCTTCAACAGGATATTC 1980  
DB 1921 ACAATTTCAAAAGCACTTAAAGAAATAGCTGAGAGAAAGTCTTCAACAGGATATTC 1980  
QY 1981 ATGAGCTTGAATAGTATGATGATGATTAAGGCACTTAATGATGATGATGATGCAAA 2040  
DB 1981 ATGAGCTTGAATAGTATGATGATGATTAAGGCACTTAATGATGATGATGATGCAAA 2040



OY 2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAAAGTACCAACCAATGCCAGTCA 2100  
DB 2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAAAGTACCAACCAATGCCAGTCA 2100  
OY 2101 GGCACAGAGAAACCTACCACTCATGGAAGGTAAAGAACTTGCAACCTGAGCCAGAAAGA 2160  
DB 2101 GGCACAGAGAAACCTACCACTCATGGAAGGTAAAGAACTTGCAACCTGAGCCAGAAAGA 2160  
OY 2161 GTAACACCCCAATGAACAGAACAAATGAAGACAGATGATCTTTCCAGAGCTGA 2220  
DB 2161 GTAACACCCCAATGAACAGAACAAATGAAGACAGATGATCTTTCCAGAGCTGA 2220  
OY 2221 AGTTAAACAATGSCACTGGTCTTTTACTTAAGTTCACAAATACAGTGAATCTTAAGAAT 2280  
DB 2221 AGTTAAACAATGSCACTGGTCTTTTACTTAAGTTCACAAATACAGTGAATCTTAAGAAT 2280  
OY 2281 TTGTCAATCTTACGCTTCCAGAGAAAGAAAGAAAGAAAGAAAGTAAAGTGT 2340  
DB 2281 TTGTCAATCTTACGCTTCCAGAGAAAGAAAGAAAGAAAGTAAAGTGT 2340  
OY 2341 CTAATTAATGCTGAACACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTGGCAACTG 2400  
DB 2341 CTAATTAATGCTGAACACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTGGCAACTG 2400  
OY 2401 AAAGATCTGTAAGAGTAGAGTATTTTCACTGTGTAAGTGAAGTGAAGTGAAGTGAAG 2460  
DB 2401 AAAGATCTGTAAGAGTAGAGTATTTTCACTGTGTAAGTGAAGTGAAGTGAAGTGAAG 2460  
OY 2461 AAAGATCTGTAAGAGTAGAGTATTTTCACTGTGTAAGTGAAGTGAAGTGAAGTGAAG 2520  
DB 2461 AAAGATCTGTAAGAGTAGAGTATTTTCACTGTGTAAGTGAAGTGAAGTGAAGTGAAG 2520  
OY 2521 GTGTAGTCAAGTGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2580  
DB 2521 GTGTAGTCAAGTGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2580  
OY 2581 ATTAATAGAAATGACACAGAAAGCTTAAAGTATCCATTGGGACATGAAGTGAAGTGAAG 2640  
DB 2581 ATTAATAGAAATGACACAGAAAGCTTAAAGTATCCATTGGGACATGAAGTGAAGTGAAG 2640  
OY 2641 GGGAAACAAGCATAGAAATGGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2700  
DB 2641 GGGAAACAAGCATAGAAATGGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2700  
OY 2701 TCAAGTTTCAAGAGGCGCAGTATTTGCTGTGTTTCAATTCAGAGAAATGCAAGAGG 2760  
DB 2701 TCAAGTTTCAAGAGGCGCAGTATTTGCTGTGTTTCAATTCAGAGAAATGCAAGAGG 2760  
OY 2761 AATGCAACATTTCTGCGCCACTGTGGTCTTAAAGAAACAAGTCCAAAGTCACTT 2820  
DB 2761 AATGCAACATTTCTGCGCCACTGTGGTCTTAAAGAAACAAGTCCAAAGTCACTT 2820  
OY 2821 TTGAATGGAACAAAGAAAGAAATCAAGAAAGATGATCTAATCAAGCTGTAC 2880  
DB 2821 TTGAATGGAACAAAGAAAGAAATCAAGAAAGATGATCTAATCAAGCTGTAC 2880  
OY 2881 AGACAGTTAATTCATCTGAGGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2940  
DB 2881 AGACAGTTAATTCATCTGAGGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2940  
OY 2941 ATGCAAAATGTAATCAAGAGGCTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3000  
DB 2941 ATGCAAAATGTAATCAAGAGGCTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3000  
OY 3001 AGCAAACTGAGTCACTTCCAAATTAACATGACCTTTTACAAACCATATGCTATAC 3060  
DB 3001 AGCAAACTGAGTCACTTCCAAATTAACATGACCTTTTACAAACCATATGCTATAC 3060  
OY 3061 CACCACTTTTCCATCAAGTATTTGTTAAACTTAATGTAAGAAATCTGCTAGAGG 3120  
DB 3061 CACCACTTTTCCATCAAGTATTTGTTAAACTTAATGTAAGAAATCTGCTAGAGG 3120

OY 3121 AAACTTGGAGAACATTCATATGTCACCTGAAGAAAGAAATGGAATGGAACATTTCCA 3180  
DB 3121 AAACTTGGAGAACATTCATATGTCACCTGAAGAAAGAAATGGAATGGAACATTTCCA 3180  
OY 3181 GTACAGTGAAGCAATTTGCCGTATTAATTAAGAAATGTTTAAAGAGCCAGCT 3240  
DB 3181 GTACAGTGAAGCAATTTGCCGTATTAATTAAGAAATGTTTAAAGAGCCAGCT 3240  
OY 3241 CAAGCAATTAATGAATAGGTTCCAGTACATTAATGAAGTGGGCTCCAGTATTAATGA 3300  
DB 3241 CAAGCAATTAATGAATAGGTTCCAGTACATTAATGAAGTGGGCTCCAGTATTAATGA 3300  
OY 3301 TAGGTTCCAGTATGAAGAAATTCAGAGCAAGTATGTAAGAAACAGAGGCCAAATTTGA 3360  
DB 3301 TAGGTTCCAGTATGAAGAAATTCAGAGCAAGTATGTAAGAAACAGAGGCCAAATTTGA 3360  
OY 3361 ATGCTATGCTTATGATTTAGGGGTTTGGCACTGAGGCTATTAACAAAGTCTTGGA 3420  
DB 3361 ATGCTATGCTTATGATTTAGGGGTTTGGCACTGAGGCTATTAACAAAGTCTTGGA 3420  
OY 3421 GTAATTTGACATCTGAAATTAAGAAAGCAAGAAATTAAGAAAGTATTCAGACTGTA 3480  
DB 3421 GTAATTTGACATCTGAAATTAAGAAAGCAAGAAATTAAGAAAGTATTCAGACTGTA 3480  
OY 3481 ATACAGATTTCTTCATATCTGATTTTCAAGTAACTTAAGAAACAGCCTTGGGAATGATC 3540  
DB 3481 ATACAGATTTCTTCATATCTGATTTTCAAGTAACTTAAGAAACAGCCTTGGGAATGATC 3540  
OY 3541 ATGCTATGAGTGTGTTGTTGTAAGACCTGATGACCTGTTAGATGATGTTGAATTAAG 3600  
DB 3541 ATGCTATGAGTGTGTTGTTGTAAGACCTGATGACCTGTTAGATGATGTTGAATTAAG 3600  
OY 3601 AAGATCTAGTGTGTTGTTGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3660  
DB 3601 AAGATCTAGTGTGTTGTTGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3660  
OY 3661 TCCAGAGAGAGGCTTACAGAGAGTCTTACGCTTACACCATACATTTGGCTCAGG 3720  
DB 3661 TCCAGAGAGAGGCTTACAGAGAGTCTTACGCTTACACCATACATTTGGCTCAGG 3720  
OY 3721 GTTACCGAAGAGGCGCAGAAATTAAGTCTCAGAAAGAACTTATCTAGTGAAGTGA 3780  
DB 3721 GTTACCGAAGAGGCGCAGAAATTAAGTCTCAGAAAGAACTTATCTAGTGAAGTGA 3780  
OY 3781 AAGAGCTTCCGCTTCCAAACATTTGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3840  
DB 3781 AAGAGCTTCCGCTTCCAAACATTTGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3840  
OY 3841 CTACTAGGCAATAGCACCGTGTCTACCGAGTGTCTGTCTAAGAACACAGAGGAATTTAT 3900  
DB 3841 CTACTAGGCAATAGCACCGTGTCTACCGAGTGTCTGTCTAAGAACACAGAGGAATTTAT 3900  
OY 3901 TATCATTTGAAGATGCTTAAATGAATGATGATGATGATGATGATGATGATGATGATGAT 3960  
DB 3901 TATCATTTGAAGATGCTTAAATGAATGATGATGATGATGATGATGATGATGATGATGAT 3960  
OY 3961 AGGAACATCACCTTAGTGAAGAAACAATGTTGCTGAGTGTGTTCTTCAAGTGA 4020  
DB 3961 AGGAACATCACCTTAGTGAAGAAACAATGTTGCTGAGTGTGTTCTTCAAGTGA 4020  
OY 4021 GTGAATTTGAAGACTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 4080  
DB 4021 GTGAATTTGAAGACTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 4080  
OY 4081 CCAAAACAATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4140  
DB 4081 CCAAAACAATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4140  
OY 4141 TTTTCAAGATGAAGAAAGAGAAAGGCGGCTTGAAGAAATTAATCAAGAGCAAGCA 4200  
DB 4141 TTTTCAAGATGAAGAAAGAGAAAGGCGGCTTGAAGAAATTAATCAAGAGCAAGCA 4200  
OY 4201 TGAATTTCAACTTATGATGAAGACAGATCTGGGTGTGAAGTGAAGCAAGCGTCTGTAAG 4260

```

Db      4201 TGGATTCAAACTTGAGTGTGAAACAGATCTGGGTGTGAGATGAAACAAGCCTCTCTGAG 4260
Qy      4261 ACTGCTCAGGGCTATTCCTCTCAGAGTGCATTTTAAACACTCAGAGAGGGATACCAATGC 4320
Db      4261 ACTGCTCAGGGCTATTCCTCTCAGAGTGCATTTTAAACACTCAGAGAGGGATACCAATGC 4320
Qy      4321 AACATTAACCTGATAAAGCTCCAGCAGAAATGCGTGAATCTAGAAAGCTGTGTAGAACAGC 4380
Db      4321 AACATTAACCTGATAAAGCTCCAGCAGAAATGCGTGAATCTAGAAAGCTGTGTAGAACAGC 4380
Qy      4381 ATGGAGAGCAGCCTTCTTAACAGCTACCTTCATCAATAGTACTCCTCTGCTGAGG 4440
Db      4381 ATGGAGAGCAGCCTTCTTAACAGCTACCTTCATCAATAGTACTCCTCTGCTGAGG 4440
Qy      4441 ACCGCGAAATCCGAAGAAAGCAATAGAGAAAAGAGTAACTTAATCTTCAAGAAAATA 4500
Db      4441 ACCGCGAAATCCGAAGAAAGCAATAGAGAAAAGAGTAACTTCAAGAAAATA 4500
Qy      4501 GTGAATACCTATTAAGCAGAAATCCAGAAAGCCTTCTGCTGACAAAGTTTGAAGGTCTG 4560
Db      4501 GTGAATACCTATTAAGCAGAAATCCAGAAAGCCTTCTGCTGACAAAGTTTGAAGGTCTG 4560
Qy      4561 CAGATAGTTCTACAGATAAAATAAAGAACAGAGTGAAGAGTCAATCCCTCTTAAT 4620
Db      4561 CAGATAGTTCTACAGATAAAATAAAGAACAGAGTGAAGAGTCAATCCCTCTTAAT 4620
Qy      4621 GCCCATCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4680
Db      4621 GCCCATCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4680
Qy      4681 ACTACCCATCTCAAGAGAGGCTCAATTAAGTTGATGATGATGATGATGATGATGATGATGAT 4740
Db      4681 ACTACCCATCTCAAGAGAGGCTCAATTAAGTTGATGATGATGATGATGATGATGATGATGAT 4740
Qy      4741 AGTCTGGGCGCAGCAGATTGACGAAACATCTTAATCTTCCAGAGCAAGATCTAGAGGAA 4800
Db      4741 AGTCTGGGCGCAGCAGATTGACGAAACATCTTAATCTTCCAGAGCAAGATCTAGAGGAA 4800
Qy      4801 CCCCTTACTGGAATCTGGAATCAAGCCTCTCTCTGATGACCTGATATCTGATCTCTG 4860
Db      4801 CCCCTTACTGGAATCTGGAATCAAGCCTCTCTCTGATGACCTGATATCTGATCTCTG 4860
Qy      4861 AAGACAGAGCCCGAGTCACTGCTGTGTGCAACATCCATCTTCAACCTCTGATGTA 4920
Db      4861 AAGACAGAGCCCGAGTCACTGCTGTGTGCAACATCCATCTTCAACCTCTGATGTA 4920
Qy      4921 AAGTCCCAATTTGAAAGTTGACAGATCTGCGCAGAGTCCAGCTGCTCTCATCTACTG 4980
Db      4921 AAGTCCCAATTTGAAAGTTGACAGATCTGCGCAGAGTCCAGCTGCTCTCATCTACTG 4980
Qy      4981 ATACTGCTGGGTATATGCAATGGAAGAGTGTGAGCAGAGGAGAAAGCCAGAAATTTGACG 5040
Db      4981 ATACTGCTGGGTATATGCAATGGAAGAGTGTGAGCAGAGGAGAAAGCCAGAAATTTGACG 5040
Qy      5041 CTTGAACGAAAGGTTGAAAGAAAGTCCATGCTGTGTGCTGTGCTGTGACCCAGAG 5100
Db      5041 CTTGAACGAAAGGTTGAAAGAAAGTCCATGCTGTGTGCTGTGCTGTGACCCAGAG 5100
Qy      5101 AATTATGCTGCTGTACAAAGTTTGCAGAAAACCAATCACTTAATCTTAATTA 5160
Db      5101 AATTATGCTGCTGTACAAAGTTTGCAGAAAACCAATCACTTAATCTTAATTA 5160
Qy      5161 CTGAAGAGACTACTCATGTGTGTATGAAACAGATGCTGAAGTTGTGTGTAACGACAC 5220
Db      5161 CTGAAGAGACTACTCATGTGTGTATGAAACAGATGCTGAAGTTGTGTGTAACGACAC 5220
Qy      5221 TGAATATATTTCTAGGAATTCGCGGAGGAAATGGGTAGTATAGTATTTCTGGGTGACCC 5280
Db      5221 TGAATATATTTCTAGGAATTCGCGGAGGAAATGGGTAGTATAGTATTTCTGGGTGACCC 5280
Qy      5281 AGTCTATTAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCTAGAGAGATGCG 5340

```

```

Db      5341 AGTCTATTAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGATGCG 5340
Qy      5341 TCAATGAGAGAAACCAACAGGTCCTCAAGAGGAGCAAGATTCACAGAGCAAGAAATCT 5400
Db      5341 TCAATGAGAGAAACCAACAGGTCCTCAAGAGGAGCAAGATTCACAGAGCAAGAAATCT 5400
Qy      5401 TCAGGGGCTGAAATCTGTGTGCTATGAGGCTTCAACCAATGCTCCACAGATCACTG 5460
Db      5401 TCAGGGGCTGAAATCTGTGTGCTATGAGGCTTCAACCAATGCTCCACAGATCACTG 5460
Qy      5461 AATGATGATGACGCTGTGTGTCTCTGTGTGTGTAAGAGCTTTCATCATCCTTG 5520
Db      5461 AATGATGATGACGCTGTGTGTCTCTGTGTGTGTAAGAGCTTTCATCATCCTTG 5520
Qy      5521 GCACAGGTGTCACCAATGCTGTGTGTGTCAGAGCAAGATGCTGACAGAGCAATGCT 5580
Db      5521 GCACAGGTGTCACCAATGCTGTGTGTGTCAGAGCAAGATGCTGACAGAGCAATGCT 5580
Qy      5581 TCCATGCAATTTGGCAGATGATGATGAGCAGCCTGTGTGACCCGAGAGTGGTGTGACA 5640
Db      5581 TCCATGCAATTTGGCAGATGATGATGAGCAGCCTGTGTGACCCGAGAGTGGTGTGACA 5640
Qy      5641 GTGTAGCACTCTACAGTGTGAGGAGCTGACACCTTACTGATACCCAGATCCCCACA 5700
Db      5641 GTGTAGCACTCTACAGTGTGAGGAGCTGACACCTTACTGATACCCAGATCCCCACA 5700
Qy      5701 GCCACTACTGA 5711
Db      5701 GCCACTACTGA 5711

RESULT 3
US-08-825-487A-1
; Sequence 1, Application US/08825487A
; Patent No. 6048689
; GENERAL INFORMATION:
; APPLICANT: Murphy, Patricia D.
; APPLICANT: White, Margie B.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING VARIATIONS IN POLYNUCLEOTIDE SEQUENCE
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESS: Howrey & Simon
; STREET: 1299 Pennsylvania Avenue., N.W.
; CITY: Washington,
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/825,487A
; FILING DATE: 28-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/060002
; FILING DATE: 26-Mar-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Albert P. Halluin
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 05371.0012.999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-463-8100
; TELEFAX: 650-463-8400
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5711 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear

```

MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
STRAIN: BRCA1  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17  
MAP POSITION: 17q21  
US-08-825-487A-1

Query Match 100.0%; Score 5711; DB 3; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 AGCTCGTAGAGACTTCTGTGACCCCGCAGCGCTGTGGGGTTCTGATTAACCTGGGCC 60
Db 1 AGCTCGTAGAGACTTCTGTGACCCCGCAGCGCTGTGGGGTTCTGATTAACCTGGGCC 60
QY 61 CCTGGGCTCAGAGAGCCCTTCACTCTGCTGTGGGTAAAGTTCAATGGACAGAAAGAA 120
Db 61 CCTGGGCTCAGAGAGCCCTTCACTCTGCTGTGGGTAAAGTTCAATGGACAGAAAGAA 120
QY 121 TGGATTTATCTGCTCTTGGCGTTGAAGATGCAAAATGTCATTATGCTATGCAAGAAA 180
Db 121 TGGATTTATCTGCTCTTGGCGTTGAAGATGCAAAATGTCATTATGCTATGCAAGAAA 180
QY 181 TCTTAGAGTGTCCCATCTGTCTGAGGTGATCAAGAACTGTCTCCAAAGTGTGACC 240
Db 181 TCTTAGAGTGTCCCATCTGTCTGAGGTGATCAAGAACTGTCTCCAAAGTGTGACC 240
QY 241 ACATATTTTGGCAATTTTGCATGTGAACTTCTCAACAGAAAGAAAGGCGCTTCAAGT 300
Db 241 ACATATTTTGGCAATTTTGCATGTGAACTTCTCAACAGAAAGAAAGGCGCTTCAAGT 300
QY 301 GTCCCTTATGTAAGATGATATTAACCAAAAGAGGCTTCAAGAAAGTACGATTTATGTC 360
Db 301 GTCCCTTATGTAAGATGATATTAACCAAAAGAGGCTTCAAGAAAGTACGATTTATGTC 360
QY 361 AACTGTGGAAGAGCTATTTGAAATCATTTGCTTTGCTTTGAGCTTGACACAGGTTTGAGT 420
Db 361 AACTGTGGAAGAGCTATTTGAAATCATTTGCTTTGAGCTTTGAGCTTGAGT 420
QY 421 ATGCAAAAGAGCTATTAATTTTGCAGAAAGAAATTAATCTCTCTGAAATCTTAAGATG 480
Db 421 ATGCAAAAGAGCTATTAATTTTGCAGAAAGAAATTAATCTCTCTGAAATCTTAAGATG 480
QY 481 AAGTTTCTATCATCCAAAGTATGGGCTTCAAGAAACCGTCCAAAGATCTTCTACAGAGTG 540
Db 481 AAGTTTCTATCATCCAAAGTATGGGCTTCAAGAAACCGTCCAAAGATCTTCTACAGAGTG 540
QY 541 AACCGGAAATCTCTTGTGAGGAAACAGTCTCAGTGTCAACTCTCTAAGCTTTGGA 600
Db 541 AACCGGAAATCTCTTGTGAGGAAACAGTCTCAGTGTCAACTCTCTAAGCTTTGGA 600
QY 601 CTGTGAGAACTCTGAGCAAAAGCAGCGGATTAACAATCTCAAAAGAGCTCTGTCTACATTG 660
Db 601 CTGTGAGAACTCTGAGCAAAAGCAGCGGATTAACAATCTCAAAAGAGCTCTGTCTACATTG 660
QY 661 AATTGGAGTCTGATCTTCTGAAATACCGTTAATTAAGCACTTATTGCGAGTGGAG 720
Db 661 AATTGGAGTCTGATCTTCTGAAATACCGTTAATTAAGCACTTATTGCGAGTGGAG 720
QY 721 ATCAAGATTTGTAACAATCAACCCCTCAAGGAACAGGAGTGAATTCAGTTTGGATTCTG 780
Db 721 ATCAAGATTTGTAACAATCAACCCCTCAAGGAACAGGAGTGAATTCAGTTTGGATTCTG 780
QY 781 CAAAAAAGGCTGTGTGTAATTTTCTGAGCGGATTAACAATCTGAGATCATCAAC 840
Db 781 CAAAAAAGGCTGTGTGTAATTTTCTGAGCGGATTAACAATCTGAGATCATCAAC 840
QY 841 CCAAGTAATTAATGATTGTAACACACTGAGAAAGCTGCACTGAGAGGCAATCCAGAAAGT 900
Db 841 CCAAGTAATTAATGATTGTAACACACTGAGAAAGCTGCACTGAGAGGCAATCCAGAAAGT 900
QY 900 CAGTAATTAATGATTGTAACACACTGAGAAAGCTGCACTGAGAGGCAATCCAGAAAGT 900
Db 900 CAGTAATTAATGATTGTAACACACTGAGAAAGCTGCACTGAGAGGCAATCCAGAAAGT 900
```

```
QY 901 ATCAGGTAATCTGTTCACAACTTGATGTGAGCCATGTGCAAAATCTCATGCCA 960
Db 901 ATCAGGTAATCTGTTCACAACTTGATGTGAGCCATGTGCAAAATCTCATGCCA 960
QY 961 GCTCATTAACAGCATGAGAACAGAGTTTATTACTCACTTAAGACAGATGATAGAAA 1020
Db 961 GCTCATTAACAGCATGAGAACAGAGTTTATTACTCACTTAAGACAGATGATAGAAA 1020
QY 1021 AGGCTGAATCTGTAAATTAAGCAACAGCTGGCTTGAAGAGGCAACATTAACGAT 1080
Db 1021 AGGCTGAATCTGTAAATTAAGCAACAGCTGGCTTGAAGAGGCAACATTAACGAT 1080
QY 1081 GGGCTGAGAGTAAGAAACATGTAATGATAGCGGACTCCAGACAGAAAAAGGTAG 1140
Db 1081 GGGCTGAGAGTAAGAAACATGTAATGATAGCGGACTCCAGACAGAAAAAGGTAG 1140
QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAAAGAAAGATGAAATAGCAGAAACTGCCATGCT 1200
Db 1141 ATCTGAATGCTGATCCCTGTGTGAGAAAGAAAGATGAAATAGCAGAAACTGCCATGCT 1200
QY 1201 CAGGAATCTCAGATATCTGAAGATGTTCTTGGATTAACCTAATTAAGCAGATTGAGA 1260
Db 1201 CAGGAATCTCAGATATCTGAAGATGTTCTTGGATTAACCTAATTAAGCAGATTGAGA 1260
QY 1261 AAGTTAATGAGTGGTTTCCAGAGATGATGAATGTTAGGTTCTGATGACTCAGATGATG 1320
Db 1261 AAGTTAATGAGTGGTTTCCAGAGATGATGAATGTTAGGTTCTGATGACTCAGATGATG 1320
QY 1321 GGGAGTCTGAATCAAAATGCCAAAGTACGTATGTTAGACGTTCTAATGAGGTAGATG 1380
Db 1321 GGGAGTCTGAATCAAAATGCCAAAGTACGTATGTTAGACGTTCTAATGAGGTAGATG 1380
QY 1381 AATTTCTGTTTCTTCAGAGAAATTAAGCTTACGCGCAGATGCTCATAGGCTTTAA 1440
Db 1381 AATTTCTGTTTCTTCAGAGAAATTAAGCTTACGCGCAGATGCTCATAGGCTTTAA 1440
QY 1441 TATGTAAAGTGAAGAGTTCATCCAAATCAGTAGAGATTAATTTGAAGACAAATAT 1500
Db 1441 TATGTAAAGTGAAGAGTTCATCCAAATCAGTAGAGATTAATTTGAAGACAAATAT 1500
QY 1501 TTGGGAAAACCTATCGAAGAGGCAAGCTCCCAACTTAAGCATGTAACTGAATATC 1560
Db 1501 TTGGGAAAACCTATCGAAGAGGCAAGCTCCCAACTTAAGCATGTAACTGAATATC 1560
QY 1561 TAAATTAAGAGCAATTTGTAATGAGCAAGATTAACAAGAGTCCCTCAAAATA 1620
Db 1561 TAAATTAAGAGCAATTTGTAATGAGCAAGATTAACAAGAGTCCCTCAAAATA 1620
QY 1621 AATTAAGCGTAAAGAGAGACTCATCAGGCTTCAATCTGAGATTTTATCAAGAAAG 1680
Db 1621 AATTAAGCGTAAAGAGAGACTCATCAGGCTTCAATCTGAGATTTTATCAAGAAAG 1680
QY 1681 CAGATTTGGCAGTTCAAAAGACTCTGAAATGATTAATCAAGGAACTTAACCAACGAGAC 1740
Db 1681 CAGATTTGGCAGTTCAAAAGACTCTGAAATGATTAATCAAGGAACTTAACCAACGAGAC 1740
QY 1741 AGAATGTCAGATGATTAATTAATTAATGATGATGATGAGAAATTAACAAGAGTAT 1800
Db 1741 AGAATGTCAGATGATTAATTAATTAATGATGATGATGAGAAATTAACAAGAGTAT 1800
QY 1801 CTATTCAGATGAGAAAAATCTTAACCAATTAAGATCACTGAGAAAAAGATCTGCTTCA 1860
Db 1801 CTATTCAGATGAGAAAAATCTTAACCAATTAAGATCACTGAGAAAAAGATCTGCTTCA 1860
QY 1861 AAACGAAAGCTGAACCTTAAGAGAGAGTATTAAGCAATTAAGAACTGGAATTAATATCC 1920
Db 1861 AAACGAAAGCTGAACCTTAAGAGAGAGTATTAAGCAATTAAGAACTGGAATTAATATCC 1920
QY 1921 ACAATTTCAAAAGCACTTAAGAAAGATAGGCTGAGAGAGAGTCTTCAACAGGATATTC 1980
Db 1921 ACAATTTCAAAAGCACTTAAGAAAGATAGGCTGAGAGAGAGTCTTCAACAGGATATTC 1980
QY 1981 ATGCGCTTGAACCTAGTAGTGAATCTTAAGCCCACTTAATTTGATGAATTTGCAAA 2040
Db 1981 ATGCGCTTGAACCTAGTAGTGAATCTTAAGCCCACTTAATTTGATGAATTTGCAAA 2040
```



QY 4201 TGAATTCAACTTAGTGAAGCAGCATCTGGTGTGAGTGAAGAAACAAGGCTCTGGAAG 4260  
Db 4201 TGAATTCAACTTAGTGAAGCAGCATCTGGTGTGAGTGAAGAAACAAGGCTCTGGAAG 4260  
QY 4261 ACTGCTCAGGGCTATCTCTCAGAGTGAACATTTTAACTCAGCAGAGGGAATACATGC 4320  
Db 4261 ACTGCTCAGGGCTATCTCTCAGAGTGAACATTTTAACTCAGCAGAGGGAATACATGC 4320  
QY 4321 AACATAACTGATTAAGCTCCAGCAGAGAAATGCTGAACCTAAGAGCTGTGTGAACAGC 4380  
Db 4321 AACATAACTGATTAAGCTCCAGCAGAGAAATGCTGAACCTAAGAGCTGTGTGAACAGC 4380  
QY 4381 ATGGAGACGACGCTTCAACAGCATCCCTTCATCAATGAATGATCTCTGCTGCTTGAAG 4440  
Db 4381 ATGGAGACGACGCTTCAACAGCATCCCTTCATCAATGAATGATCTCTGCTGCTTGAAG 4440  
QY 4441 ACCTCGGAATTCAGAAACAAGCAGCATCAGAAAAGAGATTAATTTCAACAGAAAAGTA 4500  
Db 4441 ACCTCGGAATTCAGAAACAAGCAGCATCAGAAAAGAGATTAATTTCAACAGAAAAGTA 4500  
QY 4501 GTGAATACCTTAATAGCCAGATCCAGAGGCTTTCTGCTGACAACTTGAAGTGTCTG 4560  
Db 4501 GTGAATACCTTAATAGCCAGATCCAGAGGCTTTCTGCTGACAACTTGAAGTGTCTG 4560  
QY 4561 CAGATAGTCTACCCAGTAAATAAGAACAGAGAGGAAAGGTCAATCCCTCTTAAT 4620  
Db 4561 CAGATAGTCTACCCAGTAAATAAGAACAGAGAGGAAAGGTCAATCCCTCTTAAT 4620  
QY 4621 GCCCATCATTAAGATAGGTGTATGACAGATGCTGAGAGTCTTCAAGATGAAG 4680  
Db 4621 GCCCATCATTAAGATAGGTGTATGACAGATGCTGAGAGTCTTCAAGATGAAG 4680  
QY 4681 ACTATCCATCTCAAGAGAGGCTCAATTAAGTGTGTATGTGAGAGCAACAGCTGAAG 4740  
Db 4681 ACTATCCATCTCAAGAGAGGCTCAATTAAGTGTGTATGTGAGAGCAACAGCTGAAG 4740  
QY 4741 AGTCTGGGCAACAGATTTGCGGAAACATCTTACTTCCAGAGCAGATCTAGAGGAA 4800  
Db 4741 AGTCTGGGCAACAGATTTGCGGAAACATCTTACTTCCAGAGCAGATCTAGAGGAA 4800  
QY 4801 CCCCTTAAGTGAATCTGAATCAGCTCTTCTCTGATGAACCTTGAATCTGATCTCTG 4860  
Db 4801 CCCCTTAAGTGAATCTGAATCAGCTCTTCTCTGATGAACCTTGAATCTGATCTCTG 4860  
QY 4861 AAGACAGAGCCCGAGATCAGCTGTGTGTGCAACATCACTTTCAACTCTGCAATTA 4920  
Db 4861 AAGACAGAGCCCGAGATCAGCTGTGTGTGCAACATCACTTTCAACTCTGCAATTA 4920  
QY 4921 AAGTTCCTCAATTAAGATGAGATCTGCGGAGGTCAGAGCTGCTCATCTACTG 4980  
Db 4921 AAGTTCCTCAATTAAGATGAGATCTGCGGAGGTCAGAGCTGCTCATCTACTG 4980  
QY 4981 ATACTGCTGGGTATTAATGCAATGGAAGAAAGTGTGACAGAGGAAACAGAAATGACAG 5040  
Db 4981 ATACTGCTGGGTATTAATGCAATGGAAGAAAGTGTGACAGAGGAAACAGAAATGACAG 5040  
QY 5041 CTTCAACAGAAAGGCTCAACAAAAGATGTCCATGTGTGTCTGCTGACCCCAAG 5100  
Db 5041 CTTCAACAGAAAGGCTCAACAAAAGATGTCCATGTGTGTCTGCTGACCCCAAG 5100  
QY 5101 AATTATGCTGCTATACAGATTTGCCAGAAAACAGCATCACTTAATCTAATTA 5160  
Db 5101 AATTATGCTGCTATACAGATTTGCCAGAAAACAGCATCACTTAATCTAATTA 5160  
QY 5161 CTGAAGAGACTACTACTGTGTATGAAGAAAGATGTGTGTGTGAACGAGAC 5220  
Db 5161 CTGAAGAGACTACTACTGTGTATGAAGAAAGATGTGTGTGTGAACGAGAC 5220  
QY 5221 TGAATATTTTCTTAGAATTTGCGGAGAGAAATGGGTATGTTAGTATTTCTGGGTGACC 5280  
Db 5221 TGAATATTTTCTTAGAATTTGCGGAGAGAAATGGGTATGTTAGTATTTCTGGGTGACC 5280

QY 5281 AGTCTATTAAGAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGATGTGG 5340  
Db 5281 AGTCTATTAAGAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGATGTGG 5340  
QY 5341 TCAATGAAGAAACCAACCAAGGTCAAAGGAGCAAGAAATCCAGACAGAAAGATCT 5400  
Db 5341 TCAATGAAGAAACCAACCAAGGTCAAAGGAGCAAGAAATCCAGACAGAAAGATCT 5400  
QY 5401 TCAGGGGGCTAGAAATCTGTGTATGGGCTTCAACCAACATGCCCCAGATCACTG 5460  
Db 5401 TCAGGGGGCTAGAAATCTGTGTATGGGCTTCAACCAACATGCCCCAGATCACTG 5460  
QY 5461 AATGATGTGACAGCTGTGTGTGCTTCTGTGTGAAGAGCTTTCATCACTTCACTT 5520  
Db 5461 AATGATGTGACAGCTGTGTGTGCTTCTGTGTGAAGAGCTTTCATCACTTCACTT 5520  
QY 5521 GCAAGGTGTCAACCAATTTGTGTGTGAGCAGATGCTTGAACAGAGCAATGCT 5580  
Db 5521 GCAAGGTGTCAACCAATTTGTGTGTGAGCAGATGCTTGAACAGAGCAATGCT 5580  
QY 5581 TCCATCAATTTGGGAGATGTGTGAGCACTGTGTGACCCGAGATGGGTGTGACA 5640  
Db 5581 TCCATCAATTTGGGAGATGTGTGAGCACTGTGTGACCCGAGATGGGTGTGACA 5640  
QY 5641 GTGTAGCACTCTACAGTGCAGAGCTGAGACACTAAGATATACCAATCCCA 5700  
Db 5641 GTGTAGCACTCTACAGTGCAGAGCTGAGACACTAAGATATACCAATCCCA 5700  
QY 5701 GCCACTACTGA 5711  
Db 5701 GCCACTACTGA 5711

RESULT 4  
US-09-074-476-1  
Sequence 1, Application US/09074476  
Patent No. 6130322  
GENERAL INFORMATION:  
APPLICANT: Murphy, Patricia D.  
APPLICANT: Allen, Antoinette C.  
APPLICANT: Alvarez, Christopher P.  
APPLICANT: Ciliz, Brenda S.  
APPLICANT: Olson, Sheri J.  
APPLICANT: Thurber, Denise  
APPLICANT: Zeng, Bin  
TITLE OF INVENTION: Coding Sequences of the Human  
TITLE OF INVENTION: BRCA1 Gene  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howrey & Simon  
STREET: 1299 Pennsylvania Avenue N. W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/074,476  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/074,453  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Albert P. Halluin  
REGISTRATION NUMBER: 25,227  
REFERENCE/DOCKET NUMBER: 5371.34.US01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-463-8109

TELEFAX: 650-463-8400  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5711 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
STRAIN: BRC1 (omit)  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17  
MAP POSITION: 17q21  
US-09-074-476-1

Query Match 100.0%; Score 5711; DB 3; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGCTGAGACTTCTGGACCCGACAGGCTGTGGGTTTCTGAGTAACTGGGCC 60  
DB 1 AGCTGCTGAGACTTCTGGACCCGACAGGCTGTGGGTTTCTGAGTAACTGGGCC 60  
QY 61 CTTGCGCTCAGAGGCTTCACTCTGCTGTGGTAAAGTTCAATTG3AA CAGAAAGAA 120  
DB 61 CTTGCGCTCAGAGGCTTCACTCTGCTGTGGTAAAGTTCAATTG3AA CAGAAAGAA 120  
QY 121 TGGATTATCTGCTCTTGGGTTGAAGAGTAACTAAATGTCATTAATGCTATGCAAAA 180  
DB 121 TGGATTATCTGCTCTTGGGTTGAAGAGTAACTAAATGTCATTAATGCTATGCAAAA 180  
QY 181 TCTTAGAGTGTCCATCTGTCTGGAGTTGATCAAGAAAGCTGTCTCAAGAAAGTGACC 240  
DB 181 TCTTAGAGTGTCCATCTGTCTGGAGTTGATCAAGAAAGCTGTCTCAAGAAAGTGACC 240  
QY 241 ACATATTTTCAAAATTTTGATGCTGAACTTCTCAACAGAAAGAAAGGCTTCAAGT 300  
DB 241 ACATATTTTCAAAATTTTGATGCTGAACTTCTCAACAGAAAGAAAGGCTTCAAGT 300  
QY 301 GTCTTTATGTAAGATGATATTAACAAAGAGGCTTCAAGAAAGTACGAGATTAGTC 360  
DB 301 GTCTTTATGTAAGATGATATTAACAAAGAGGCTTCAAGAAAGTACGAGATTAGTC 360  
QY 361 AACTGTGTAAGAGCTATTTGAAAATCAATTTGTGTTTCACTTGAACAAGTTGAGT 420  
DB 361 AACTGTGTAAGAGCTATTTGAAAATCAATTTGTGTTTCACTTGAACAAGTTGAGT 420  
QY 421 ATGCAAAAGAGCTATTTTGAAGAAAGAAATACTCTCTGAGACATCTAAAGATG 480  
DB 421 ATGCAAAAGAGCTATTTTGAAGAAAGAAATACTCTCTGAGACATCTAAAGATG 480  
QY 481 AAGTTTCTATCAATCAAGATATGGGCTACAGAAACGCTGCCAAAGACTTCAAGAGT 540  
DB 481 AAGTTTCTATCAATCAAGATATGGGCTACAGAAACGCTGCCAAAGACTTCAAGAGT 540  
QY 541 AACCAGAAATCTCTCTTCTGAGAAACAGCTCTCACTGTCCTTCAACTCTTGA 600  
DB 541 AACCAGAAATCTCTCTTCTGAGAAACAGCTCTCACTGTCCTTCAACTCTTGA 600  
QY 601 CTGTGAGAACTCTGAGAGCAAGAGCGAGATCAACTCTCAAGAGAGCTCTGTCTACATTTG 660  
DB 601 CTGTGAGAACTCTGAGAGCAAGAGCGAGATCAACTCTCAAGAGAGCTCTGTCTACATTTG 660  
QY 661 AATTGGATCTGATCTTCTGAGAGTACCGTTAATTAAGCACTTAATGCAAGTGTGAG 720  
DB 661 AATTGGATCTGATCTTCTGAGAGTACCGTTAATTAAGCACTTAATGCAAGTGTGAG 720  
QY 721 ATCAAGAAATGTTTCAAAATCAAGAGTCAAGAGTCAAGAGTCAAGTGTGATTTCTG 780  
DB 721 ATCAAGAAATGTTTCAAAATCAAGAGTCAAGAGTCAAGAGTCAAGTGTGATTTCTG 780  
QY 781 CAAAAAGGCTGTTGTAATTTTCTGAGACGAGATGTAACAAATATGAGACATCATCAC 840

DB 781 CAAAAAGGCTGTTGTAATTTTCTGAGACGAGATGTAACAAATATGAGACATCATCAC 840  
QY 841 CAGATAATATGATTTTGAACACAGAGAGGCTGAGAGGCTCCGAAAGT 900  
DB 841 CAGATAATATGATTTTGAACACAGAGAGGCTGAGAGGCTCCGAAAGT 900  
QY 901 ATCAGAGTATGTTCTGTTCAAACTTGCATGTGAGAGCCATGTGCACAATATCATGCCA 960  
DB 901 ATCAGAGTATGTTCTGTTCAAACTTGCATGTGAGAGCCATGTGCACAATATCATGCCA 960  
QY 961 GCTCATTACAGCATGAGAACAGCAGTTATTACTCACTAAAGACAGATGTAGAAA 1020  
DB 961 GCTCATTACAGCATGAGAACAGCAGTTATTACTCACTAAAGACAGATGTAGAAA 1020  
QY 1021 AGGCTGAATCTGTATTAATTAAGCAACAGCTGGCTTGAAGAGCCATTAACGAT 1080  
DB 1021 AGGCTGAATCTGTATTAATTAAGCAACAGCTGGCTTGAAGAGCCATTAACGAT 1080  
QY 1081 GGGCTGAGATTAAGAAACATGTAATGATAGGCGGACTCCAGACAGAAAAAGGTAG 1140  
DB 1081 GGGCTGAGATTAAGAAACATGTAATGATAGGCGGACTCCAGACAGAAAAAGGTAG 1140  
QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGAAATGAACAGAACTGCATGCT 1200  
DB 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGAAATGAACAGAACTGCATGCT 1200  
QY 1201 CAGAGATCTTAAGATCTGAAGATGTTCTTGGATTAACATTAATGACAGATTGAGA 1260  
DB 1201 CAGAGATCTTAAGATCTGAAGATGTTCTTGGATTAACATTAATGACAGATTGAGA 1260  
QY 1261 AAGTTATGAGTGGTTTCCAGAGATGATGAACGTTTGAAGTCTCATGATG 1320  
DB 1261 AAGTTATGAGTGGTTTCCAGAGATGATGAACGTTTGAAGTCTCATGATG 1320  
QY 1321 GGGAGTCTGAATCAAAATGCCAAAGTCTGATGATTTGAAGAGTATG 1380  
DB 1321 GGGAGTCTGAATCAAAATGCCAAAGTCTGATGATTTGAAGAGTATG 1380  
QY 1381 AATATCTGTTCTTCAAGAGAAATATGACTTACTGCGCAGTATCTCATAGGCTTTAA 1440  
DB 1381 AATATCTGTTCTTCAAGAGAAATATGACTTACTGCGCAGTATCTCATAGGCTTTAA 1440  
QY 1441 TATGTAAGTGAAGAGTCACTCCAAATCACTAAGAGATTAATGAGACAAATAT 1500  
DB 1441 TATGTAAGTGAAGAGTCACTCCAAATCACTAAGAGATTAATGAGACAAATAT 1500  
QY 1501 TTGGGAAAACCTATCGGAGAGGCAAGCTCCCAACTTAACCATGTAACTGAAATC 1560  
DB 1501 TTGGGAAAACCTATCGGAGAGGCAAGCTCCCAACTTAACCATGTAACTGAAATC 1560  
QY 1561 TAAATATAGAGCAATTTTACTAGAGCAAGATTAATCAAGAGCGTCCCTCAAAATA 1620  
DB 1561 TAAATATAGAGCAATTTTACTAGAGCAAGATTAATCAAGAGCGTCCCTCAAAATA 1620  
QY 1621 AATTAAGGCTTAAGAGAGCTTCAATCAGGCTTCACTCTGAGATTTTATCAAGAAAG 1680  
DB 1621 AATTAAGGCTTAAGAGAGCTTCAATCAGGCTTCACTCTGAGATTTTATCAAGAAAG 1680  
QY 1681 CAGATTTGGAGTTCAAAAGACTCTGAAATGATTAATCAGGAGCTTAACCAAGGAGC 1740  
DB 1681 CAGATTTGGAGTTCAAAAGACTCTGAAATGATTAATCAGGAGCTTAACCAAGGAGC 1740  
QY 1741 AGAATGCTAGATGATGATTAATTAATAGTGTCTATGAGATTAAGCAAGAGGTAT 1800  
DB 1741 AGAATGCTAGATGATGATTAATTAATAGTGTCTATGAGATTAAGCAAGAGGTAT 1800  
QY 1801 CTATTCAGATGAGAAAAATCTTAACCAATTAATCACTGAGAAAAAGATCTGCTTCA 1860  
DB 1801 CTATTCAGATGAGAAAAATCTTAACCAATTAATCACTGAGAAAAAGATCTGCTTCA 1860  
QY 1861 AAGCAAGCTGAACCTATTAAGCAGATTAAGCAATATGAACTGAAATTAATATCC 1920



Db 1861 AAAGAAAGCTGAACCTATAGACAGAGATTAAGCAATATGAACTCGAATTAATATCC 1920  
Qy 1921 ACAATTTAAAAAGCATTTAAAAAGAAATAGGCTGAGAGAGAAAGTCTTACCAAGGATATTC 1980  
Db 1921 ACAATTTAAAAAGCATTTAAAAAGAAATAGGCTGAGAGAGAAAGTCTTACCAAGGATATTC 1980  
Qy 1981 ATGGCTTTGAACTGATAGTCAGTGAATCTAAGCCCACTAATTTGACTGAATTTGCAAA 2040  
Db 1981 ATGGCTTTGAACTGATAGTCAGTGAATCTAAGCCCACTAATTTGACTGAATTTGCAAA 2040  
Qy 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATTAAGAAAAAAAGTACAAACCAATGCGACTCA 2100  
Db 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATTAAGAAAAAAAGTACAAACCAATGCGACTCA 2100  
Qy 2101 GGCACACACAAAACCTCAACTCTGTAAGGTAAGAACTGCAACTGAGGCCAAGAA 2160  
Db 2101 GGCACACACAAAACCTCAACTCTGTAAGGTAAGAACTGCAACTGAGGCCAAGAA 2160  
Qy 2161 GTAAACAGCCAAATGAAACAGACAGTAAAGACATGACAGTACTTTCCAGAGCTGA 2220  
Db 2161 GTAAACAGCCAAATGAAACAGACAGTAAAGACATGACAGTACTTTCCAGAGCTGA 2220  
Qy 2221 AGTTAACAAATGCACTGCTGTTCTTTTACTAAGTGTCAAAATACCAAGTGAACCTTAAGAAAT 2280  
Db 2221 AGTTAACAAATGCACTGCTGTTCTTTTACTAAGTGTCAAAATACCAAGTGAACCTTAAGAAAT 2280  
Qy 2281 TTGTGATTCCTAGGCTTCCAAAGAAAGAAAAAGAAAGAACTGAAACAGTTAAATGT 2340  
Db 2281 TTGTGATTCCTAGGCTTCCAAAGAAAGAAAAAGAAAGAACTGAAACAGTTAAATGT 2340  
Qy 2341 CTAAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGAGAAAGGTTTTGCAAACTG 2400  
Db 2341 CTAAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGAGAAAGGTTTTGCAAACTG 2400  
Qy 2401 AAAGATCTGAGAGAGTAGACAGTATTTCACTGTAAGTGTACTGATTAATGCACTCAGG 2460  
Db 2401 AAAGATCTGAGAGAGTAGACAGTATTTCACTGTAAGTGTACTGATTAATGCACTCAGG 2460  
Qy 2461 AAAGATCTGTTACTGGAAGTTAGCACTCTGTAAGTGTACTGATTAATGCACTCAGG 2520  
Db 2461 AAAGATCTGTTACTGGAAGTTAGCACTCTGTAAGTGTACTGATTAATGCACTCAGG 2520  
Qy 2521 GTGTGAGTCAAGTGTGACAGATTTGAAAAACCCCAAGGACTAATCATGCTGTTCCAAAG 2580  
Db 2521 GTGTGAGTCAAGTGTGACAGATTTGAAAAACCCCAAGGACTAATCATGCTGTTCCAAAG 2580  
Qy 2581 ATAAATAGAAATGACACAGAAAGCTTTTAAGTATTCATTGGGACATGAAGTTAACCAAGTC 2640  
Db 2581 ATAAATAGAAATGACACAGAAAGCTTTTAAGTATTCATTGGGACATGAAGTTAACCAAGTC 2640  
Qy 2641 GGGAAACAGATAGAAATGGAAGAAAGTGAATTTGATGCTCAATTTTTCAGAAATACAT 2700  
Db 2641 GGGAAACAGATAGAAATGGAAGAAAGTGAATTTGATGCTCAATTTTTCAGAAATACAT 2700  
Qy 2701 TCAAGTTTCAAAGCGCGAGTCATTTGCTGTTTTCAATCCAGAAATCAGAAAGG 2760  
Db 2701 TCAAGTTTCAAAGCGCGAGTCATTTGCTGTTTTCAATCCAGAAATCAGAAAGG 2760  
Qy 2761 AATGTGCAACATTTCTGCGCCACTCTGGGTCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
Db 2761 AATGTGCAACATTTCTGCGCCACTCTGGGTCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
Qy 2821 TTGAAATGTGAACAAAGGAAGAAATCAAGAAAGAAATGAGTCTAATATCAAGCTGTAC 2880  
Db 2821 TTGAAATGTGAACAAAGGAAGAAATCAAGAAAGAAATGAGTCTAATATCAAGCTGTAC 2880  
Qy 2881 AGACAGTTAATATCATGCGAGCTTTCTGTGTTGTGTCAGAAAGATPAAGCAGTTGATA 2940  
Db 2881 AGACAGTTAATATCATGCGAGCTTTCTGTGTTGTGTCAGAAAGATPAAGCAGTTGATA 2940  
Qy 2941 ATGCCAAATGTATATCAAGAGAGCTCTAGTTTTGTCTATCATCTCAGTTGAGAGCA 3000  
Db 2941 ATGCCAAATGTATATCAAGAGAGCTCTAGTTTTGTCTATCATCTCAGTTGAGAGCA 3000

Qy 3001 ACGAACTGGACTCATTACTCCAATTAACATGGAAGCTTTTACAAAAACCATATCGTATAC 3060  
Db 3001 ACGAACTGGACTCATTACTCCAATTAACATGGAAGCTTTTACAAAAACCATATCGTATAC 3060  
Qy 3061 CACCACTTTTCCCATCAAGTCAATTTGTTTAAAACTAAATGTAAGAAAAATCTGCTAGAGG 3120  
Db 3061 CACCACTTTTCCCATCAAGTCAATTTGTTTAAAACTAAATGTAAGAAAAATCTGCTAGAGG 3120  
Qy 3121 AAAAATTGAGAAACATTCAATGTCACCTGAAAGAAATGGAATGAGAACATTCCAA 3180  
Db 3121 AAAAATTGAGAAACATTCAATGTCACCTGAAAGAAATGGAATGAGAACATTCCAA 3180  
Qy 3181 GTACAGTGAACAATTAAGCGCTAATPAACATTGAGAAATGTTTTTAAAGAGCCAGCT 3240  
Db 3181 GTACAGTGAACAATTAAGCGCTAATPAACATTGAGAAATGTTTTTAAAGAGCCAGCT 3240  
Qy 3241 CAAGCAATATTAATGAAGTAGTTCAGTACTAATGAAGTGGCTCCAGTATTATGAAA 3300  
Db 3241 CAAGCAATATTAATGAAGTAGTTCAGTACTAATGAAGTGGCTCCAGTATTATGAAA 3300  
Qy 3301 TAGGTTCAAGTATGAAAAATTTCAAGCAGAACTAAGTAAACAGAGGCCAAAAATTGA 3360  
Db 3301 TAGGTTCAAGTATGAAAAATTTCAAGCAGAACTAAGTAAACAGAGGCCAAAAATTGA 3360  
Qy 3361 ATGCTATGCTTAGATTAAGGGGTTTTTGCAACTGAGGCTAATAACAAAGTCTTCTGAA 3420  
Db 3361 ATGCTATGCTTAGATTAAGGGGTTTTTGCAACTGAGGCTAATAACAAAGTCTTCTGAA 3420  
Qy 3421 GTAAATGTAAAGACTCTGAATTAATAAAGCAAGAAATGAAAGAGTAGTTCAAGCTGTTA 3480  
Db 3421 GTAAATGTAAAGACTCTGAATTAATAAAGCAAGAAATGAAAGAGTAGTTCAAGCTGTTA 3480  
Qy 3481 ATACAGATTTCTCCATATCTGATTTCAATTAATCTTAAGAACAGGCTTAAGGAAGTAGTC 3540  
Db 3481 ATACAGATTTCTCCATATCTGATTTCAATTAATCTTAAGAACAGGCTTAAGGAAGTAGTC 3540  
Qy 3541 ATGCAATCTCAGGTTTTGTTCTGAGACACCTGATGACCTGTAAGATGATGTAATAAAGG 3600  
Db 3541 ATGCAATCTCAGGTTTTGTTCTGAGACACCTGATGACCTGTAAGATGATGTAATAAAGG 3600  
Qy 3601 AAGATACATGTTTTGCTGAAAAATGACATTAAGAAAGTTGCTGTTTTAGCAAAAGCG 3660  
Db 3601 AAGATACATGTTTTGCTGAAAAATGACATTAAGAAAGTTGCTGTTTTAGCAAAAGCG 3660  
Qy 3661 TCCAGAGAGAGAGCTTAGCAGAGTCTTGCCCTTACCCATACATTTGGCTCAGG 3720  
Db 3661 TCCAGAGAGAGAGCTTAGCAGAGTCTTGCCCTTACCCATACATTTGGCTCAGG 3720  
Qy 3721 GTTAACGGAAGGGGCCCAAGAAATTAAGATCCTCAGAAAGAACTTACTAGTAGAGATG 3780  
Db 3721 GTTAACGGAAGGGGCCCAAGAAATTAAGATCCTCAGAAAGAACTTACTAGTAGAGATG 3780  
Qy 3781 AAGAGCTTCCCTGCTTCCAAACATTTGTTTGTAAAGTAAACAATATACCTTCCAGT 3840  
Db 3781 AAGAGCTTCCCTGCTTCCAAACATTTGTTTGTAAAGTAAACAATATACCTTCCAGT 3840  
Qy 3841 CTACTAGGCAATAGACCGTTGCTACCGAGTGTCTGTAAAGAACACAGAGAAATTTAT 3900  
Db 3841 CTACTAGGCAATAGACCGTTGCTACCGAGTGTCTGTAAAGAACACAGAGAAATTTAT 3900  
Qy 3901 TATCATTTGAAGATAGGTTAAATGAAGTGAAGTAAACAGATTAATTTGGCAAGGCAATCTC 3960  
Db 3901 TATCATTTGAAGATAGGTTAAATGAAGTGAAGTAAACAGATTAATTTGGCAAGGCAATCTC 3960  
Qy 3961 AGGAACATCACTTAGTAGAGGAAAAAAATGTTCTGCTAGCTGTTTTCTTCAAGTGA 4020  
Db 3961 AGGAACATCACTTAGTAGAGGAAAAAAATGTTCTGCTAGCTGTTTTCTTCAAGTGA 4020  
Qy 4021 GTGAATTTGAAGACTGACTGCAAAATCAAAACCCAGATCCTTTCTTGAATTTGTTCTT 4080  
Db 4021 GTGAATTTGAAGACTGACTGCAAAATCAAAACCCAGATCCTTTCTTGAATTTGTTCTT 4080



QY 4081 CCAACAAATGAGGCATCATCTGTAAGCCAGAGGAGTTGGTCTGAGTGAACAAGAAATTTGG 4140  
 DB 4081 CCAACAAATGAGGCATCATCTGTAAGCCAGAGGAGTTGGTCTGAGTGAACAAGAAATTTGG 4140  
 QY 4141 TTTCAGATGATGAAGAAAGAGAAACGGGCTTGAAGAAATTAATCAAGAAAGAGAAAGCA 4200  
 DB 4141 TTTCAGATGATGAAGAAAGAGAAACGGGCTTGAAGAAATTAATCAAGAAAGAGAAAGCA 4200  
 QY 4201 TGAATTCAACTTAAGTGAAGACAGCATCTGGGTGTGAGAGTGAACAAGCGTCTCTGAAG 4260  
 DB 4201 TGAATTCAACTTAAGTGAAGACAGCATCTGGGTGTGAGAGTGAACAAGCGTCTCTGAAG 4260  
 QY 4261 ACTGCTCAGGCGCTATCTCTCAGAGTGAACATTTTAACCACTCAGCAGAGGAGATCCATGC 4320  
 DB 4261 ACTGCTCAGGCGCTATCTCTCAGAGTGAACATTTTAACCACTCAGCAGAGGAGATCCATGC 4320  
 QY 4321 AACATTAACCTGATTAACCTCAGAGAAATGGGTGAATCTGAAGCTGTGTGAACAAGC 4380  
 DB 4321 AACATTAACCTGATTAACCTCAGAGAAATGGGTGAATCTGAAGCTGTGTGAACAAGC 4380  
 QY 4381 ATGGAGACAGCCTTCTTAACAGTACCTTCCATCATTAAGTGAATCTCTGCGCCCTTGAAG 4440  
 DB 4381 ATGGAGACAGCCTTCTTAACAGTACCTTCCATCATTAAGTGAATCTCTGCGCCCTTGAAG 4440  
 QY 4441 ACCTGCGAAATCCAGAAACAAAGCATCAGAAAAAGCAGATTAATCACTTCAAGAAAAAGTA 4500  
 DB 4441 ACCTGCGAAATCCAGAAACAAAGCATCAGAAAAAGCAGATTAATCACTTCAAGAAAAAGTA 4500  
 QY 4501 GTGAAATACCTTAAGCCAGAAATCCAGAAAGCCCTTCTGCTGACAAAGTTGAAGTGTCTG 4560  
 DB 4501 GTGAAATACCTTAAGCCAGAAATCCAGAAAGCCCTTCTGCTGACAAAGTTGAAGTGTCTG 4560  
 QY 4561 CAGATAGTCTCAACAGTAATAAATAAGAACAGAGAGTGAAGGTCAATCCCTTCTTAAT 4620  
 DB 4561 CAGATAGTCTCAACAGTAATAAATAAGAACAGAGAGTGAAGGTCAATCCCTTCTTAAT 4620  
 QY 4621 GCCCATCATTAAGTGAAGTGTGATCAATGCAAGTTGCTGAGAGTCTTCAAGATGA 4680  
 DB 4621 GCCCATCATTAAGTGAAGTGTGATCAATGCAAGTTGCTGAGAGTCTTCAAGATGA 4680  
 QY 4681 ACTAACCATTCAAGAGAGAGTCAATTAAGTTGTGATGTGAGAGCAACAGCTGGAAG 4740  
 DB 4681 ACTAACCATTCAAGAGAGAGTCAATTAAGTTGTGATGTGAGAGCAACAGCTGGAAG 4740  
 QY 4741 AGTGTGGGCAACGATTTGACGGAACATCTTACTTCCAGAGCAAGATCTGAAGGAA 4800  
 DB 4741 AGTGTGGGCAACGATTTGACGGAACATCTTACTTCCAGAGCAAGATCTGAAGGAA 4800  
 QY 4801 CCCCTTAACCTGAATCTGAATCAGCTCTTCTCTGATGAACCTGAATCTGATCTTCTG 4860  
 DB 4801 CCCCTTAACCTGAATCTGAATCAGCTCTTCTCTGATGAACCTGAATCTGATCTTCTG 4860  
 QY 4861 AAGAAGAGCCCAAGAGTCAAGCTGTGTGCAACATACCATCTTCAACCTCTGATTTGA 4920  
 DB 4861 AAGAAGAGCCCAAGAGTCAAGCTGTGTGCAACATACCATCTTCAACCTCTGATTTGA 4920  
 QY 4921 AAGTTCCTCCCAATGAAGTTGACAGAAATCTGCCAGGGTCCAGCTGCTCATATCTACTG 4980  
 DB 4921 AAGTTCCTCCCAATGAAGTTGACAGAAATCTGCCAGGGTCCAGCTGCTCATATCTACTG 4980  
 QY 4981 ATACTGCTGGGTATTAATGCAATGGAAGAAAGTGTGACAGAGAGAACCCGAATTTGACAG 5040  
 DB 4981 ATACTGCTGGGTATTAATGCAATGGAAGAAAGTGTGACAGAGAGAACCCGAATTTGACAG 5040  
 QY 5041 CTTCAACAGAAAGGTCAACAAAAGATGTCATGAGTGTGTGCTGAGCTGACCCCAAG 5100  
 DB 5041 CTTCAACAGAAAGGTCAACAAAAGATGTCATGAGTGTGTGCTGAGCTGACCCCAAG 5100  
 QY 5101 AATTATGCTGTCTATACAAAGTTGCCAGAAAACCAATCACTTAATTAATTAATTA 5160  
 DB 5101 AATTATGCTGTCTATACAAAGTTGCCAGAAAACCAATCACTTAATTAATTAATTA 5160  
 QY 5161 CTGAAGAGACTACTGTTGTATGAACAAGATGCTGAGTTGTGTGAGACGACAC 5220

DB 5161 CTGAAGAGACTACTGTTGTATGAACAAGATGCTGAGTTGTGTGAGACGACAC 5220  
 QY 5221 TGAATTTTCTTCAAGAAATTCAGGAGAGAAATGGGAGTATGATCTATTTCTGGGTGACCC 5280  
 DB 5221 TGAATTTTCTTCAAGAAATTCAGGAGAGAAATGGGAGTATGATCTATTTCTGGGTGACCC 5280  
 QY 5281 AGCTATTAAGAAGAAAGAAATGCTGAATGAGATGATTTTGAAGTCAAGAGATGTGG 5340  
 DB 5281 AGCTATTAAGAAGAAAGAAATGCTGAATGAGATGATTTTGAAGTCAAGAGATGTGG 5340  
 QY 5341 TCAATGAGAAACCAACCAAGTCCAAAGCAGACAGAAAGATCCAGAGACAGAAAGATCT 5400  
 DB 5341 TCAATGAGAAACCAACCAAGTCCAAAGCAGACAGAAAGATCCAGAGACAGAAAGATCT 5400  
 QY 5401 TCAAGGGGCTGAAGAAATGTTGTGATGAGGCTTTCACCAATGCCCAGATCAACTGG 5460  
 DB 5401 TCAAGGGGCTGAAGAAATGTTGTGATGAGGCTTTCACCAATGCCCAGATCAACTGG 5460  
 QY 5461 AATGATGTGACAGCTGTGTGCTTCTGAGTGAAGAGCTTTCATTCACCTTG 5520  
 DB 5461 AATGATGTGACAGCTGTGTGCTTCTGAGTGAAGAGCTTTCATTCACCTTG 5520  
 QY 5521 GCAAGGTGTCCACCAATTTGTGTGTGACGCAAGTGTGAGACAGAAATGGCT 5580  
 DB 5521 GCAAGGTGTCCACCAATTTGTGTGTGACGCAAGTGTGAGACAGAAATGGCT 5580  
 QY 5581 TCCATGCAATTTGGGAGATGTGTGAGCAGCTGTGTGACCCAGAGATGGGTGTGACA 5640  
 DB 5581 TCCATGCAATTTGGGAGATGTGTGAGCAGCTGTGTGACCCAGAGATGGGTGTGACA 5640  
 QY 5641 GTGAGACACTCTCAAGTGTGAGAGAGTGAACACTTACCTGATACCCCAATCCCCACA 5700  
 DB 5641 GTGAGACACTCTCAAGTGTGAGAGAGTGAACACTTACCTGATACCCCAATCCCCACA 5700  
 QY 5701 GCCACTACTGA 5711  
 DB 5701 GCCACTACTGA 5711

RESULT 5  
 US-08-798-691-5  
 Sequence 5, Application US/08798691  
 Patent No. 5750400  
 GENERAL INFORMATION:  
 APPLICANT: Murphy, Patricia D.  
 APPLICANT: Allen, Antoinette C.  
 APPLICANT: Alvarez, Christopher P.  
 APPLICANT: Critz, Brenda S.  
 APPLICANT: O'Leon, Sheri J.  
 APPLICANT: Schelter, Denise B.  
 APPLICANT: Zeng, Bin  
 TITLE OF INVENTION: Coding Sequences of the Human  
 TITLE OF INVENTION: BRCA1 Gene  
 NUMBER OF SEQUENCES: 72  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: ONCOMED  
 STREET: 200 Perry Parkway  
 CITY: Gaithersburg  
 STATE: MD  
 COUNTRY: USA  
 ZIP: 20877  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/798,691  
 FILING DATE: 12-Feb-97  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Thomas Gallegos



Db 1801 CTATTCGAATGAGAAAAATCTTAACCCAAATAGATCACTCGAAAAAAGAAATCTGCTTTCA 1860  
Qy 1861 AAAAGAAAGCTGAACCTTAAGACAGAGTATAGCAATATGGAATGAACTGGAATTAATATCC 1920  
Db 1861 AAAGAAAGCTGAACCTTAAGACAGAGTATAGCAATATGGAATGAACTGGAATTAATATCC 1920  
Qy 1921 ACAATTCAAAAGCACTTAAGAAATAGGCTGAGAGAGAACTCTTCAACAGGATATTC 1980  
Db 1921 ACAATTCAAAAGCACTTAAGAAATAGGCTGAGAGAGAACTCTTCAACAGGATATTC 1980  
Qy 1981 ATGGGCTTGAACCTATGATGATGAGAAATCTAACCCCACTTAATTTGATCTGAATTCGAAA 2040  
Db 1981 ATGGGCTTGAACCTATGATGATGAGAAATCTAACCCCACTTAATTTGATCTGAATTCGAAA 2040  
Qy 2041 TTGATAGTTGTTCTAGAGATGAGATTAAGAAAAAAGTACAAACCAATGCGAGTCA 2100  
Db 2041 TTGATAGTTGTTCTAGAGATGAGATTAAGAAAAAAGTACAAACCAATGCGAGTCA 2100  
Qy 2101 GGCAACAGCAGAAACCTTAACCTCATGAGAGGTAAAGAACTGCAACTGAGCCAAAGAA 2160  
Db 2101 GGCAACAGCAGAAACCTTAACCTCATGAGAGGTAAAGAACTGCAACTGAGCCAAAGAA 2160  
Qy 2161 GTAAACAAAGCCAAATGAACAGACAAAGTAAAGACATGACAGTATCTTTCCAGAGCTGA 2220  
Db 2161 GTAAACAAAGCCAAATGAACAGACAAAGTAAAGACATGACAGTATCTTTCCAGAGCTGA 2220  
Qy 2221 AGTTAAACAAATGACCTGCTCTTTTCTAAGCTTCAATTAACCAAGGAACTTAAAGAT 2280  
Db 2221 AGTTAAACAAATGACCTGCTCTTTTCTAAGCTTCAATTAACCAAGGAACTTAAAGAT 2280  
Qy 2281 TTGTCATCTGAGCTTCAAGAGAGAAAGAAAGAAAGAACTGAAGAACTGTAAGTGT 2340  
Db 2281 TTGTCATCTGAGCTTCAAGAGAGAAAGAAAGAAAGAAAGAACTGTAAGTGT 2340  
Qy 2341 CTAAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTGCAGAACTG 2400  
Db 2341 CTAAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTGCAGAACTG 2400  
Qy 2401 AAAGATCTGAGAGATGAGATGATTTCACTGCTGATCTGATTAATGAGCACTGAG 2460  
Db 2401 AAAGATCTGAGAGATGAGATGATTTCACTGCTGATCTGATTAATGAGCACTGAG 2460  
Qy 2461 AAAGATCTGCTGATGAGAGATGAGATCTGAGAGAGGCAAAAGCAAGAACTGAATTAAT 2520  
Db 2461 AAAGATCTGCTGATGAGAGATGAGATCTGAGAGAGGCAAAAGCAAGAACTGAATTAAT 2520  
Qy 2521 GTGTGAGTCAAGTGTGAGCAATTTGAAAAAAGGCAAGGCACTAATTCATGTTGTTCAAG 2580  
Db 2521 GTGTGAGTCAAGTGTGAGCAATTTGAAAAAAGGCAAGGCACTAATTCATGTTGTTCAAG 2580  
Qy 2581 ATAAATTAAGATGACAGAGAGGCTTTAAGTATCCATTTGGAGCATGAAGTTAACACAGTGC 2640  
Db 2581 ATAAATTAAGATGACAGAGAGGCTTTAAGTATCCATTTGGAGCATGAAGTTAACACAGTGC 2640  
Qy 2641 GGGGAAACAGATGAGAAATGAGAAAGTGAAGTGAAGTCAATTTTGGAGAAATCAT 2700  
Db 2641 GGGGAAACAGATGAGAAATGAGAAAGTGAAGTGAAGTCAATTTTGGAGAAATCAT 2700  
Qy 2701 TCAAGTTTCAAAAGCGCAGTCAATTTGCTGTTTCAAAATCCAGAAATGCAAGAGG 2760  
Db 2701 TCAAGTTTCAAAAGCGCAGTCAATTTGCTGTTTCAAAATCCAGAAATGCAAGAGG 2760  
Qy 2761 AATGTGCAACATTTCTGCGCCACTCTGCGGCTTTAAAGAAAGTCAAAAGTCACTT 2820  
Db 2761 AATGTGCAACATTTCTGCGCCACTCTGCGGCTTTAAAGAAAGTCAAAAGTCACTT 2820  
Qy 2821 TTGAATGAGAAACAAAGAGAAATCAAGAGAAAGTGAAGTGAATTAATCAAGCTGATC 2880  
Db 2821 TTGAATGAGAAACAAAGAGAAATCAAGAGAAAGTGAAGTGAATTAATCAAGCTGATC 2880  
Qy 2881 AGACAGTTAATATCATGCAAGGCTTCTGTGTGTGTGTCAGAAAGATAGCAGCTGATA 2940  
Db 2881 AGACAGTTAATATCATGCAAGGCTTCTGTGTGTGTGTCAGAAAGATAGCAGCTGATA 2940

Qy 2941 ATGCCAAATGATATCAAAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAAGGCA 3000  
Db 2941 ATGCCAAATGATATCAAAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAAGGCA 3000  
Qy 3001 ACGAACTGAGCTCATTAATCTCAAAATTAACATGAGCTTTTCAAAACCCATATCTATAC 3060  
Db 3001 ACGAACTGAGCTCATTAATCTCAAAATTAACATGAGCTTTTCAAAACCCATATCTATAC 3060  
Qy 3061 CACACCTTTTCCATCAATCAATTTGTTTAAATCTAAATGAGAAATCTGCTAAGG 3120  
Db 3061 CACACCTTTTCCATCAATCAATTTGTTTAAATCTAAATGAGAAATCTGCTAAGG 3120  
Qy 3121 AAAAATTGAGAAACATTCAATGCTCACTGAAAGAGAAATGAGAAATGAGAACTTCCAA 3180  
Db 3121 AAAAATTGAGAAACATTCAATGCTCACTGAAAGAGAAATGAGAAATGAGAACTTCCAA 3180  
Qy 3181 GTACAGTGAACCAATTAAGCCGTAATTAACATTAAGAAATGTTTTTAAAGAGCAGCT 3240  
Db 3181 GTACAGTGAACCAATTAAGCCGTAATTAACATTAAGAAATGTTTTTAAAGAGCAGCT 3240  
Qy 3241 CAAGCAATTAATTAAGAGTGGTTCCAGTACTAATGAAGTGGCTCCAGTATTAATGAA 3300  
Db 3241 CAAGCAATTAATTAAGAGTGGTTCCAGTACTAATGAAGTGGCTCCAGTATTAATGAA 3300  
Qy 3301 TAGGTTCCAGTATGAAGAAACATTCAAGCAGAACTAAGGTAGAAACAGAGGCAAAATTTGA 3360  
Db 3301 TAGGTTCCAGTATGAAGAAACATTCAAGCAGAACTAAGGTAGAAACAGAGGCAAAATTTGA 3360  
Qy 3361 ATGCTATGCTTAAGATTAAGGAGGTTTTCAGACCTGAGGTCTAATTAACAAAGCTTCTGAAA 3420  
Db 3361 ATGCTATGCTTAAGATTAAGGAGGTTTTCAGACCTGAGGTCTAATTAACAAAGCTTCTGAAA 3420  
Qy 3421 GTAAATTTGAAGCATCTGAAATTAAGAAAGCAAGAAATGAAGAAATGTTTCAAGCTGTA 3480  
Db 3421 GTAAATTTGAAGCATCTGAAATTAAGAAAGCAAGAAATGAAGAAATGTTTCAAGCTGTA 3480  
Qy 3481 ATACAGATTTCTCCATCTCATCTGATTTCAATTAACATTAAGAAACAGCCATAGGAAATGATC 3540  
Db 3481 ATACAGATTTCTCCATCTCATCTGATTTCAATTAACATTAAGAAACAGCCATAGGAAATGATC 3540  
Qy 3541 ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGATGATTAAGG 3600  
Db 3541 ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGATGATTAAGG 3600  
Qy 3601 AAGATCTAGGTTTGTCTGAGAAATGACATTAAGAAAGTCTGCTGTTTGAAGAAAGG 3660  
Db 3601 AAGATCTAGGTTTGTCTGAGAAATGACATTAAGAAAGTCTGCTGTTTGAAGAAAGG 3660  
Qy 3661 TCCAGAGAGAGAGCTTGAAGAGAGTCTGAGCCCTTCAACCAATACATTTGGCTGAGG 3720  
Db 3661 TCCAGAGAGAGAGCTTGAAGAGAGTCTGAGCCCTTCAACCAATACATTTGGCTGAGG 3720  
Qy 3721 GTTACGAGAGAGGAGGCAAAATTAAGTCTCAGAGAGAACTTATCTAGTGAAGATG 3780  
Db 3721 GTTACGAGAGAGGAGGCAAAATTAAGTCTCAGAGAGAACTTATCTAGTGAAGATG 3780  
Qy 3781 AAGAGCTTCCCTGCTTCAACACTTGTATTTGGTAAAGTAAACAAATATACCTTCTCAGT 3840  
Db 3781 AAGAGCTTCCCTGCTTCAACACTTGTATTTGGTAAAGTAAACAAATATACCTTCTCAGT 3840  
Qy 3841 CTACTAGGATAGACCGTTGCTACCGAGTGTCTGTATTAAGAAACAGAGAGAAATTTAT 3900  
Db 3841 CTACTAGGATAGACCGTTGCTACCGAGTGTCTGTATTAAGAAACAGAGAGAAATTTAT 3900  
Qy 3901 TATCATTTGAAGAAATAGCTTAAATGATGACAGTAAACAGATTAATTTGGCAAGGCACTTC 3960  
Db 3901 TATCATTTGAAGAAATAGCTTAAATGATGACAGTAAACAGATTAATTTGGCAAGGCACTTC 3960  
Qy 3961 AGGAACATCACTTATGAGAGAAACAAATGTTCTGCTAGCTTGTCTTCAACAGTGA 4020  
Db 3961 AGGAACATCACTTATGAGAGAAACAAATGTTCTGCTAGCTTGTCTTCAACAGTGA 4020

QY 4021 GTGATTTGGAAGACTTGACCTGCAATATCAAAACACCCAGGATCTTTCTTGATGGTCTT 4080  
 DB 4021 GTGATTTGGAAGACTTGACCTGCAATATCAAAACACCCAGGATCTTTCTTGATGGTCTT 4080  
 QY 4081 CCAAAACAAATGAGGCAATCTGTAAGAGCCAGGAGTTGGTCTGAGTGACAAAGAAATGG 4140  
 DB 4081 CCAAAACAAATGAGGCAATCTGTAAGAGCCAGGAGTTGGTCTGAGTGACAAAGAAATGG 4140  
 QY 4141 TTTTCAGATGATGAAGAAAGAGAAACGGGCTTGGAAGAAATATCAAGAAAGAGAAAGCA 4200  
 DB 4141 TTTTCAGATGATGAAGAAAGAGAAACGGGCTTGGAAGAAATATCAAGAAAGAGAAAGCA 4200  
 QY 4201 TGAATTAACCTTGAATGAGCAACATCTGGGTGAGAGTGAAGCAAGCGTCTGTAAG 4260  
 DB 4201 TGAATTAACCTTGAATGAGCAACATCTGGGTGAGAGTGAAGCAAGCGTCTGTAAG 4260  
 QY 4261 ACTGCTCAGGGCTATCTCTCTCAGAGTGACATTTTAACTCAGCAGAGGGATACATGC 4320  
 DB 4261 ACTGCTCAGGGCTATCTCTCTCAGAGTGACATTTTAACTCAGCAGAGGGATACATGC 4320  
 QY 4321 AACATACTGATTAAGCTCCAGCAGAAATGGCTGAATCTGAAGCTGTGTAAGAACAC 4380  
 DB 4321 AACATACTGATTAAGCTCCAGCAGAAATGGCTGAATCTGAAGCTGTGTAAGAACAC 4380  
 QY 4381 ATGGAGAGCAGGCTTCTTAACAGCTACCTTCATCATTAAGTACTCTTCTGCTTGAAG 4440  
 DB 4381 ATGGAGAGCAGGCTTCTTAACAGCTACCTTCATCATTAAGTACTCTTCTGCTTGAAG 4440  
 QY 4441 ACCTGCAAAATCCAGAAACAAAGCAATCAGAAAAAGAGATTAATCTTCAAGAAAAATA 4500  
 DB 4441 ACCTGCAAAATCCAGAAACAAAGCAATCAGAAAAAGAGATTAATCTTCAAGAAAAATA 4500  
 QY 4501 GTGATTAACCTTAAGCCAGAAATCCAGAAAGCCCTTTCTGCTGAACAAGTTGAAGTGTCTG 4560  
 DB 4501 GTGATTAACCTTAAGCCAGAAATCCAGAAAGCCCTTTCTGCTGAACAAGTTGAAGTGTCTG 4560  
 QY 4561 CAGATAGTCTTACCAAGTAAATTAAGAAACAGAGAGTGAAGAGTCACTCCCTCTAAT 4620  
 DB 4561 CAGATAGTCTTACCAAGTAAATTAAGAAACAGAGAGTGAAGAGTCACTCCCTCTAAT 4620  
 QY 4621 GCCCATCATTAAGATGATAGTGTGTAACATGCAACAGTTGCTGAGAGTCTTCAAGAAATGAA 4680  
 DB 4621 GCCCATCATTAAGATGATAGTGTGTAACATGCAACAGTTGCTGAGAGTCTTCAAGAAATGAA 4680  
 QY 4681 ACTTCCCATCTCAAGAGAGAGCTCATTAAGTGTGTAAGTGAAGAGCAACAGCTGCAAG 4740  
 DB 4681 ACTTCCCATCTCAAGAGAGAGCTCATTAAGTGTGTAAGTGAAGAGCAACAGCTGCAAG 4740  
 QY 4741 AGTCTGGGCCCACGATTTGACGAAACATCTTACTTGCCAAAGGCAAGATCTAGAGGAA 4800  
 DB 4741 AGTCTGGGCCCACGATTTGACGAAACATCTTACTTGCCAAAGGCAAGATCTAGAGGAA 4800  
 QY 4801 CCCCTTAACCTGGAATCTGGAATCAGCCCTTCTCTGATGACCTGGAATCTGATCTTCTG 4860  
 DB 4801 CCCCTTAACCTGGAATCTGGAATCAGCCCTTCTCTGATGACCTGGAATCTGATCTTCTG 4860  
 QY 4861 AAGACAGAGCCCGAGTCAAGCTGTGTGGAACAATCCATCTTCAACCTCTCATTGA 4920  
 DB 4861 AAGACAGAGCCCGAGTCAAGCTGTGTGGAACAATCCATCTTCAACCTCTCATTGA 4920  
 QY 4921 AAGTTCCTCCATTTAAAGTTGACAGAAATCTGCCAGGGTCCAGCTGCTGCTATCTACTG 4980  
 DB 4921 AAGTTCCTCCATTTAAAGTTGACAGAAATCTGCCAGGGTCCAGCTGCTGCTATCTACTG 4980  
 QY 4981 ATACTGCTGGGTATATGATGATGAAGAAAGTGTGAGAGGAGGAAAGCAAGATTTGACAG 5040  
 DB 4981 ATACTGCTGGGTATATGATGATGAAGAAAGTGTGAGAGGAGGAAAGCAAGATTTGACAG 5040  
 QY 5041 CTTTCAACAGAAAGGCTCAACAAAGATGCTCAATGCTGTGTCTGCTGCAAGCCCAAG 5100  
 DB 5041 CTTTCAACAGAAAGGCTCAACAAAGATGCTCAATGCTGTGTCTGCTGCAAGCCCAAG 5100  
 QY 5101 AATTTATGCTGCTGTACAGTTTGCCAGAAACACCATCATCTTAACTTAATTA 5160

DB 5101 AATTTATGCTGCTGTGTACAGTTTGCCAGAAACACCATCATCTTAACTTAATTA 5160  
 QY 5161 CTGAAGAGACTTACTCATGTTGTTATGAAAACAGATGCTGAGTTGTGTGAAACGACAC 5220  
 DB 5161 CTGAAGAGACTTACTCATGTTGTTATGAAAACAGATGCTGAGTTGTGTGAAACGACAC 5220  
 QY 5221 TGAATATTTTCTAGGAATTCGGGAGGAAATGGGAGTGTAGCTATTTCTGGGTGACC 5280  
 DB 5221 TGAATATTTTCTAGGAATTCGGGAGGAAATGGGAGTGTAGCTATTTCTGGGTGACC 5280  
 QY 5281 AGCTATTAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGATGTGG 5340  
 DB 5281 AGCTATTAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGATGTGG 5340  
 QY 5341 TCAATGGAAGAAACCAACAGGCTCAAGAGGAGCAGAGCAAGAAATCT 5400  
 DB 5341 TCAATGGAAGAAACCAACAGGCTCAAGAGGAGCAGAGCAAGAAATCT 5400  
 QY 5401 TCAAGGGGCTTGAATGCTGTGATGAGGCTTCAACATGCTCCAGACAGATCACTGG 5460  
 DB 5401 TCAAGGGGCTTGAATGCTGTGATGAGGCTTCAACATGCTCCAGACAGATCACTGG 5460  
 QY 5461 AATGATGTAACAGCTGTGTGCTTCTGTGTAAGAGCTTTCATCTACCTTG 5520  
 DB 5461 AATGATGTAACAGCTGTGTGCTTCTGTGTAAGAGCTTTCATCTACCTTG 5520  
 QY 5521 GCACAGGTGTCACCAATGTTGTTGTGACAGCCAGATGCTTGAACAGATGCT 5580  
 DB 5521 GCACAGGTGTCACCAATGTTGTTGTGACAGCCAGATGCTTGAACAGATGCT 5580  
 QY 5581 TCAATGAATTTGGCAGATGTGAGCACTGTGTGACCCAGATGGGTGTGACA 5640  
 DB 5581 TCAATGAATTTGGCAGATGTGAGCACTGTGTGACCCAGATGGGTGTGACA 5640  
 QY 5641 GTGAGCACTTCAACAGTGCAGAGCTGAGCACTTCACTGATATCCAGATCCCCACA 5700  
 DB 5641 GTGAGCACTTCAACAGTGCAGAGCTGAGCACTTCACTGATATCCAGATCCCCACA 5700  
 QY 5701 GCCACTACTGA 5711  
 DB 5701 GCCACTACTGA 5711

RESULT 6  
 US-08-825-487A-5  
 : Sequence 5, Application US/08825487A  
 : Patent No. 6048689  
 : GENERAL INFORMATION:  
 : APPLICANT: Murphy, Patricia D.  
 : TITLE OF INVENTION: METHODS FOR IDENTIFYING VARIATIONS IN POLYNUCLEOTIDE SEQUENCES  
 : NUMBER OF SEQUENCES: 110  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Howrey & Simon  
 : STREET: 1299 Pennsylvania Avenue., N.W.  
 : CITY: Washington,  
 : STATE: DC  
 : COUNTRY: USA  
 : ZIP: 20004  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patent in Release #1.0, Version #1.30  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/825,487A  
 : FILING DATE: 28-Mar-1997  
 : CLASSIFICATION: 435  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: PCT/US98/060002  
 : FILING DATE: 26-Mar-1998  
 : CLASSIFICATION: 435

QY	721	ATCAAGATTGTATCAAAATCAACCCCTCAAGAAACAGGGATGAATCACTTTGGATTCTG	780
Db	721	ATCAAGAAATGTATCAAAATCAACCCCTCAAGAAACAGGGATGAATCACTTTGGATTCTG	780
QY	781	CAAAAAAGCGCTGTGTGAATTTTCTGAGCGAGTGAACAAATCTGAACATCATCAAC	840
Db	781	CAAAAAAGCGCTGTGTGAATTTTCTGAGCGAGTGAACAAATCTGAACATCATCAAC	840
QY	841	CCAGTAATATGATTTGGAACCACTGGAAGCGTGCAGCTGAGAGGCATCCAGAAAAGT	900
Db	841	CCAGTAATATGATTTGGAACCACTGGAAGCGTGCAGCTGAGAGGCATCCAGAAAAGT	900
QY	901	ATCAGGGTAGTTCTGTTCGAACCTTGCACTGTGGACCATGTGGCAAAATCTCATGCCA	960
Db	901	ATCAGGGTAGTTCTGTTCGAACCTTGCACTGTGGACCATGTGGCAAAATCTCATGCCA	960
QY	961	GCTCATTTACAGATAGAAACAGCACTTTATTACTCATTAAGACAGAAATGTATGA	1020
Db	961	GCTCATTTACAGATAGAAACAGCACTTTATTACTCATTAAGACAGAAATGTATGA	1020
QY	1021	AGCGTGAATTCGTATATAAAAGCAACAGCCTGTAGCAAGAGCCAACTAACAT	1080
Db	1021	AGCGTGAATTCGTATATAAAAGCAACAGCCTGTAGCAAGAGCCAACTAACAT	1080
QY	1081	GGCGTGAAGTAAAGGAAACATGTATGTAGGCGGACTCCGACAGAAAAAAGTGA	1140
Db	1081	GGCGTGAAGTAAAGGAAACATGTATGTAGGCGGACTCCGACAGAAAAAAGTGA	1140
QY	1141	ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGGAATGACAGAACTGCCATGT	1200
Db	1141	ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGGAATGACAGAACTGCCATGT	1200
QY	1201	CAGAGATCCTAGAGATCTGAAGATGTTCCCTGGAATACCTAATATGACAGACTTCGA	1260
Db	1201	CAGAGATCCTAGAGATCTGAAGATGTTCCCTGGAATACCTAATATGACAGACTTCGA	1260
QY	1261	AAGTAAATGAGTGGTTTTCCAGAAAGTATGAACCTGTATGCTTGATGATCATATGAT	1320
Db	1261	AAGTAAATGAGTGGTTTTCCAGAAAGTATGAACCTGTATGCTTGATGATCATATGAT	1320
QY	1321	GGGAGTCTGAATCAATCCCAAGTAGCTGATGATTTGACGTTCTAATAGAGTAGATG	1380
Db	1321	GGGAGTCTGAATCAATCCCAAGTAGCTGATGATTTGACGTTCTAATAGAGTAGATG	1380
QY	1381	AATATTCCTGCTCTTCAGAGAAAATAGACTTAATGCGCAAGATCTCATAGGCTTTAA	1440
Db	1381	AATATTCCTGCTCTTCAGAGAAAATAGACTTAATGCGCAAGATCTCATAGGCTTTAA	1440
QY	1441	TATGTAAAGTGAAGAGTTCACCTCAATCAGTAGAGATGAATTTGAAAGCAAAATAT	1500
Db	1441	TATGTAAAGTGAAGAGTTCACCTCAATCAGTAGAGATGAATTTGAAAGCAAAATAT	1500
QY	1501	TTGGGAAAACCTATCGAAGAAAGGCMAAGCTCCCAACTTAAGCCATGTAACTGAAAATC	1560
Db	1501	TTGGGAAAACCTATCGAAGAAAGGCMAAGCTCCCAACTTAAGCCATGTAACTGAAAATC	1560
QY	1561	TAAATATATGAGACATTTGTTACTGAGCCAAGATATATCAAGAGCGTCCCTCAAAATA	1620
Db	1561	TAAATATATGAGACATTTGTTACTGAGCCAAGATATATCAAGAGCGTCCCTCAAAATA	1620
QY	1621	AATTAAACGTAAGAGACCTTACATAGGCTTCACTGAGGATTTTATCAAGAAAG	1680
Db	1621	AATTAAACGTAAGAGACCTTACATAGGCTTCACTGAGGATTTTATCAAGAAAG	1680
QY	1681	CAGATTTGGCAGTTCAAAAAGCTCCTGAATATGATTAATCAGGGAATTAACCAAGCGAGC	1740
Db	1681	CAGATTTGGCAGTTCAAAAAGCTCCTGAATATGATTAATCAGGGAATTAACCAAGCGAGC	1740
QY	1741	AGAAATGTCAAATGATGAATATTAATAATAGTGTATGAGATTAATAAACAAGGTGATT	1800
Db	1741	AGAAATGTCAAATGATGAATATTAATAATAGTGTATGAGATTAATAAACAAGGTGATT	1800

QY 1801 CTATTGAGATGAGAAAAATCTTAACCCATAGAAATCACTCGAAGAAAAAGAAATCTGCTTCA 1860  
Db 1801 CTATTGAGATGAGAAAAATCTTAACCCATAGAAATCACTCGAAGAAAAAGAAATCTGCTTCA 1860  
QY 1861 AAACGAAAGCTGAACTTATAGCAGAGATATAGCAATATGCAATCTCGAAATTAATATCC 1920  
Db 1861 AAACGAAAGCTGAACTTATAGCAGAGATATAGCAATATGCAATCTCGAAATTAATATCC 1920  
QY 1921 ACAATTCAGAACGACTTAAAGAAATAGGCTGAGAGAGAACTCTTCAACGAGCATATTC 1980  
Db 1921 ACAATTCAGAACGACTTAAAGAAATAGGCTGAGAGAGAACTCTTCAACGAGCATATTC 1980  
QY 1981 ATGCGCTTGAATAGTACGATAGAAATCTAAGCCCACTTAATGTAATGCAATTC 2040  
Db 1981 ATGCGCTTGAATAGTACGATAGAAATCTAAGCCCACTTAATGTAATGCAATTC 2040  
QY 2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAAAAAGTACAAACCAATGCCAGTCA 2100  
Db 2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAAAAAGTACAAACCAATGCCAGTCA 2100  
QY 2101 GGCAACAGCAAAACCTTACAACTATGSAAGSTAAAGAACTTCACTGAGCCAGAAAGA 2160  
Db 2101 GGCAACAGCAAAACCTTACAACTATGSAAGSTAAAGAACTTCACTGAGCCAGAAAGA 2160  
QY 2161 GTAACAGGCAATGAAAGAGACAGAAAGTAAAGAACTGACAGTATCTTCCAGAGCTGA 2220  
Db 2161 GTAACAGGCAATGAAAGAGACAGAAAGTAAAGAACTGACAGTATCTTCCAGAGCTGA 2220  
QY 2221 AGTTACAAATGACACTGCTGTTCTTTTACTAAGTGTTCAAATACCAAGTAACTTAAAGAT 2280  
Db 2221 AGTTACAAATGACACTGCTGTTCTTTTACTAAGTGTTCAAATACCAAGTAACTTAAAGAT 2280  
QY 2281 TTGTCAATCTTACCTTCCAGAGAAAGAAAGAAAGAACTTAAAGAAAGTAAAGT 2340  
Db 2281 TTGTCAATCTTACCTTCCAGAGAAAGAAAGAAAGAACTTAAAGAAAGTAAAGT 2340  
QY 2341 CTAAATATGCTGAAGAGACCCCAAGAACTCATGTGTTAAGTGAAGAGGGTTTGCAAACTG 2400  
Db 2341 CTAAATATGCTGAAGAGACCCCAAGAACTCATGTGTTAAGTGAAGAGGGTTTGCAAACTG 2400  
QY 2401 AAAGATCTGTAGAGATGACAGATTTTCACTGGTACCTGTTACTGATTAATGCACTCAG 2460  
Db 2401 AAAGATCTGTAGAGATGACAGATTTTCACTGGTACCTGTTACTGATTAATGCACTCAG 2460  
QY 2461 AAAGATCTGTAGAGATGACAGATTTTCACTGGTACCTGTTACTGATTAATGCACTCAG 2520  
Db 2461 AAAGATCTGTAGAGATGACAGATTTTCACTGGTACCTGTTACTGATTAATGCACTCAG 2520  
QY 2521 GTGTAGTCAAGTGTGACAGATTTGAAAGACCCCAAGGAACTAAATTCATGCTGTTCCAAAG 2580  
Db 2521 GTGTAGTCAAGTGTGACAGATTTGAAAGACCCCAAGGAACTAAATTCATGCTGTTCCAAAG 2580  
QY 2581 ATAAATGAAATGACACAGAAAGCTTAAATTCATTTGGAAGATGAAGTTAAACAAGT 2640  
Db 2581 ATAAATGAAATGACACAGAAAGCTTAAATTCATTTGGAAGATGAAGTTAAACAAGT 2640  
QY 2641 GGGAAACAGCATAGAAATGGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2700  
Db 2641 GGGAAACAGCATAGAAATGGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2700  
QY 2701 TCAAGGTTCAAGGCGCAGTATTTGCTGTTTCAATCCAGAAATGAGAGAGAG 2760  
Db 2701 TCAAGGTTCAAGGCGCAGTATTTGCTGTTTCAATCCAGAAATGAGAGAGAG 2760  
QY 2761 AATGTGCAACATTTCTGCGCACTGCGGTCTTTAAAGAAACAAGTCCAAAGTCACTT 2820  
Db 2761 AATGTGCAACATTTCTGCGCACTGCGGTCTTTAAAGAAACAAGTCCAAAGTCACTT 2820  
QY 2821 TTGAATGTGAACAAAGAAAGAAATCAAGAAAGATGATGATTAATCAAGCTGTAC 2880  
Db 2821 TTGAATGTGAACAAAGAAAGAAATCAAGAAAGATGATGATTAATCAAGCTGTAC 2880  
QY 2881 AAGACGTTAATATCACTGAGGCTTCCGTGTTGTGTAAGAAAGTAAAGCCAGTTGATA 2940

Db 2881 AAGACGTTAATATCACTGAGGCTTCCGTGTTGTGTAAGAAAGTAAAGCCAGTTGATA 2940  
QY 2941 ATGCCAAATGTATGATCAAGAGAGCTCTAGTTTGTCTATCATCTCACTTCAAGAGCA 3000  
Db 2941 ATGCCAAATGTATGATCAAGAGAGCTCTAGTTTGTCTATCATCTCACTTCAAGAGCA 3000  
QY 3001 ACGAATCTGAGCTCATTTCTCCAAATTAACATGAGCTTTTCAAAACCATATGCTATAC 3060  
Db 3001 ACGAATCTGAGCTCATTTCTCCAAATTAACATGAGCTTTTCAAAACCATATGCTATAC 3060  
QY 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAACTTAAAGTAAAGAAATCTGCTAGAG 3120  
Db 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAACTTAAAGTAAAGAAATCTGCTAGAG 3120  
QY 3121 AAACTTTGAGAACATTTCAATGTACCTGAAAGAAATGGAAATGAAACATTTCCAA 3180  
Db 3121 AAACTTTGAGAACATTTCAATGTACCTGAAAGAAATGGAAATGAAACATTTCCAA 3180  
QY 3181 GTACAGTGAACATTTAGCCGTTAATCAATTAAGAAATGTTTAAAGAGCAGCT 3240  
Db 3181 GTACAGTGAACATTTAGCCGTTAATCAATTAAGAAATGTTTAAAGAGCAGCT 3240  
QY 3241 CAAGCAATTTAATGAAAGTATGAGTTCAGTACTAATGAAGTGGCTCAGATTAATGA 3300  
Db 3241 CAAGCAATTTAATGAAAGTATGAGTTCAGTACTAATGAAGTGGCTCAGATTAATGA 3300  
QY 3301 TAGGTTCCAGTATGAAACATTTCAAGCAAACTAGTGAAGAAAGAGGCGCAAAATTTGA 3360  
Db 3301 TAGGTTCCAGTATGAAACATTTCAAGCAAACTAGTGAAGAAAGAGGCGCAAAATTTGA 3360  
QY 3361 ATGCTATGCTAATGATTAAGGGGTTTGCAACCTGAGCTCAATTAAGAAAGTCTCTGGA 3420  
Db 3361 ATGCTATGCTAATGATTAAGGGGTTTGCAACCTGAGCTCAATTAAGAAAGTCTCTGGA 3420  
QY 3421 GTAAATGTAAGCATCTGAAATTAAGAAAGCAAGATATGAAGATGATTCAGACTGTA 3480  
Db 3421 GTAAATGTAAGCATCTGAAATTAAGAAAGCAAGATATGAAGATGATTCAGACTGTA 3480  
QY 3481 ATACAGATTTCTTCCATATCTGATTTCAATTAAGTAACTTGAACAGCTTATGGAAGTATG 3540  
Db 3481 ATACAGATTTCTTCCATATCTGATTTCAATTAAGTAACTTGAACAGCTTATGGAAGTATG 3540  
QY 3541 ATGCAATCAAGTGTGTTCTGAGACACTGATGACCTGTTAATGATGATGATGATGATG 3600  
Db 3541 ATGCAATCAAGTGTGTTCTGAGACACTGATGACCTGTTAATGATGATGATGATGATG 3600  
QY 3601 AAGATATGATTTGCTGAAATGACATTTAAGAAAGTCTGCTGTTTAAAGAAAGCG 3660  
Db 3601 AAGATATGATTTGCTGAAATGACATTTAAGAAAGTCTGCTGTTTAAAGAAAGCG 3660  
QY 3661 TCCAGAGAGAGAGCTTACAGAGAGTCTAGGCTTTTCAACCATACATTTGGCTCAGG 3720  
Db 3661 TCCAGAGAGAGAGCTTACAGAGAGTCTAGGCTTTTCAACCATACATTTGGCTCAGG 3720  
QY 3721 GTTACGGAAGAGGGGCAAGAAATTAAGTCTCAGAGAGAACTTATCTGAGAGATG 3780  
Db 3721 GTTACGGAAGAGGGGCAAGAAATTAAGTCTCAGAGAGAACTTATCTGAGAGATG 3780  
QY 3781 AAGACCTTCCCTGCTTCAACACTTGTATTTGTAAGTAAACAATATACCTTCTCAGT 3840  
Db 3781 AAGACCTTCCCTGCTTCAACACTTGTATTTGTAAGTAAACAATATACCTTCTCAGT 3840  
QY 3841 CTACTAGGATATGACCGTGTGCTACCGAGTGTCTGTAAAGAAACAAGAGGAAATTAAT 3900  
Db 3841 CTACTAGGATATGACCGTGTGCTACCGAGTGTCTGTAAAGAAACAAGAGGAAATTAAT 3900  
QY 3901 TATCATTTGAAGAAATGCTTAAATGATCTGAGTAAACAGGTAAATTTGGCAAGGATCTC 3960  
Db 3901 TATCATTTGAAGAAATGCTTAAATGATCTGAGTAAACAGGTAAATTTGGCAAGGATCTC 3960  
QY 3961 AGGAACATCACTTGTGAGAGAAACAATATGTTCTGAGTGTGTTTCTTCAAGTGA 4020

Db 3961 AGGAACATCACCCTTAGTGAGGAAACAAATGTTCTGTAGCTTGTCTTCTTCAAGTGCA 4020  
 Qy 4021 GTGAATTTGAGAGCTTGTGCTGCAATATACAAACACCCAGGATCCTTCTTGTATGTTCTT 4080  
 Db 4021 GTGAATTTGAGAGCTTGTGCTGCAATATACAAACACCCAGGATCCTTCTTGTATGTTCTT 4080  
 Qy 4081 CCAACCAATATGAGGATCAGTCTGAAAGCCAGGAGTTGCTGTAGTGAACAAGAAATGG 4140  
 Db 4081 CCAACCAATATGAGGATCAGTCTGAAAGCCAGGAGTTGCTGTAGTGAACAAGAAATGG 4140  
 Qy 4141 TTTTCAGATGATGAGAAAGAGAACGGGCTTGGAAAGAAATATATCAAGAGAGCAAGCA 4200  
 Db 4141 TTTTCAGATGATGAGAAAGAGAACGGGCTTGGAAAGAAATATATCAAGAGAGCAAGCA 4200  
 Qy 4201 TGGATTCAAACTTAGTGTAGAGGATCTGGGTGTAGAGTGAACAAGCCCTCTGTGAAG 4260  
 Db 4201 TGGATTCAAACTTAGTGTAGAGGATCTGGGTGTAGAGTGAACAAGCCCTCTGTGAAG 4260  
 Qy 4261 ACTGCTCAGGGCTATCCTCTCAGAGTGAATTTTAAACACTCAGCAGAGAGGATACCATGC 4320  
 Db 4261 ACTGCTCAGGGCTATCCTCTCAGAGTGAATTTTAAACACTCAGCAGAGAGGATACCATGC 4320  
 Qy 4321 AACATACCTGTATTAAGCTCCAGCAGAAATGGCTGAATAGAGCTGTGTGAACACGC 4380  
 Db 4321 AACATACCTGTATTAAGCTCCAGCAGAAATGGCTGAATAGAGCTGTGTGAACACGC 4380  
 Qy 4381 ATGGAGGACAGCCTTCTAAAGCTACCCCTTCAATATAGTGAATCTCTGCTGCTTGAAG 4440  
 Db 4381 ATGGAGGACAGCCTTCTAAAGCTACCCCTTCAATATAGTGAATCTCTGCTGCTTGAAG 4440  
 Qy 4441 ACCTGCGAAATTCAGAAACAAAGCAGATCAGAAAGAGAGTATTAATCTTCAAGAAAGTA 4500  
 Db 4441 ACCTGCGAAATTCAGAAACAAAGCAGATCAGAAAGAGAGTATTAATCTTCAAGAAAGTA 4500  
 Qy 4501 GTGAATACCTTATTAAGCAGAAATTCAGAAAGCCTTCTGCTGCAAGATTGAGGTCTG 4560  
 Db 4501 GTGAATACCTTATTAAGCAGAAATTCAGAAAGCCTTCTGCTGCAAGATTGAGGTCTG 4560  
 Qy 4561 CAGATAGTTCTTACCGATTAATAAAGAAACGAGAGTGAAGAGTCAATCCCTTCTTAAT 4620  
 Db 4561 CAGATAGTTCTTACCGATTAATAAAGAAACGAGAGTGAAGAGTCAATCCCTTCTTAAT 4620  
 Qy 4621 GCCCATCATTTAGATGATAGTGTGATCATGCAAGTTGCTGGAGTCTTCAAGATAGA 4680  
 Db 4621 GCCCATCATTTAGATGATAGTGTGATCATGCAAGTTGCTGGAGTCTTCAAGATAGA 4680  
 Qy 4681 ACTACCATCTTCAAGAGAGCTCTTAAAGTTGTGATGTGAGAGCAACAGCTGGAAG 4740  
 Db 4681 ACTACCATCTTCAAGAGAGCTCTTAAAGTTGTGATGTGAGAGCAACAGCTGGAAG 4740  
 Qy 4741 AGTCTGGGCGCACAGATTTGAGAGGAAACATCTTACTTGGCAAGGCAAGATCTAGAGGAA 4800  
 Db 4741 AGTCTGGGCGCACAGATTTGAGAGGAAACATCTTACTTGGCAAGGCAAGATCTAGAGGAA 4800  
 Qy 4801 CCCCTTACCTGGAATCTGGAATCAGGCTCTTCTGTAGTGAACCTGAATCTGATCTG 4860  
 Db 4801 CCCCTTACCTGGAATCTGGAATCAGGCTCTTCTGTAGTGAACCTGAATCTGATCTG 4860  
 Qy 4861 AAGACAGAGCCCGACAGTCAAGCTGTGTGGCAATACCATCTTCAACCTTGTGATGA 4920  
 Db 4861 AAGACAGAGCCCGACAGTCAAGCTGTGTGGCAATACCATCTTCAACCTTGTGATGA 4920  
 Qy 4921 AAGTTCCTGCAATTTGAAAGTTGCAAGATCTGCCAGAGGTCAGCTGTCTCATCTACTG 4980  
 Db 4921 AAGTTCCTGCAATTTGAAAGTTGCAAGATCTGCCAGAGGTCAGCTGTCTCATCTACTG 4980  
 Qy 4981 ATACTGTGGGTATATGCAATGAGAAAGTGTGAGCAGGAGAGGACAGAAATGACAG 5040  
 Db 4981 ATACTGTGGGTATATGCAATGAGAAAGTGTGAGCAGGAGAGGACAGAAATGACAG 5040  
 Qy 5041 CTTCAACAGAAAGGCTCAACAAAGATGTCCATGATGTGTGTGTGAGCCCTGACCCAGAG 5100  
 Db 5041 CTTCAACAGAAAGGCTCAACAAAGATGTCCATGATGTGTGTGTGAGCCCTGACCCAGAG 5100

Qy 5101 AATTATGCTGCTGTACAAAGTTTGGCAGAAAAACACATCATCTTAATCTAATTA 5160  
 Db 5101 AATTATGCTGCTGTACAAAGTTTGGCAGAAAAACACATCATCTTAATCTAATTA 5160  
 Qy 5161 CTGAAGAGACTATCTCATGTTGTTATGAAACAGATGCTGAGTTGTGTGAAACGACAC 5220  
 Db 5161 CTGAAGAGACTATCTCATGTTGTTATGAAACAGATGCTGAGTTGTGTGAAACGACAC 5220  
 Qy 5221 TGAATATTTTCTAGAAATTCGGAGAGAAATGGGTAGTATGATTTCTGGGGTGAACC 5280  
 Db 5221 TGAATATTTTCTAGAAATTCGGAGAGAAATGGGTAGTATGATTTCTGGGGTGAACC 5280  
 Qy 5281 AGCTATTTAAAGAAAGAAATATGCTGAATGAGCATGATTTTGAAGTCAAGAGATGTGG 5340  
 Db 5281 AGCTATTTAAAGAAAGAAATATGCTGAATGAGCATGATTTTGAAGTCAAGAGATGTGG 5340  
 Qy 5341 TCAATGAGAAAGAACCAAGGTCCTCAAGCGAGAGAAATCCAGAGACAGAAAGATCT 5400  
 Db 5341 TCAATGAGAAAGAACCAAGGTCCTCAAGCGAGAGAAATCCAGAGACAGAAAGATCT 5400  
 Qy 5401 TCAAGGGGCTAGAAATCTGTTGCTATGAGGCTTCAACAAATGCTCCACATCACTGG 5460  
 Db 5401 TCAAGGGGCTAGAAATCTGTTGCTATGAGGCTTCAACAAATGCTCCACATCACTGG 5460  
 Qy 5461 AATGATGATACAGCTGTGTGTGCTGCTGTGTGTGAAGAGCTTCAATCATTACCCCTTG 5520  
 Db 5461 AATGATGATACAGCTGTGTGTGCTGCTGTGTGTGAAGAGCTTCAATCATTACCCCTTG 5520  
 Qy 5521 GCACAGGTGTCACCAATTTGTTGTGACAGCCAGATGCTGACAGAGCAATGAGT 5580  
 Db 5521 GCACAGGTGTCACCAATTTGTTGTGACAGCCAGATGCTGACAGAGCAATGAGT 5580  
 Qy 5581 TCCATGCAATTTGGGCAATGTGTGAGGCACTGTGTGTGACCCAGAGATGGGTGGACA 5640  
 Db 5581 TCCATGCAATTTGGGCAATGTGTGAGGCACTGTGTGTGACCCAGAGATGGGTGGACA 5640  
 Qy 5641 GTGTAGCACTTACCAAGTGCAGAGCTGAGACCTACTGATCCAGATCCCCCA 5700  
 Db 5641 GTGTAGCACTTACCAAGTGCAGAGCTGAGACCTACTGATCCAGATCCCCCA 5700  
 Qy 5701 GCCACTACTGA 5711  
 Db 5701 GCCACTACTGA 5711

RESULT 7  
 US-09-074-476-3  
 ; Sequence 3, Application US/09074476  
 ; Patent No. 6130322  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Murphy, Patricia D.  
 ; APPLICANT: Allen, Antonette C.  
 ; APPLICANT: Alvares, Christopher P.  
 ; APPLICANT: Clitz, Brenda S.  
 ; APPLICANT: Olson, Sheri J.  
 ; APPLICANT: Thurder, Denise  
 ; APPLICANT: Zeng, Bin  
 ; TITLE OF INVENTION: Coding Sequences of the Human  
 ; TITLE OF INVENTION: BRCA1 Gene  
 ; NUMBER OF SEQUENCES: 72  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Howrey & Simon  
 ; STREET: 1299 Pennsylvania Avenue N. W.  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20004  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30



CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/074,476  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/074,453  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Albert P. Halluin  
REGISTRATION NUMBER: 25,227  
REFERENCE/DOCKET NUMBER: 5371.34.US01  
TELEPHONE: 650-463-8109  
TELEFAX: 650-463-8400  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5711 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
STRAIN: BRCA1 (om12)  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17  
MAP POSITION: 17q21  
US-09-074-476-3

Query Match 100.0%; Score 5709.4; DB 3; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCTGGCTGAGACTTCTCTGAGACCCGCGACAGGCTGTGGGTTTCTGAGTAACTGGGCC 60  
DB 1 AGCTGGCTGAGACTTCTCTGAGACCCGCGACAGGCTGTGGGTTTCTGAGTAACTGGGCC 60  
QY 61 CCGGCGCTCAGAGGCTTACCCCTGTGCTGGGTTAAAGTTCATTGGAAAGAAAGAA 120  
DB 61 CCGGCGCTCAGAGGCTTACCCCTGTGCTGGGTTAAAGTTCATTGGAAAGAAAGAA 120  
QY 121 TGGATTATCTGCTCTTCCGCTTGAAGAGTACAAATGTCTAATATGCTATGACAGAAA 180  
DB 121 TGGATTATCTGCTCTTCCGCTTGAAGAGTACAAATGTCTAATATGCTATGACAGAAA 180  
QY 121 TGGATTATCTGCTCTTCCGCTTGAAGAGTACAAATGTCTAATATGCTATGACAGAAA 180  
DB 121 TGGATTATCTGCTCTTCCGCTTGAAGAGTACAAATGTCTAATATGCTATGACAGAAA 180  
QY 181 TCTTGAAGTCCCATCTGTCTGAGGTTGATCAAGAACTGTCTCCCAAAAGTGTGACC 240  
DB 181 TCTTGAAGTCCCATCTGTCTGAGGTTGATCAAGAACTGTCTCCCAAAAGTGTGACC 240  
QY 241 ACATATTTTGCAGAAATTTTGCATGCGAAACTTCTCAACGAGAAAGAGGCTTGCACAGT 300  
DB 241 ACATATTTTGCAGAAATTTTGCATGCGAAACTTCTCAACGAGAAAGAGGCTTGCACAGT 300  
QY 301 GTCTTTATGTAAAGATGATATATACCAAAAGAGGCTTCAAGAAAGTACGAGATTAGTC 360  
DB 301 GTCTTTATGTAAAGATGATATATACCAAAAGAGGCTTCAAGAAAGTACGAGATTAGTC 360  
QY 301 GTCTTTATGTAAAGATGATATATACCAAAAGAGGCTTCAAGAAAGTACGAGATTAGTC 360  
DB 301 GTCTTTATGTAAAGATGATATATACCAAAAGAGGCTTCAAGAAAGTACGAGATTAGTC 360  
QY 361 AACTTGTGAAGAGCTATTTGAAATCATTTTGTCTTTTCAAGTTGACACAGGTTTGGAGT 420  
DB 361 AACTTGTGAAGAGCTATTTGAAATCATTTTGTCTTTTCAAGTTGACACAGGTTTGGAGT 420  
QY 421 ATGCAACAGGCTATATTTTGCAGAAAGAGAAATTAATCTCTGAAACATCTAAAGATG 480  
DB 421 ATGCAACAGGCTATATTTTGCAGAAAGAGAAATTAATCTCTGAAACATCTAAAGATG 480  
QY 481 AAGTTTATATCATCAAGATATGGGCTACAGAAACCGTCCAAAGACCTTCTACAGAGTG 540  
DB 481 AAGTTTATATCATCAAGATATGGGCTACAGAAACCGTCCAAAGACCTTCTACAGAGTG 540  
QY 541 AACCCGAAATCTTCTCTTGCAGAAACCAAGTCTCAAGTCTCACTCTTAACTTTGAA 600  
DB 541 AACCCGAAATCTTCTCTTGCAGAAACCAAGTCTCAAGTCTCACTCTTAACTTTGAA 600  
QY 541 AACCCGAAATCTTCTCTTGCAGAAACCAAGTCTCAAGTCTCACTCTTAACTTTGAA 600  
DB 541 AACCCGAAATCTTCTCTTGCAGAAACCAAGTCTCAAGTCTCACTCTTAACTTTGAA 600

QY 601 CTGTGAGAACTCTGAGACAAAGCAGCGATATACACTCAAAAGACGTCTGTCTACATTTG 660  
DB 601 CTGTGAGAACTCTGAGACAAAGCAGCGATATACACTCAAAAGACGTCTGTCTACATTTG 660  
QY 661 AATTGGGATCTGATTTCTTGAAGATACCGTTAATAGGCACTTATTTGCACTGGGAG 720  
DB 661 AATTGGGATCTGATTTCTTGAAGATACCGTTAATAGGCACTTATTTGCACTGGGAG 720  
QY 721 ATCAAGATTTGTTCAAAATCAACCCCTCAAGGACCAAGGAGTGAATCACTTGGATTTG 780  
DB 721 ATCAAGATTTGTTCAAAATCAACCCCTCAAGGACCAAGGAGTGAATCACTTGGATTTG 780  
QY 781 CAAAAAGGCTGCTGTGAAATTTTCTGAGACGATGTAAACAAATACGAAATCATCTAAC 840  
DB 781 CAAAAAGGCTGCTGTGAAATTTTCTGAGACGATGTAAACAAATACGAAATCATCTAAC 840  
QY 841 CCAGTAATATGATTTGAAACCACTGAGAAACCGTGCAGCTGAGAGCATCCAGAAAGT 900  
DB 841 CCAGTAATATGATTTGAAACCACTGAGAAACCGTGCAGCTGAGAGCATCCAGAAAGT 900  
QY 901 ATCAGGATATGTTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCAAAATCTCATGGCA 960  
DB 901 ATCAGGATATGTTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCAAAATCTCATGGCA 960  
QY 961 GCTCATTTACACATGAGAACGACAGTTTATTTACTCATCAAAAGACGATGATGAGAA 1020  
DB 961 GCTCATTTACACATGAGAACGACAGTTTATTTACTCATCAAAAGACGATGATGAGAA 1020  
QY 1021 AGCTGAATTTCTGTAATTAAGCAACAGCTGCTGCTTTCAGAGGACCAATTAACAGAT 1080  
DB 1021 AGCTGAATTTCTGTAATTAAGCAACAGCTGCTGCTTTCAGAGGACCAATTAACAGAT 1080  
QY 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGCGGACCTCCAGCAAGAAAGGATG 1140  
DB 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGCGGACCTCCAGCAAGAAAGGATG 1140  
QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGAAATGAGAACTGCCATGCT 1200  
DB 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGAAATGAGAACTGCCATGCT 1200  
QY 1201 CAGAGATCTAGAGATCTGAAGATGTTCTTGGATTAACCTAATATGACAGATTCAGA 1260  
DB 1201 CAGAGATCTAGAGATCTGAAGATGTTCTTGGATTAACCTAATATGACAGATTCAGA 1260  
QY 1261 AAGTTAATGAGTGTTCAGAGAGTGAATGAACTGTTGATGATGATGATGATGATG 1320  
DB 1261 AAGTTAATGAGTGTTCAGAGAGTGAATGAACTGTTGATGATGATGATGATGATG 1320  
QY 1321 GGGAGTCTGAATCAAAATGCCAAAGTGAATGATGATGATGATGATGATGATGATG 1380  
DB 1321 GGGAGTCTGAATCAAAATGCCAAAGTGAATGATGATGATGATGATGATGATGATG 1380  
QY 1381 AATATTTCTGTTCTTCAAGAAATAGACTTACCTGAGGACGATCTCATGAGGCTTTAA 1440  
DB 1381 AATATTTCTGTTCTTCAAGAAATAGACTTACCTGAGGACGATCTCATGAGGCTTTAA 1440  
QY 1441 TATGTAAAGTGAAGAGTCACTTCAATCAATGATGATGATGATGATGATGATGATG 1500  
DB 1441 TATGTAAAGTGAAGAGTCACTTCAATCAATGATGATGATGATGATGATGATGATG 1500  
QY 1501 TTGGGAAACCTATCTGAAAGAGGACCTCCCAACTTAAGGATTAAGGATTAAGGATTA 1560  
DB 1501 TTGGGAAACCTATCTGAAAGAGGACCTCCCAACTTAAGGATTAAGGATTAAGGATTA 1560  
QY 1561 TAAATTAAGAGCAATTTGTTAATGAGCAAGATTAATCAAGAGGTCCTTCAAAATA 1620  
DB 1561 TAAATTAAGAGCAATTTGTTAATGAGCAAGATTAATCAAGAGGTCCTTCAAAATA 1620  
QY 1621 AATTAAAGCTTAAAGAGAGCTTACATGAGGCTTCACTGAGGATTTTATCAAGAAAG 1680  
DB 1621 AATTAAAGCTTAAAGAGAGCTTACATGAGGCTTCACTGAGGATTTTATCAAGAAAG 1680  
QY 1681 CAGATTTGGAGTTCAAAAGACTCCTGAATGATTAATCAAGGAACTAAACCAAGGAGC 1740

```
Db 1681 CAAATTTGGAGTTCAAAAGACTCTCTGAATGATMAATTCAGGGGAACTACAAACGAGC 1740
Qy 1741 AGATGGTCAAGTGAATATTTACTAATGTGCTCATGGAATATAAACAAGGATTT 1800
Db 1741 AGAATGGTCAAGTGAATATTTACTAATGTGCTCATGGAATATAAACAAGGATTT 1800
Qy 1801 CTATTCAGAAATGAGAAAATCTTAACCAATAGATCACTCGAATAAAGAAATCTGCTTCA 1860
Db 1801 CTATTCAGAAATGAGAAAATCTTAACCAATAGATCACTCGAATAAAGAAATCTGCTTCA 1860
Qy 1861 AAACGAAAGCTGAACCTATAAGCAGCATATAGCAATATGGAATCTGGAATTAATATCC 1920
Db 1861 AAACGAAAGCTGAACCTATAAGCAGCATATAGCAATATGGAATCTGGAATTAATATCC 1920
Qy 1921 ACAATTCAAAGACCTTAAAAAGATAGGCTGAGAGAGAAAGTCTTCTACAGGCAATATTC 1980
Db 1921 ACAATTCAAAGACCTTAAAAAGATAGGCTGAGAGAGAAAGTCTTCTACAGGCAATATTC 1980
Qy 1981 ATGCGCTTGAATAGTATGATGATGAATCTAAGCCCACTAATTTGATGAAATTCGAAA 2040
Db 1981 ATGCGCTTGAATAGTATGATGATGAATCTAAGCCCACTAATTTGATGAAATTCGAAA 2040
Qy 2041 TTGATAGTTGTTCTAGCAGTGAAGATATAAGAAAAAAAGTACAAACCAATGCAATGCA 2100
Db 2041 TTGATAGTTGTTCTAGCAGTGAAGATATAAGAAAAAAAGTACAAACCAATGCAATGCA 2100
Qy 2101 GGCACAGCAGAAAACCTTAACCTCATGGAAGTAAAGAACTGCACTGAGCCCAAGAA 2160
Db 2101 GGCACAGCAGAAAACCTTAACCTCATGGAAGTAAAGAACTGCACTGAGCCCAAGAA 2160
Qy 2161 GTAACAGGCCAAATGAACAGACATGAAGGATTAAGAACTGATATCTTTCCAGAGCTGA 2220
Db 2161 GTAACAGGCCAAATGAACAGACATGAAGGATTAAGAACTGATATCTTTCCAGAGCTGA 2220
Qy 2221 AGTTAAACAAATGCACTGTTCTTTTCTAAGTGTTCAAATACCAATGAACTTAAGAA 2280
Db 2221 AGTTAAACAAATGCACTGTTCTTTTCTAAGTGTTCAAATACCAATGAACTTAAGAA 2280
Qy 2281 TTGTCATCTCTAGCTTCCAGAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGTGT 2340
Db 2281 TTGTCATCTCTAGCTTCCAGAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGTGT 2340
Qy 2341 CTAAATATGCTGAAGCCCAAGATCTCATGTTAATGAGAAAGGTTTTCGAACTG 2400
Db 2341 CTAAATATGCTGAAGCCCAAGATCTCATGTTAATGAGAAAGGTTTTCGAACTG 2400
Qy 2401 AAAGATCTGAGAGATGAGATATTCATCTGATCCTGATCTGATTTGCACTCAGG 2460
Db 2401 AAAGATCTGAGAGATGAGATATTCATCTGATCCTGATCTGATTTGCACTCAGG 2460
Qy 2461 AAAGATCTGAGATGAGATATTCATCTGATCCTGATCTGATTTGCACTCAGG 2520
Db 2461 AAAGATCTGAGATGAGATATTCATCTGATCCTGATCTGATTTGCACTCAGG 2520
Qy 2521 GTGTGATCTGATGATGATTTGAAACCCCAAGGAGCTTAATCATGTTTTCGAAAG 2580
Db 2521 GTGTGATCTGATGATGATTTGAAACCCCAAGGAGCTTAATCATGTTTTCGAAAG 2580
Qy 2581 ATATATGAATGACACAGAGGCTTTAATGATCATTGGGACATGAAAGTTAACCAAGTC 2640
Db 2581 ATATATGAATGACACAGAGGCTTTAATGATCATTGGGACATGAAAGTTAACCAAGTC 2640
Qy 2641 GGGAAAACAGCATAGAAATGGAAGAAAGTGAATGATGCTCATGATTTTCAGAAATCAT 2700
Db 2641 GGGAAAACAGCATAGAAATGGAAGAAAGTGAATGATGCTCATGATTTTCAGAAATCAT 2700
Qy 2701 TCAAGGTTTCAAGGCGCAGTCAATTTGCTGTTTCAATCCAGGAAATGCAAGAGG 2760
Db 2701 TCAAGGTTTCAAGGCGCAGTCAATTTGCTGTTTCAATCCAGGAAATGCAAGAGG 2760
Qy 2761 AATGTGCAACATTTCTGCGCACTCTGAGTCTTAAGAAACAAAGTCAAAAGTCACTT 2820
Db 2761 AATGTGCAACATTTCTGCGCACTCTGAGTCTTAAGAAACAAAGTCAAAAGTCACTT 2820
Db 2761 AATGTGCAACATTTCTGCGCACTCTGAGTCTTAAGAAACAAAGTCAAAAGTCACTT 2820
Qy 2821 TTGAATGTGAACAAAGAGAAAGAAATCAGAGAAAGATGATCTAATATCAAGCTGTAC 2880
Db 2821 TTGAATGTGAACAAAGAGAAAGAAATCAGAGAAAGATGATCTAATATCAAGCTGTAC 2880
Qy 2881 AGACAGTTAATATCATGCAAGGCTTCTGTTGTTGCTGAGAAAGATAGCCAGTTGATA 2940
Db 2881 AGACAGTTAATATCATGCAAGGCTTCTGTTGTTGCTGAGAAAGATAGCCAGTTGATA 2940
Qy 2941 ATGCAATATGATATCAAGAGAGGCTTAAGGTTTGTCTATATCATCTCAGTTCAAGGCA 3000
Db 2941 ATGCAATATGATATCAAGAGAGGCTTAAGGTTTGTCTATATCATCTCAGTTCAAGGCA 3000
Qy 3001 ACGAAATGACATCTACTCCAAATTAACATGACCTTTTACAAACCAATATGCTATAC 3060
Db 3001 ACGAAATGACATCTACTCCAAATTAACATGACCTTTTACAAACCAATATGCTATAC 3060
Qy 3061 CACCACTTTTCCATCAAGTCAATTTGTAAAATAATGTAAGAAATCTGCTAGAGG 3120
Db 3061 CACCACTTTTCCATCAAGTCAATTTGTAAAATAATGTAAGAAATCTGCTAGAGG 3120
Qy 3121 AAAAATTGAGAAACATTCATATGTCACCTGAAAAGAAATGGAAATGAGAACTTCCAA 3180
Db 3121 AAAAATTGAGAAACATTCATATGTCACCTGAAAAGAAATGGAAATGAGAACTTCCAA 3180
Qy 3181 GTACAGTACACAAATTAAGCCCTTAATACATTAAGAAATGTTTTTAAAGAGCCAGCT 3240
Db 3181 GTACAGTACACAAATTAAGCCCTTAATACATTAAGAAATGTTTTTAAAGAGCCAGCT 3240
Qy 3241 CAAGCAATATTAATGAAGTGTCCAGTCTAATGAAGTGGGCTCAGATTAATGAAA 3300
Db 3241 CAAGCAATATTAATGAAGTGTCCAGTCTAATGAAGTGGGCTCAGATTAATGAAA 3300
Qy 3301 TAGGTTCAAGTATGAAGAAACATTCAGACAGAACTAGGTAGAAACAGAGGCGCAAAATGA 3360
Db 3301 TAGGTTCAAGTATGAAGAAACATTCAGACAGAACTAGGTAGAAACAGAGGCGCAAAATGA 3360
Qy 3361 ATGCTATGCTTAATTAAGGTTTTCGACACCTGAGTCTTAATGAAGTCTTCTGAA 3420
Db 3361 ATGCTATGCTTAATTAAGGTTTTCGACACCTGAGTCTTAATGAAGTCTTCTGAA 3420
Qy 3421 GTAAATGTAAGCACTCCGAAATTAAGAAAGAAATGAAGAAAGTGTCAAGCTGTA 3480
Db 3421 GTAAATGTAAGCACTCCGAAATTAAGAAAGAAATGAAGAAAGTGTCAAGCTGTA 3480
Qy 3481 ATACAGATTTCTCTCCATATCTGATTTCAATTAATAGAACAGCTATGGAAGTATGC 3540
Db 3481 ATACAGATTTCTCTCCATATCTGATTTCAATTAATAGAACAGCTATGGAAGTATGC 3540
Qy 3541 ATGCAATCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGTAATAAGG 3600
Db 3541 ATGCAATCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGTAATAAGG 3600
Qy 3601 AAGATTAATATTTTCTGAAATGACATTAAGAAAGTTCTGCTGTTTTCGAAAGCG 3660
Db 3601 AAGATTAATATTTTCTGAAATGACATTAAGAAAGTTCTGCTGTTTTCGAAAGCG 3660
Qy 3661 TCCAGAGAGAGAGCTTAGCAGAGAGTCTAGACCCTTTCACCCATACATTTGGCTCAGG 3720
Db 3661 TCCAGAGAGAGAGCTTAGCAGAGAGTCTAGACCCTTTCACCCATACATTTGGCTCAGG 3720
Qy 3721 GTTACGAGAGAGGCGCCAAAGAAATTAAGTCTCAGAGAGAACTTAATCTAGTGAAGATG 3780
Db 3721 GTTACGAGAGAGGCGCCAAAGAAATTAAGTCTCAGAGAGAACTTAATCTAGTGAAGATG 3780
Qy 3781 AAGAGCTTCCCTGCTTCCAACTCTGTTATTTGGTAAAGTAAACATATCTTCTCAGT 3840
Db 3781 AAGAGCTTCCCTGCTTCCAACTCTGTTATTTGGTAAAGTAAACATATCTTCTCAGT 3840
Qy 3841 CTACTAGCATATGACAGGTTGCTACAGAGTGTCTGTCTAAGAACACAGAGAGAAATTTAT 3900
Db 3841 CTACTAGCATATGACAGGTTGCTACAGAGTGTCTGTCTAAGAACACAGAGAGAAATTTAT 3900
```

QY 3901 TATCATGGAAGATAGCTTAATGACTGCACTAACAGGTATATATGGCAAAAGGCATCTC 3960  
 Db 3901 TATCATGGAAGATAGCTTAATGACTGCACTAACAGGTATATATGGCAAAAGGCATCTC 3960  
 QY 3961 AGGAACATCACCTTAGTAGGAGAAACAAATGTTCTGCTAGCTGTTTCTTCAAGTGA 4020  
 Db 3961 AGGAACATCACCTTAGTAGGAGAAACAAATGTTCTGCTAGCTGTTTCTTCAAGTGA 4020  
 QY 4021 GTGAATGGAAGACTTGAATGCAAAATACAAACCCCGAGATCCCTTCTGATTTGGTCTT 4080  
 Db 4021 GTGAATGGAAGACTTGAATGCAAAATACAAACCCCGAGATCCCTTCTGATTTGGTCTT 4080  
 QY 4081 CCAAAACAAATAGGAGCATGCTGTAAGCCAGGAGTTGCTGTAAGTGAACAAGAAATGG 4140  
 Db 4081 CCAAAACAAATAGGAGCATGCTGTAAGCCAGGAGTTGCTGTAAGTGAACAAGAAATGG 4140  
 QY 4141 TTTGAGATGATGAAGAAAGAGAAACGGGCTTGAAGAAATATCAAGAAAGCAAGCA 4200  
 Db 4141 TTTGAGATGATGAAGAAAGAGAAACGGGCTTGAAGAAATATCAAGAAAGCAAGCA 4200  
 QY 4201 TGAATTCAACTTAGTGAAGACAGCATCTGGGTGAGAGTGAACAAGCCTCTGAG 4260  
 Db 4201 TGAATTCAACTTAGTGAAGACAGCATCTGGGTGAGAGTGAACAAGCCTCTGAG 4260  
 QY 4261 ACTGCTAGGGCTATCCCTCTGAGAGTGAATTTTAAACACTCAGAGAGGATTCATG 4320  
 Db 4261 ACTGCTAGGGCTATCCCTCTGAGAGTGAATTTTAAACACTCAGAGAGGATTCATG 4320  
 QY 4321 AACATACTGATTAAGCTCCAGAGAGAAATGCTGTAAGAACTGTGTTAGAACAGC 4380  
 Db 4321 AACATACTGATTAAGCTCCAGAGAGAAATGCTGTAAGAACTGTGTTAGAACAGC 4380  
 QY 4381 ATGGAGAGCAGCTTCTTAACGCTACCTTCCATCATTAAGTGAATCCTCTGCTGAG 4440  
 Db 4381 ATGGAGAGCAGCTTCTTAACGCTACCTTCCATCATTAAGTGAATCCTCTGCTGAG 4440  
 QY 4441 ACCTGCGAAATCCAGAAACAGACATGAGAAAGAGATTAATCAAGAAAGTA 4500  
 Db 4441 ACCTGCGAAATCCAGAAACAGACATGAGAAAGAGATTAATCAAGAAAGTA 4500  
 QY 4501 GTGAATACCTTAATAGCCAGAAATCCAGAGGCTTCTGCTGTAACAAGTTGAGGTGCTG 4560  
 Db 4501 GTGAATACCTTAATAGCCAGAAATCCAGAGGCTTCTGCTGTAACAAGTTGAGGTGCTG 4560  
 QY 4561 CAGATAGTTCTTAACGATTAATAAGAACAGAGAGTGAAGAGTCAATCCCTCTTAAT 4620  
 Db 4561 CAGATAGTTCTTAACGATTAATAAGAACAGAGAGTGAAGAGTCAATCCCTCTTAAT 4620  
 QY 4621 GCCCATCATTAAGATGATGAGTGTACATGCAAGTGTCTGAGAGTCTTCAAGAAAGTA 4680  
 Db 4621 GCCCATCATTAAGATGATGAGTGTACATGCAAGTGTCTGAGAGTCTTCAAGAAAGTA 4680  
 QY 4681 ACTACCATCTCAAGAGAGGCTCATTAAGTGTGATGAGAGAGCAAGCTGAG 4740  
 Db 4681 ACTACCATCTCAAGAGAGGCTCATTAAGTGTGATGAGAGAGCAAGCTGAG 4740  
 QY 4741 AGTCTGGGCCACAGATTTGACGAAACATCTTACTTGCCAAAGACAGATCTAAGAGGAA 4800  
 Db 4741 AGTCTGGGCCACAGATTTGACGAAACATCTTACTTGCCAAAGACAGATCTAAGAGGAA 4800  
 QY 4801 CCCCTTACTGGAATCTGGAATCAGGCTTCTCTGATGAGCCCTGGAATCTATCTTCTG 4860  
 Db 4801 CCCCTTACTGGAATCTGGAATCAGGCTTCTCTGATGAGCCCTGGAATCTATCTTCTG 4860  
 QY 4861 AAGACAGAGCCCAAGAGTCAAGTGTGTCAGACATCACTTCAACCTCTGATGGA 4920  
 Db 4861 AAGACAGAGCCCAAGAGTCAAGTGTGTCAGACATCACTTCAACCTCTGATGGA 4920  
 QY 4921 AAGTTCCCAATGAAAGTTGCAAGATCTGCCAGGGTCCAGCTGCTCATCTACTG 4980  
 Db 4921 AAGTTCCCAATGAAAGTTGCAAGATCTGCCAGGGTCCAGCTGCTCATCTACTG 4980

QY 4981 ATACTGCGGTATTAATGCAATGGAAGAAAGTGTGAGCAGGAGAAACCAATTTGACAG 5040  
 Db 4981 ATACTGCGGTATTAATGCAATGGAAGAAAGTGTGAGCAGGAGAAACCAATTTGACAG 5040  
 QY 5041 CTTCAACAGAAAGGCTCAACAAAGAAATGTCATGTTGTTCTGCTGACCCCAAG 5100  
 Db 5041 CTTCAACAGAAAGGCTCAACAAAGAAATGTCATGTTGTTCTGCTGACCCCAAG 5100  
 QY 5101 AATTATGCTGCTGATCAAGTTTCCAGAAACCAATCACTTAATCTAATTA 5160  
 Db 5101 AATTATGCTGCTGATCAAGTTTCCAGAAACCAATCACTTAATCTAATTA 5160  
 QY 5161 CTGAAGAGACTACTCATGTTGTTATGAAAAAGATGCTGAGTTGTGTGAAACGAC 5220  
 Db 5161 CTGAAGAGACTACTCATGTTGTTATGAAAAAGATGCTGAGTTGTGTGAAACGAC 5220  
 QY 5221 TGAATATTTTCTAGGAATTCGGGAGAGAAATGGTATGTTAGTTTCTGGTGA 5280  
 Db 5221 TGAATATTTTCTAGGAATTCGGGAGAGAAATGGTATGTTAGTTTCTGGTGA 5280  
 QY 5281 AGTCTATTAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTGAAGAGAGATGG 5340  
 Db 5281 AGTCTATTAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTGAAGAGATGG 5340  
 QY 5341 TCAATGGAAGAAACCAACAGGTCCAAGCGAGCAAGAGATCCAGAGACAGAAAGATCT 5400  
 Db 5341 TCAATGGAAGAAACCAACAGGTCCAAGCGAGCAAGAGATCCAGAGACAGAAAGATCT 5400  
 QY 5401 TCAGGGGGCTAGAAATCTGTTGCTATGAGGCTTCAACCAATGCCACAGATCACTGG 5460  
 Db 5401 TCAGGGGGCTAGAAATCTGTTGCTATGAGGCTTCAACCAATGCCACAGATCACTGG 5460  
 QY 5461 AATGATGATGACAGCTGTGAGTCTCTGTGTGAGAGAGCTTCAATCACTG 5520  
 Db 5461 AATGATGATGACAGCTGTGAGTCTCTGTGTGAGAGAGCTTCAATCACTG 5520  
 QY 5521 GCACAGGTGTCACCCCAATGTTGTTGAGCAGCAGATGCTGAGACAGAGCAATGGCT 5580  
 Db 5521 GCACAGGTGTCACCCCAATGTTGTTGAGCAGCAGATGCTGAGACAGAGCAATGGCT 5580  
 QY 5581 TCATGCAATTTGGGAGATGTTGAGGACCTGTGTGACCCGAGAGTGGGTGTTGACA 5640  
 Db 5581 TCATGCAATTTGGGAGATGTTGAGGACCTGTGTGACCCGAGAGTGGGTGTTGACA 5640  
 QY 5641 GTGTAAGACTCTTACAGTGTGAGAGGCTGGAACACTTCTGATACCCAGATCCCA 5700  
 Db 5641 GTGTAAGACTCTTACAGTGTGAGAGGCTGGAACACTTCTGATACCCAGATCCCA 5700  
 QY 5701 GCCACTACTGA 5711  
 Db 5701 GCCACTACTGA 5711

RESULT 8  
 US-08-798-691-3  
 ; Sequence 3, Application US/08798691  
 ; Patent No. 5750400  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Murphy, Patricia D.  
 ; APPLICANT: Allen, Antoinette C.  
 ; APPLICANT: Alvarez, Christopher P.  
 ; APPLICANT: Critz, Brenda S.  
 ; APPLICANT: Olson, Sheri J.  
 ; APPLICANT: Schelter, Denise B.  
 ; APPLICANT: Zeng, Bin  
 ; TITLE OF INVENTION: Coding Sequences of the Human  
 ; TITLE OF INVENTION: BRCA1 Gene  
 ; NUMBER OF SEQUENCES: 72  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: ONCORMED  
 ; STREET: 200 Perry Parkway  
 ; CITY: Gaithersburg  
 ; STATE: MD

```

? COUNTRY: USA
? ZIP: 20877
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/798,691
? FILING DATE: 12-Feb-97
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: Thomas Gallagos
? REGISTRATION NUMBER: 32,692
? REFERENCE/DOCKET NUMBER: PA-0054CIP
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 301-527-2051
? TELEFAX: 301-208-6997
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 5711 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: not relevant
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? ORIGINAL SOURCE:
? ORGANISM: Homo sapiens
? STRAIN: BRCA1
? POSITION IN GENOME:
? CHROMOSOME/SEGMENT: 17
? MAP POSITION: 17q21
? US-08-798-691-3

Query Match      99.8%; Score 5701.4; DB 1; Length 5711;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5705; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

```

QY 541 AACCCGAAAATCTTCCCTTGAGAAAACAGCTCTCAAGTGTCCAACTCTAACCCTTGAA 600
DB 541 AACCCGAAAATCTTCCCTTGAGAAAACAGCTCTCAAGTGTCCAACTCTAACCCTTGAA 600
QY 601 CTGTGAGAACTCTGAGAACAAAGCAGGGGATACAACTCCAAAAGACGTCTGTACATTG 660
DB 601 CTGTGAGAACTCTGAGAACAAAGCAGGGGATACAACTCCAAAAGACGTCTGTACATTG 660
QY 661 AATTGGGATCTGATCTTCTGAGATACCGTTAATTAAGGCAACTTATTCAGTGGGAG 720
DB 661 AATTGGGATCTGATCTTCTGAGATACCGTTAATTAAGGCAACTTATTCAGTGGGAG 720
QY 721 ATCAAGAATTGTTCAAAATCACCCCTCAAGGAACAGGAGATGAATCAGTTGGATTCTG 780
DB 721 ATCAAGAATTGTTCAAAATCACCCCTCAAGGAACAGGAGATGAATCAGTTGGATTCTG 780
QY 781 CAAAAAGGCTGCTTGGAATTTTCTGAGACGATGTAACTGAATCTGAACATCAAC 840
DB 781 CAAAAAGGCTGCTTGGAATTTTCTGAGACGATGTAACTGAATCTGAACATCAAC 840
QY 841 CCAGTAATTAATGATTGAAACCACTGAGAACGCTGACGTGAGAGCATCCAGAAAAGT 900
DB 841 CCAGTAATTAATGATTGAAACCACTGAGAACGCTGACGTGAGAGCATCCAGAAAAGT 900
QY 901 ATCAGGGTAGTTCTGTTCAAACTTGCACTGAGACCATGTGGCAAAATCTCATGGCA 960
DB 901 ATCAGGGTAGTTCTGTTCAAACTTGCACTGAGACCATGTGGCAAAATCTCATGGCA 960
QY 961 GCTCATTAACAGCATGAGAACAGAGTTTATTACTCACTAAAGACAGAAATGATAGAAA 1020
DB 961 GCTCATTAACAGCATGAGAACAGAGTTTATTACTCACTAAAGACAGAAATGATAGAAA 1020
QY 1021 AGGCTGAATTTGTAATTAAGCAAAACAGCTGCTTACAGAGAGCCAACTAACAT 1080
DB 1021 AGGCTGAATTTGTAATTAAGCAAAACAGCTGCTTACAGAGAGCCAACTAACAT 1080
QY 1081 GGGCTGGAATGTAAGAAACATGTAATGATAGACGCACTCCAGACAGAAAAAAGTAG 1140
DB 1081 GGGCTGGAATGTAAGAAACATGTAATGATAGACGCACTCCAGACAGAAAAAAGTAG 1140
QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAGATGAATTAACAGAACTGCCATGCT 1200
DB 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAGATGAATTAACAGAACTGCCATGCT 1200
QY 1201 CAGAGAACTCTAAGATATCTGAAGATGTTCTTGATTAACCTAATATGACGATTCGA 1260
DB 1201 CAGAGAACTCTAAGATATCTGAAGATGTTCTTGATTAACCTAATATGACGATTCGA 1260
QY 1261 AAGTTAATGAGTGGTTTCCAGAGTGAATGAACTGTAAGTTCTGATGATCTCACTGATG 1320
DB 1261 AAGTTAATGAGTGGTTTCCAGAGTGAATGAACTGTAAGTTCTGATGATCTCACTGATG 1320
QY 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGTAATGGAAGTTCTAATAGAGTAGATG 1380
DB 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGTAATGGAAGTTCTAATAGAGTAGATG 1380
QY 1381 AATAATTCGTGTTCTTCAAGAAAATAGACTTAAGTGGCAGATGATCTCATAGAGCTTTAA 1440
DB 1381 AATAATTCGTGTTCTTCAAGAAAATAGACTTAAGTGGCAGATGATCTCATAGAGCTTTAA 1440
QY 1441 TATGTAAGAGTGAAGAGTTCACTCCAAATCAATGATGAGATTAATTTGAAGACAAAATAT 1500
DB 1441 TATGTAAGAGTGAAGAGTTCACTCCAAATCAATGATGAGATTAATTTGAAGACAAAATAT 1500
QY 1501 TTGGGAAAACCTATTCGAGAAAGGCAAGCTCCCAACTTAAGCATATTAAGCTGAAAATC 1560
DB 1501 TTGGGAAAACCTATTCGAGAAAGGCAAGCTCCCAACTTAAGCATATTAAGCTGAAAATC 1560
QY 1561 TAAATTAAGAGCAATTTGTTACTGAGCCAAGATTAATCAAGAGCGTCCCTCACAAATTA 1620
DB 1561 TAAATTAAGAGCAATTTGTTACTGAGCCAAGATTAATCAAGAGCGTCCCTCACAAATTA 1620
QY 1621 AATTAAAGCGTAAAGAGACCTTACATCAGGCTTTCATCTGAGAGATTTTATCAAGAAAG 1680

```

```
Db 1621 AATTAAAGCTAAAGAGACCTACATCAGGCTTCATCTGAGGATTTTATCAAGAAAG 1680
Qy 1681 CAGATTTGGCAGTTCAAAAGACCTCTGAAATGATPAAACAGGAACTTAACCAACGAGC 1740
Db 1681 CAGATTTGGCAGTTCAAAAGACCTCTGAAATGATPAAACAGGAACTTAACCAACGAGC 1740
Qy 1741 AGAATGCTCAGTGTGATTAATTAATTAATGTCATGATGATTAATTAATTAATTAATTAAT 1800
Db 1741 AGAATGCTCAGTGTGATTAATTAATTAATGTCATGATGATTAATTAATTAATTAATTAAT 1800
Qy 1801 CTATTCAGATGAGAAAAATCTTAACCAATGAAATCACTCGAAAAAGATCTGTTTCA 1860
Db 1801 CTATTCAGATGAGAAAAATCTTAACCAATGAAATCACTCGAAAAAGATCTGTTTCA 1860
Qy 1861 AAAGAAAGCTGAACTTAAGCAGCAGATATGAAATGAACTGCAATTAATTAATTC 1920
Db 1861 AAAGAAAGCTGAACTTAATGAGCAGATATGAAATGAACTGCAATTAATTAATTC 1920
Qy 1921 ACAATTCAAAAGCAGCTTAAGAAATAGCTGAGAGAGAGATCTTCTACAGCAGATTC 1980
Db 1921 ACAATTCAAAAGCAGCTTAAGAAATAGCTGAGAGAGAGATCTTCTACAGCAGATTC 1980
Qy 1981 ATGCGCTTGAACCTAGTACAGTAAATCTAAGCCCACTAATTTGACTGAATTCGAAA 2040
Db 1981 ATGCGCTTGAACCTAGTACAGTAAATCTAAGCCCACTAATTTGACTGAATTCGAAA 2040
Qy 2041 TTGATAGTCTTCTAGCAGTGAAGATTAAGAAAAAAAGTCAACCAATTCGACGCA 2100
Db 2041 TTGATAGTCTTCTAGCAGTGAAGATTAAGAAAAAAAGTCAACCAATTCGACGCA 2100
Qy 2101 GGACAGAGAGAAACCTAACAATGAGAAAGTAAAGAACTGCAACTGAGCCCAAGAA 2160
Db 2101 GGACAGAGAGAAACCTAACAATGAGAAAGTAAAGAACTGCAACTGAGCCCAAGAA 2160
Qy 2161 GTAAACAAGCCAAATGAAAGACAGTAAAGACATGACAGTATCTTTCCAGAGCTGA 2220
Db 2161 GTAAACAAGCCAAATGAAAGACAGTAAAGACATGACAGTATCTTTCCAGAGCTGA 2220
Qy 2221 AGTTAAACAATGAGCAGCTGCTCTTTACTAGTGTCAATACAGTGAACCTTAAGAT 2280
Db 2221 AGTTAAACAATGAGCAGCTGCTCTTTACTAGTGTCAATACAGTGAACCTTAAGAT 2280
Qy 2281 TTGTCATCTAGCTTCTCAAGAGAGAGAAAGAACTAGAAACAGTTAAAGTGT 2340
Db 2281 TTGTCATCTAGCTTCTCAAGAGAGAGAAAGAACTAGAAACAGTTAAAGTGT 2340
Qy 2341 CTAAATTAATGCTGAGAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTGCAC 2400
Db 2341 CTAAATTAATGCTGAGAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTGCAC 2400
Qy 2401 AAAGATCTGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2460
Db 2401 AAAGATCTGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2460
Qy 2461 AAAGATCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2520
Db 2461 AAAGATCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2520
Qy 2521 GTGAGAGTCACTGAGCAGATTTGAAAACCCCAAGAGCTAATTCATGTTTCCAAAG 2580
Db 2521 GTGAGAGTCACTGAGCAGATTTGAAAACCCCAAGAGCTAATTCATGTTTCCAAAG 2580
Qy 2581 ATATATGAATGACACAGAGAGCTTTAAGTATCCATTGGACATGAAGTGAACCAAGTC 2640
Db 2581 ATATATGAATGACACAGAGAGCTTTAAGTATCCATTGGACATGAAGTGAACCAAGTC 2640
Qy 2641 GGGAAACAAGATGAATGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2700
Db 2641 GGGAAACAAGATGAATGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2700
Qy 2701 TCAAGTTTCAAGGCGCAGTCAATTTGCTGTTTCAATCAAGAAATGACAGAGAGG 2760
Db 2701 TCAAGTTTCAAGGCGCAGTCAATTTGCTGTTTCAATCAAGAAATGACAGAGAGG 2760

Db 2701 TCAAGTTTCAAGGCGCAGTCAATTTGCTGTTTCAATCAAGAAATGACAGAGAGG 2760
Qy 2761 AATGTGCAACATTCCTGCCCCACCTGAGGCTCTTAAGAAACAAAGTCCAAAGTCACTT 2820
Db 2761 AATGTGCAACATTCCTGCCCCACCTGAGGCTCTTAAGAAACAAAGTCCAAAGTCACTT 2820
Qy 2821 TTGAATGTGAACAAAGAGAGAAATCAAGAGAAAGAAATGAGTCTAATATCAAGCTGTAC 2880
Db 2821 TTGAATGTGAACAAAGAGAGAAATCAAGAGAAAGAAATGAGTCTAATATCAAGCTGTAC 2880
Qy 2881 AGACATTAATATATCTGACAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2940
Db 2881 AGACATTAATATATCTGACAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2940
Qy 2941 ATGCCAATGATGATCAAGAGAGAGCTCTAGTGTGCTATCACTCACTGCTGAGAGCA 3000
Db 2941 ATGCCAATGATGATCAAGAGAGAGCTCTAGTGTGCTATCACTCACTGCTGAGAGCA 3000
Qy 3001 ACGAAACTGACCTGATTAACCTCAAAATPAAACATGACCTTTTACAAACCCATATGCTATC 3060
Db 3001 ACGAAACTGACCTGATTAACCTCAAAATPAAACATGACCTTTTACAAACCCATATGCTATC 3060
Qy 3061 CACCACTTTTCCATCAAGTCAATTTGTTAAACATAATGTAAGAAATTCGCTAGAGG 3120
Db 3061 CACCACTTTTCCATCAAGTCAATTTGTTAAACATAATGTAAGAAATTCGCTAGAGG 3120
Qy 3121 AAAAATTGAGGACATTCATGATGACCTGAAAGAAAGTGGAAATGAGAAATTCCTCAA 3180
Db 3121 AAAAATTGAGGACATTCATGATGACCTGAAAGAAAGTGGAAATGAGAAATTCCTCAA 3180
Qy 3181 GTACAGTGAAGCAATTAAGCCGTAATPAACTAATGAGAAATGTTTTTAAAGAGCCAGCT 3240
Db 3181 GTACAGTGAAGCAATTAAGCCGTAATPAACTAATGAGAAATGTTTTTAAAGAGCCAGCT 3240
Qy 3241 CAAGCAATTAATTAAGAGTGTGCTCCAGTACTAATGAAAGTGGCTCCAGATTTAATGAAA 3300
Db 3241 CAAGCAATTAATTAAGAGTGTGCTCCAGTACTAATGAAAGTGGCTCCAGATTTAATGAAA 3300
Qy 3301 TAGGTTCAAGTGAAGAAACCTCAAGAGAACTGAGTGAAGAAAGAGGAGCCAAATTTGA 3360
Db 3301 TAGGTTCAAGTGAAGAAACCTCAAGAGAACTGAGTGAAGAAAGAGGAGCCAAATTTGA 3360
Qy 3361 ATGCTATGCTTGAATGAAGGCTTTTGCACCTGAGGCTTAATPAAACAAAGCTTCTGAAA 3420
Db 3361 ATGCTATGCTTGAATGAAGGCTTTTGCACCTGAGGCTTAATPAAACAAAGCTTCTGAAA 3420
Qy 3421 GTAAATTTGAGACCTCGAATTAAGAAAGCAAGAAATGAGAAAGTGTGAGACTGTTA 3480
Db 3421 GTAAATTTGAGACCTCGAATTAAGAAAGCAAGAAATGAGAAAGTGTGAGACTGTTA 3480
Qy 3481 ATACAGATTTCTCCATATCTGATTCAGATTAAGAAACAGCTATGAGGAGTGTGTC 3540
Db 3481 ATACAGATTTCTCCATATCTGATTCAGATTAAGAAACAGCTATGAGGAGTGTGTC 3540
Qy 3541 ATGCATCTCAGGTTTGTCTGAGACCTGATGACCTGTTAGATGATGTGAAATPAAAG 3600
Db 3541 ATGCATCTCAGGTTTGTCTGAGACCTGATGACCTGTTAGATGATGTGAAATPAAAG 3600
Qy 3601 AAGATTAATGATTTGCTGAGAAATGACATTAAGAAAGTGTGCTGCTGTTTAAAGAGCG 3660
Db 3601 AAGATTAATGATTTGCTGAGAAATGACATTAAGAAAGTGTGCTGCTGTTTAAAGAGCG 3660
Qy 3661 TCCAGAGAGAGACCTTAAGCAGAGTCTAGCCCTTCAACCATAACATTTGCTCAGG 3720
Db 3661 TCCAGAGAGAGACCTTAAGCAGAGTCTAGCCCTTCAACCATAACATTTGCTCAGG 3720
Qy 3721 GTTACCGAAGAGGAGCCAAAGAAATTAAGTCTCAGAGAGAACTTAATCTAGAGATG 3780
Db 3721 GTTACCGAAGAGGAGCCAAAGAAATTAAGTCTCAGAGAGAACTTAATCTAGAGATG 3780
Qy 3781 AAGAGCTTCCCTGCTTCAACATCTGTTATTTGTTAAGTAAACATATACCTTCTCAGT 3840
Db 3781 AAGAGCTTCCCTGCTTCAACATCTGTTATTTGTTAAGTAAACATATACCTTCTCAGT 3840
```

QY 3841 CTAATGACATAGACCGGTTGCTACCGAGTGTCTGTCTAAGAACAGAGGAGATTAT 3900  
 DB 3841 CTAATGACATAGACCGGTTGCTACCGAGTGTCTGTCTAAGAACAGAGGAGATTAT 3900  
 QY 3901 TATCATGGAAGAAATAGCTTAATAGTACAGTAAACAGGTAATATTGGCAAAAGCATCTC 3960  
 DB 3901 TATCATGGAAGAAATAGCTTAATAGTACAGTAAACAGGTAATATTGGCAAAAGCATCTC 3960  
 QY 3961 AGGAACATCACTTAAGTGAAGAAACAAATGTCTGCTAGCTTTTCTTCAAGTGA 4020  
 DB 3961 AGGAACATCACTTAAGTGAAGAAACAAATGTCTGCTAGCTTTTCTTCAAGTGA 4020  
 QY 4021 GTGAATGGAAGACTTGACTGCAATATACAAACCCAGAGATCTTTCTGATGTTGGTCTT 4080  
 DB 4021 GTGAATGGAAGACTTGACTGCAATATACAAACCCAGAGATCTTTCTGATGTTGGTCTT 4080  
 QY 4081 CCAAAACAATGAGGATCACTGTAAGACCAAGGAGTTGTCTGATGACAAAGAAATTGG 4140  
 DB 4081 CCAAAACAATGAGGATCACTGTAAGACCAAGGAGTTGTCTGATGACAAAGAAATTGG 4140  
 QY 4141 TTTCAATGATGAAGAAAGAGAAACGGGCTTGAAGAAATATATCAAGAAAGCA 4200  
 DB 4141 TTTCAATGATGAAGAAAGAGAAACGGGCTTGAAGAAATATATCAAGAAAGCA 4200  
 QY 4201 TGGATTAACCTTGAAGGAGAGATCTGGGTGTGAGTGAAGCAAGCGCTCTGAG 4260  
 DB 4201 TGGATTAACCTTGAAGGAGAGATCTGGGTGTGAGTGAAGCAAGCGCTCTGAG 4260  
 QY 4261 ACTGCTCAGGGCTATTCCTCTCAGAGTGAATTTTAAACCACTCAGCAGAGGATACATGC 4320  
 DB 4261 ACTGCTCAGGGCTATTCCTCTCAGAGTGAATTTTAAACCACTCAGCAGAGGATACATGC 4320  
 QY 4321 AACCTAACCTGATTAAGCTCCAGCAGAAATGGCTGAACCTAAGAACTGTGTTAAACAC 4380  
 DB 4321 AACCTAACCTGATTAAGCTCCAGCAGAAATGGCTGAACCTAAGAACTGTGTTAAACAC 4380  
 QY 4381 ATGGAGAGCGGCTTCTTAACAGCTAACCCCTTCATATAGTGAATCCCTCCCTGAGG 4440  
 DB 4381 ATGGAGAGCGGCTTCTTAACAGCTAACCCCTTCATATAGTGAATCCCTCCCTGAGG 4440  
 QY 4441 ACCTGCGAAATCCAGAACCAAGCATATGAGAAAGAGAGATTAATCTTCAAGAAAGTA 4500  
 DB 4441 ACCTGCGAAATCCAGAACCAAGCATATGAGAAAGAGAGATTAATCTTCAAGAAAGTA 4500  
 QY 4501 GTGAATACCTTAAGCCAGAAATCCAGAAAGGCTTTCTGCTGACAAAGTTGAGGTGCTG 4560  
 DB 4501 GTGAATACCTTAAGCCAGAAATCCAGAAAGGCTTTCTGCTGACAAAGTTGAGGTGCTG 4560  
 QY 4561 CAGATAGTCTTCAACAGTAAATAAGAACCAAGAGTGAAGAGTCAATCCCTCTTAAT 4620  
 DB 4561 CAGATAGTCTTCAACAGTAAATAAGAACCAAGAGTGAAGAGTCAATCCCTCTTAAT 4620  
 QY 4621 GCCCATCATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4680  
 DB 4621 GCCCATCATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4680  
 QY 4681 ACTACCATCTCAAGAGAGCTCAATTAAGTGTGTGATGATGATGATGATGATGATGATGAT 4740  
 DB 4681 ACTACCATCTCAAGAGAGCTCAATTAAGTGTGTGATGATGATGATGATGATGATGATGAT 4740  
 QY 4741 AGTCTGGGCGCAACAGATTGACGAAACATCTTCTGATGATGATGATGATGATGATGATGAT 4800  
 DB 4741 AGTCTGGGCGCAACAGATTGACGAAACATCTTCTGATGATGATGATGATGATGATGATGAT 4800  
 QY 4801 CCCCTTACTGGAATCTGGAATCAAGCTCTTCTCTGATGATGATGATGATGATGATGATGAT 4860  
 DB 4801 CCCCTTACTGGAATCTGGAATCAAGCTCTTCTCTGATGATGATGATGATGATGATGATGAT 4860  
 QY 4861 AAGACAGAGCCCAAGAGTCAAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 4920  
 DB 4861 AAGACAGAGCCCAAGAGTCAAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 4920

QY 4921 AAGTCCCAATGAAAGTTGACAAATCTGCCAGGCTCCAGCTGCTGCTCATACTACTG 4980  
 DB 4921 AAGTCCCAATGAAAGTTGACAAATCTGCCAGGCTCCAGCTGCTGCTCATACTACTG 4980  
 QY 4981 ATACTGCTGGGTATTAATGCAATGGAAGAAAGTGTGACAGGAGAGACCCAGAAATTGACAG 5040  
 DB 4981 ATACTGCTGGGTATTAATGCAATGGAAGAAAGTGTGACAGGAGAGACCCAGAAATTGACAG 5040  
 QY 5041 CTTCAAGAAAGGCTCAACAAAGAAATGTCACATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5100  
 DB 5041 CTTCAAGAAAGGCTCAACAAAGAAATGTCACATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5100  
 QY 5101 AATTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5160  
 DB 5101 AATTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5160  
 QY 5161 CTGAAGAGACTACTCATGTTGTTATGAAAACAGATGCTGAGTTGTGTGTAACGACAC 5220  
 DB 5161 CTGAAGAGACTACTCATGTTGTTATGAAAACAGATGCTGAGTTGTGTGTAACGACAC 5220  
 QY 5221 TGAATATTTTCTGAAATGTCGAGAGAAATGGGTAGTACTATTTCTGGGTGACCC 5280  
 DB 5221 TGAATATTTTCTGAAATGTCGAGAGAAATGGGTAGTACTATTTCTGGGTGACCC 5280  
 QY 5281 AGTCTATTTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGAGATGAG 5340  
 DB 5281 AGTCTATTTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGAGATGAG 5340  
 QY 5341 TCAATGAGAGAAACCAACAGAGTCCAAAGCGAGCAAGAAATCCAGAGACAGAAAGATCT 5400  
 DB 5341 TCAATGAGAGAAACCAACAGAGTCCAAAGCGAGCAAGAAATCCAGAGACAGAAAGATCT 5400  
 QY 5401 TCAAGGGGCTTGAATATGTTGCTATGAGGCTTCAACCAATGCTCCCAAGATCACTGG 5460  
 DB 5401 TCAAGGGGCTTGAATATGTTGCTATGAGGCTTCAACCAATGCTCCCAAGATCACTGG 5460  
 QY 5461 AATGATGATGACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5520  
 DB 5461 AATGATGATGACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5520  
 QY 5521 GCACAGGCTGTCACCCCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 5580  
 DB 5521 GCACAGGCTGTCACCCCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 5580  
 QY 5581 TCCATGCAATTTGGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5640  
 DB 5581 TCCATGCAATTTGGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5640  
 QY 5641 GTGAGACACTTACCAAGTGCAGAGAGTGAACCTTACTGATATCCCAAGATCCCAAGAT 5700  
 DB 5641 GTGAGACACTTACCAAGTGCAGAGAGTGAACCTTACTGATATCCCAAGATCCCAAGAT 5700  
 QY 5701 GCCACTACTGA 5711  
 DB 5701 GCCACTACTGA 5711

RESULT 9  
 US-08-825-487A-3  
 ; Sequence 3, Application US/08825487A  
 ; Patent No. 6048689  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Murphy, Patricia D.  
 ; APPLICANT: White, Marja B.  
 ; TITLE OF INVENTION: METHODS FOR IDENTIFYING VARIATIONS IN POLYNUCLEOTIDE SEQUENCE  
 ; NUMBER OF SEQUENCES: 110  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Howrey & Simon  
 ; STREET: 1299 Pennsylvania Avenue., N.W.  
 ; CITY: Washington,  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20004

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/825,487A  
 FILING DATE: 28-MAR-1997  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US98/060002  
 FILING DATE: 26-Mar-1998  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Albert P. Halluin  
 REGISTRATION NUMBER: 25,227  
 REFERENCE/DOCKET NUMBER: 05371.0012.999  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-463-8100  
 TELEFAX: 650-463-8400  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5711 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: not relevant  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
 STRAIN: BRCA1  
 POSITION IN GENOME:  
 CHROMOSOME/SEGMENT: 17  
 MAP POSITION: 17q21  
 US-08-825-487A-3

Query Match 99.8%; Score 5701.4; DB 3; Length 5711;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 5705; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

QY 1 AGCTGCTGAGACTTCTCTGAGACCCCGCACAGGCTGTGGGTTTCTCAGATPACTGGGCC 60
DB 1 AGCTGCTGAGACTTCTCTGAGACCCCGCACAGGCTGTGGGTTTCTCAGATPACTGGGCC 60
QY 61 CCTGGCTCAGAGGCTTCAACCTCTGCTGGGTTAAAGTTCATTGGAACGAAAGAA 120
DB 61 CCTGGCTCAGAGGCTTCAACCTCTGCTGGGTTAAAGTTCATTGGAACGAAAGAA 120
QY 121 TGGATTATCTGCTCTTGGCGGTTGAAGAGTACAAATGTCAATTAATGTCAGAGAAA 180
DB 121 TGGATTATCTGCTCTTGGCGGTTGAAGAGTACAAATGTCAATTAATGTCAGAGAAA 180
QY 181 TCTTAGAGTGTCCATCTGTCTGAGTTGATCAAGAACTGTCTCCCAAAAGTGTGACC 240
DB 181 TCTTAGAGTGTCCATCTGTCTGAGTTGATCAAGAACTGTCTCCCAAAAGTGTGACC 240
QY 241 ACATATTTTGAAGATTTTGCATGCTGAAACCTTCTCAACGAGAAAGAGGCTTCAACAGT 300
DB 241 ACATATTTTGAAGATTTTGCATGCTGAAACCTTCTCAACGAGAAAGAGGCTTCAACAGT 300
QY 301 GTTCCTTATGTAAAGATATATTAACAAAGAGGCTTCAAGAAAGTACGAGATTAGTGC 360
DB 301 GTTCCTTATGTAAAGATATATTAACAAAGAGGCTTCAAGAAAGTACGAGATTAGTGC 360
QY 361 AACTTGTGAAGAGCTATTGAAATCATTTGTGCTTTTCAAGTTCACACAGGTTGGAGT 420
DB 361 AACTTGTGAAGAGCTATTGAAATCATTTGTGCTTTTCAAGTTCACACAGGTTGGAGT 420
QY 421 ATGCAAAAGAGCTATTTTGAAGAAAGGAAATTAACCTCCCTGAATCTAAAGAGT 480
DB 421 ATGCAAAAGAGCTATTTTGAAGAAAGGAAATTAACCTCCCTGAATCTAAAGAGT 480
QY 481 AAGTTTCTATCATCAAGATATGGGCTACAGAAACCGTGCCTCAAGAGT 540
DB 481 AAGTTTCTATCATCAAGATATGGGCTACAGAAACCGTGCCTCAAGAGT 540

```

```

DB 481 AAGTTTCTATCATCAAGATATGGGCTACAGAAACCGTGCCTCAAGAGT 540
QY 541 AACCCGAAAATCCTTCTCTGAGAGAAACAGCTCAGTGTCCACTCTTAACCTGGAA 600
DB 541 AACCCGAAAATCCTTCTCTGAGAGAAACAGCTCAGTGTCCACTCTTAACCTGGAA 600
QY 601 CTGTGAGAACTCTGAGACAAAGCAGGATACCACTCAAAAGAGTCTGTCTACATTTG 660
DB 601 CTGTGAGAACTCTGAGACAAAGCAGGATACCACTCAAAAGAGTCTGTCTACATTTG 660
QY 661 AATTGGATCTGATTTCTTGAAGATACCTTAATTAAGGCACTTATTCAGTGTGGAG 720
DB 661 AATTGGATCTGATTTCTTGAAGATACCTTAATTAAGGCACTTATTCAGTGTGGAG 720
QY 721 ATCAAGATTTCTTCAAAATCAACCTTCAAGGAAACAGGAGTGAATCAGTTGATCTG 780
DB 721 ATCAAGATTTCTTCAAAATCAACCTTCAAGGAAACAGGAGTGAATCAGTTGATCTG 780
QY 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGACGATGTAACTAAATCTGAATCATCAAC 840
DB 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGACGATGTAACTAAATCTGAATCATCAAC 840
QY 841 CCAATATATATGATTTGAACCACTGAGAAAGGCTGACCTGAGAGGCTATCAAGAAAGT 900
DB 841 CCAATATATATGATTTGAACCACTGAGAAAGGCTGACCTGAGAGGCTATCAAGAAAGT 900
QY 901 ATCAGGGATGTTCTGTTCAAACTTGCATGTGAGCCATGTGGCAAAATCTCATGCCA 960
DB 901 ATCAGGGATGTTCTGTTCAAACTTGCATGTGAGCCATGTGGCAAAATCTCATGCCA 960
QY 961 GCTCATTTACAGCATGAGAACAGCAGTTTACTCACTAAAGACAGATGATGATAGAA 1020
DB 961 GCTCATTTACAGCATGAGAACAGCAGTTTACTCACTAAAGACAGATGATGATAGAA 1020
QY 1021 AGGCTGAATTTCTGATTAATTAAGCAACAGCTGCTTGAAGAGGCCAATTAACAGAT 1080
DB 1021 AGGCTGAATTTCTGATTAATTAAGCAACAGCTGCTTGAAGAGGCCAATTAACAGAT 1080
QY 1081 GGGCTGGAAGTAAAGAAACATGTATGATGAGGAGCTCCAGACAGAAAAAGGATG 1140
DB 1081 GGGCTGGAAGTAAAGAAACATGTATGATGAGGAGCTCCAGACAGAAAAAGGATG 1140
QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGGAATTAAGCAAACTGCATGCT 1200
DB 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGGAATTAAGCAAACTGCATGCT 1200
QY 1201 CAGAGATCTTGAAGATCTGAAGATGTTCTTGGATTAACCTAAATAGCAGCAATTGAGA 1260
DB 1201 CAGAGATCTTGAAGATCTGAAGATGTTCTTGGATTAACCTAAATAGCAGCAATTGAGA 1260
QY 1261 AAGTTAATGAGTGGTTTCCAGAGTGAATGAACCTTAAAGTTCTGAGACCTCAGATG 1320
DB 1261 AAGTTAATGAGTGGTTTCCAGAGTGAATGAACCTTAAAGTTCTGAGACCTCAGATG 1320
QY 1321 GGGAGTCTGAATCAAAATGCCAAAGTGAATGATTAAGAGCTTAAATAGAGTATG 1380
DB 1321 GGGAGTCTGAATCAAAATGCCAAAGTGAATGATTAAGAGCTTAAATAGAGTATG 1380
QY 1381 AATATTTCTGTTCTTCAAGAGAAATGACTTACTGCGCAGTGAATCTCATAGAGCTTTAA 1440
DB 1381 AATATTTCTGTTCTTCAAGAGAAATGACTTACTGCGCAGTGAATCTCATAGAGCTTTAA 1440
QY 1441 TATGTAAAGTGAAGAGTCACTTCCAAATCAATGAGAGATTAATTTGAACCAAAATAT 1500
DB 1441 TATGTAAAGTGAAGAGTCACTTCCAAATCAATGAGAGATTAATTTGAACCAAAATAT 1500
QY 1501 TTGGGAAAACCTATCGAAGAAAGCAAGCTCCCAACTTAAGCATATTAAGCTGAAATTC 1560
DB 1501 TTGGGAAAACCTATCGAAGAAAGCAAGCTCCCAACTTAAGCATATTAAGCTGAAATTC 1560
QY 1561 TAAATTAAGAGCAATTTGTTACTGAGCCAGATATTAAGAGAGGCTCCCTCAAAATA 1620
DB 1561 TAAATTAAGAGCAATTTGTTACTGAGCCAGATATTAAGAGAGGCTCCCTCAAAATA 1620

```



QY 1621 AATTAAAGCTTAAAGAGAGACCTTACATCAGGCTTCATCTGAGGATTTTATCAAGAAG 1680  
|||  
Db 1621 AATTAAAGCTTAAAGAGAGACCTTACATCAGGCTTCATCTGAGGATTTTATCAAGAAG 1680  
QY 1681 CAGATTGGCAGTTCAAAAGACTCTCTGAATGATTAATCAAGGAACTAACCAACGAGAGC 1740  
|||  
Db 1681 CAGATTGGCAGTTCAAAAGACTCTCTGAATGATTAATCAAGGAACTAACCAACGAGAGC 1740  
QY 1741 AGAATGCTCAAGTGTGATTAATTAATTAATGCTGATGAGAAATTAACCAAAAGGTGATT 1800  
|||  
Db 1741 AGAATGCTCAAGTGTGATTAATTAATTAATGCTGATGAGAAATTAACCAAAAGGTGATT 1800  
QY 1801 CTATTCAAGATGAGAAAAATCTTAACCCCAATGATATCACTGAAAAAGATCTGCTTTCA 1860  
|||  
Db 1801 CTATTCAAGATGAGAAAAATCTTAACCCCAATGATATCACTGAAAAAGATCTGCTTTCA 1860  
QY 1861 AAACGAAAGCTGAACCTTAAGCAGCAGTATTAAGCAATATGGAATCTGAAATTAATATCC 1920  
|||  
Db 1861 AAACGAAAGCTGAACCTTAAGCAGCAGTATTAAGCAATATGGAATCTGAAATTAATATCC 1920  
QY 1921 ACAATTCAAAAGCACCTTAAAAAGAAATAGGCTGAGAGAAAGTCTTCAACAGGCATATTC 1980  
|||  
Db 1921 ACAATTCAAAAGCACCTTAAAAAGAAATAGGCTGAGAGAAAGTCTTCAACAGGCATATTC 1980  
QY 1981 ATGGGCTTGAACCTAGTACGTAGAAATCTAAGGCCCACTTAATTGTACTGAATTGCAAA 2040  
|||  
Db 1981 ATGGGCTTGAACCTAGTACGTAGAAATCTAAGGCCCACTTAATTGTACTGAATTGCAAA 2040  
QY 2041 TTGATAGTTGTTCTTAGCAGTGAAGATTAAGAAAAAAGTAAACCAAAATGCGAGTCA 2100  
|||  
Db 2041 TTGATAGTTGTTCTTAGCAGTGAAGATTAAGAAAAAAGTAAACCAAAATGCGAGTCA 2100  
QY 2101 GGCACAGAGAAACCTTAACAATCATGAAAGTAAAGAACTGCAACTGAGCCAAAGAAAGA 2160  
|||  
Db 2101 GGCACAGAGAAACCTTAACAATCATGAAAGTAAAGAACTGCAACTGAGCCAAAGAAAGA 2160  
QY 2161 GTAAACAAGCCAAATGAACAGACAACTAAGAAAGCATGACAGTATCTTCCAGAGCTGA 2220  
|||  
Db 2161 GTAAACAAGCCAAATGAACAGACAACTAAGAAAGCATGACAGTATCTTCCAGAGCTGA 2220  
QY 2221 AGTTAAACAATGCAACTGTTCTTTTACTAAGTGTCAATACAGTAACTTAAGAAT 2280  
|||  
Db 2221 AGTTAAACAATGCAACTGTTCTTTTACTAAGTGTCAATACAGTAACTTAAGAAT 2280  
QY 2281 TTGTCAATCTTAGCTTCCAGAGAAAGAAAGAAAGAACTAGAAA CAGTTAAAGTGT 2340  
|||  
Db 2281 TTGTCAATCTTAGCTTCCAGAGAAAGAAAGAAAGAAAGAACTAGAAA CAGTTAAAGTGT 2340  
QY 2341 CTAATTAATGCTGAGAAACCCCAAAAGATCTCATGTTAAGTGAAGAAAGGTTTGGCAACTG 2400  
|||  
Db 2341 CTAATTAATGCTGAGAAACCCCAAAAGATCTCATGTTAAGTGAAGAAAGGTTTGGCAACTG 2400  
QY 2401 AAAGATCTGTAGAGAGTGAAGTATTTTCACTGTACTGTACTGATTAAGGCACTCAGG 2460  
|||  
Db 2401 AAAGATCTGTAGAGAGTGAAGTATTTTCACTGTACTGTACTGATTAAGGCACTCAGG 2460  
QY 2461 AAAGATCTGTACTGTAGAGTGAAGTACTTAAGGAGGCAAAAACAGAACCAATTAAT 2520  
|||  
Db 2461 AAAGATCTGTACTGTAGAGTGAAGTACTTAAGGAGGCAAAAACAGAACCAATTAAT 2520  
QY 2521 GTGTGAGTCAAGTGTGACAGATTTTGAACCCCAAGGAACTAATGATGTTTCCAAAG 2580  
|||  
Db 2521 GTGTGAGTCAAGTGTGACAGATTTTGAACCCCAAGGAACTAATGATGTTTCCAAAG 2580  
QY 2581 AATAATAGAAATGACACAGAAAGCTTAAATGATTCATGAGGACATGAAGTTAAACCAAGTC 2640  
|||  
Db 2581 AATAATAGAAATGACACAGAAAGCTTAAATGATTCATGAGGACATGAAGTTAAACCAAGTC 2640  
QY 2641 GGGAAACAGCATAGAAATGGAAGAAAGTGAACCTTGATGCTCAGTATTTGGAGAAATACAT 2700  
|||  
Db 2641 GGGAAACAGCATAGAAATGGAAGAAAGTGAACCTTGATGCTCAGTATTTGGAGAAATACAT 2700

QY 2701 TCAAGTTTCAAAAGGCCAGTCAATTTGCTCTGTTTCAATTCAGAAATGACAGAAAGG 2760  
|||  
Db 2701 TCAAGTTTCAAAAGGCCAGTCAATTTGCTCTGTTTCAATTCAGAAATGACAGAAAGG 2760  
QY 2761 AATGTGCAACATTTCTGTGCCCACTCTGGGCTTTAAGAAACAAAGTCCAAAGTCACTT 2820  
|||  
Db 2761 AATGTGCAACATTTCTGTGCCCACTCTGGGCTTTAAGAAACAAAGTCCAAAGTCACTT 2820  
QY 2821 TTGAATGTGAACAAAGGAAAGAAATTCAGAAAGAAAGTCAATTAATCAAGCTGTAC 2880  
|||  
Db 2821 TTGAATGTGAACAAAGGAAAGAAATTCAGAAAGAAAGTCAATTAATCAAGCTGTAC 2880  
QY 2881 AGACAGTAAATATCATCTGACAGGCTTCTGTGTGTGTGACAGAAAGATAGCCAGTGTATA 2940  
|||  
Db 2881 AGACAGTAAATATCATCTGACAGGCTTCTGTGTGTGTGACAGAAAGATAGCCAGTGTATA 2940  
QY 2941 ATGCCAAATGTAGTATCAAAAGAGGCTTAGGTTTGTCTATCATCTCAGTTCAAGAGCA 3000  
|||  
Db 2941 ATGCCAAATGTAGTATCAAAAGAGGCTTAGGTTTGTCTATCATCTCAGTTCAAGAGCA 3000  
QY 3001 ACGAAACTGACATCTATCTCCAAATTAACATGACATTTTCAAAACCCATATGCTATAC 3060  
|||  
Db 3001 ACGAAACTGACATCTATCTCCAAATTAACATGACATTTTCAAAACCCATATGCTATAC 3060  
QY 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAACCTAAATGTAAAGAAATGCTGAGAGG 3120  
|||  
Db 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAACCTAAATGTAAAGAAATGCTGAGAGG 3120  
QY 3121 AAAACTTTGAGAAACATTCATGTCACCTGAAAGAAAGTGAATGAGAACATTCGA 3180  
|||  
Db 3121 AAAACTTTGAGAAACATTCATGTCACCTGAAAGAAAGTGAATGAGAACATTCGA 3180  
QY 3181 GTACAGTGAACAAATTTAGCCGTATTAACATTAAGAAATGTTTAAAGAGCAGCT 3240  
|||  
Db 3181 GTACAGTGAACAAATTTAGCCGTATTAACATTAAGAAATGTTTAAAGAGCAGCT 3240  
QY 3241 CAAGCAATTAATTAAGAGTAGTTCACAGTACTAATTAAGAGTGGGCTCCAGTAAATGAA 3300  
|||  
Db 3241 CAAGCAATTAATTAAGAGTAGTTCACAGTACTAATTAAGAGTGGGCTCCAGTAAATGAA 3300  
QY 3241 CAAGCAATTAATTAAGAGTAGTTCACAGTACTAATTAAGAGTGGGCTCCAGTAAATGAA 3300  
|||  
Db 3241 CAAGCAATTAATTAAGAGTAGTTCACAGTACTAATTAAGAGTGGGCTCCAGTAAATGAA 3300  
QY 3301 TAGGTTCCAGTATGAAACATTCAGAGCAACTAGTAGAAACAGAGGCAAAATTTGA 3360  
|||  
Db 3301 TAGGTTCCAGTATGAAACATTCAGAGCAACTAGTAGAAACAGAGGCAAAATTTGA 3360  
QY 3361 ATGCTATCTTAGATTAAGAGGTTTGGCAACTGAGAGTCTAATAACAAAGTCTTCTGGA 3420  
|||  
Db 3361 ATGCTATCTTAGATTAAGAGGTTTGGCAACTGAGAGTCTAATAACAAAGTCTTCTGGA 3420  
QY 3421 GTAATGTAAAGCATCTGAAATTAAGAAAGCAAGAAATTAAGAAAGTACTGACCTGTA 3480  
|||  
Db 3421 GTAATGTAAAGCATCTGAAATTAAGAAAGCAAGAAATTAAGAAAGTACTGACCTGTA 3480  
QY 3481 ATAAGATTTCTTCCATATCTGATTTCAAGATTAAGTGAACAGCTTAAGGAAAGTATG 3540  
|||  
Db 3481 ATAAGATTTCTTCCATATCTGATTTCAAGATTAAGTGAACAGCTTAAGGAAAGTATG 3540  
QY 3541 ATGATCTCAGGTTTGTCTGAGACACTGATGACCTGTATGATGATGTTGAAATTAAGG 3600  
|||  
Db 3541 ATGATCTCAGGTTTGTCTGAGACACTGATGACCTGTATGATGATGTTGAAATTAAGG 3600  
QY 3601 AAGATCTAGTGTGTGCAAAATGACATTAAGAAAGTGTGCTGTTTAAAGCAAAAGCG 3660  
|||  
Db 3601 AAGATCTAGTGTGTGCAAAATGACATTAAGAAAGTGTGCTGTTTAAAGCAAAAGCG 3660  
QY 3661 TCCAGAGAGAGAGCTTAGCAGAGTCTTACCCCTTCAACCATATACATTTGGCTCAGG 3720  
|||  
Db 3661 TCCAGAGAGAGAGCTTAGCAGAGTCTTACCCCTTCAACCATATACATTTGGCTCAGG 3720  
QY 3721 GTTACCGAAGAGGAGCCAAAGAAATTAAGTCTCAGAAAGAACTTATCTAGTGAAGATG 3780  
|||  
Db 3721 GTTACCGAAGAGGAGCCAAAGAAATTAAGTCTCAGAAAGAACTTATCTAGTGAAGATG 3780  
QY 3781 AAGAGCTTCCCTGCTTCCAAACCTTGTATTTGGTAAAGTAAACATATACCTTCTCAGT 3840  
|||

Db 3781 AAGAGCTTCCTGCTCCAACTCTGTTATTTGGTAAAGTAACAATATACCTTCTGAGT 3840  
Qy 3841 CTACTAGGCATAGACCCGTTGCTACCGAGTGTCTGTCTAAGAACACAGAGGAAATTTAT 3900  
Db 3841 CTACTAGGCATAGACCCGTTGCTACCGAGTGTCTGTCTAAGAACACAGAGGAAATTTAT 3900  
Qy 3901 TATCATTTGAAGAAATGCTTAAATGACTGACATACCAAGTAATATTGGCAAAAGGATCTC 3960  
Db 3901 TATCATTTGAAGAAATGCTTAAATGACTGACATACCAAGTAATATTGGCAAAAGGATCTC 3960  
Qy 3961 AGAATCATCACCTTAGTAGAGAAACAAATGTTCTGTAGCTGTTTCTTCAAGTCA 4020  
Db 3961 AGAATCATCACCTTAGTAGAGAAACAAATGTTCTGTAGCTGTTTCTTCAAGTCA 4020  
Qy 4021 GTGAATTTGGAAGACTTGAAGTGAACCAACCCAGAGATCTTTCTTGAATGGTCTT 4080  
Db 4021 GTGAATTTGGAAGACTTGAAGTGAACCAACCCAGAGATCTTTCTTGAATGGTCTT 4080  
Qy 4081 CCAAAACAATAGAGCATCAGTCTGAAGCCAGGGAGTTGTCTGTGACAAAGAAATGG 4140  
Db 4081 CCAAAACAATAGAGCATCAGTCTGAAGCCAGGGAGTTGTCTGTGACAAAGAAATGG 4140  
Qy 4141 TTTGATGATGAAGAAAGAGGAGCGGCTTGGAGAAATATATGAAGAGCAAGCA 4200  
Db 4141 TTTGATGATGAAGAAAGAGGAGCGGCTTGGAGAAATATATGAAGAGCAAGCA 4200  
Qy 4201 TGGATTTCAAACTTAGAGTGAAGCAGCATCTGGGTGTGAAGTGAACAAAGCTCTGAG 4260  
Db 4201 TGGATTTCAAACTTAGAGTGAAGCAGCATCTGGGTGTGAAGTGAACAAAGCTCTGAG 4260  
Qy 4261 ACTGCTCAGGGCTATCTCTCAGAGTGAATTTTAAACAATCAGAGAGGATACCAATGC 4320  
Db 4261 ACTGCTCAGGGCTATCTCTCAGAGTGAATTTTAAACAATCAGAGAGGATACCAATGC 4320  
Qy 4321 AACATPAACCTGTAAGCTCCAGAGAAATGGCTGAAGTGAAGCTGTTGAGAAACAGC 4380  
Db 4321 AACATPAACCTGTAAGCTCCAGAGAAATGGCTGAAGTGAAGCTGTTGAGAAACAGC 4380  
Qy 4381 ATGGAGGCAAGCTTCTAACAAGCTACCTTCATCATTAAGTGAATCTTCTGCTTGAAG 4440  
Db 4381 ATGGAGGCAAGCTTCTAACAAGCTACCTTCATCATTAAGTGAATCTTCTGCTTGAAG 4440  
Qy 4441 AACTGCGAAATCCAGAAACAAAGCAATCAGAAACAAAGCAATCTTCAAGAAAGTA 4500  
Db 4441 AACTGCGAAATCCAGAAACAAAGCAATCAGAAACAAAGCAATCTTCAAGAAAGTA 4500  
Qy 4501 GTGAATACCCCTTAAGCCAGAAATCCAGAGGCTTCTGCTGAACAAGTTTGAAGTGTCTG 4560  
Db 4501 GTGAATACCCCTTAAGCCAGAAATCCAGAGGCTTCTGCTGAACAAGTTTGAAGTGTCTG 4560  
Qy 4561 CAGATAGTTCTAACAAGTAATAAGAACAGAGTGAAGGTCATCCCTCTTAAT 4620  
Db 4561 CAGATAGTTCTAACAAGTAATAAGAACAGAGTGAAGGTCATCCCTCTTAAT 4620  
Qy 4621 GCCCATCATTAAGTATAGTGTGTATGATGACAGATGCTGCGAGTCTTCAAGATAGAA 4680  
Db 4621 GCCCATCATTAAGTATAGTGTGTATGATGACAGATGCTGCGAGTCTTCAAGATAGAA 4680  
Qy 4681 ACTACCAATCTCAAGAGGAGCTCATTAAGGTTGTGATGTGAGAGCAACAGCTGGAAG 4740  
Db 4681 ACTACCAATCTCAAGAGGAGCTCATTAAGGTTGTGATGTGAGAGCAACAGCTGGAAG 4740  
Qy 4741 AGTCTGGGCAACAGATTTGACGAAACATCTTACTTGGCAAGGCAAGATCTAGAGGAA 4800  
Db 4741 AGTCTGGGCAACAGATTTGACGAAACATCTTACTTGGCAAGGCAAGATCTAGAGGAA 4800  
Qy 4801 CCCCTTACCTGGAATCTGGAATCAGCTCTTCTGTGATGACCTTGAATCTGATCTTCTG 4860  
Db 4801 CCCCTTACCTGGAATCTGGAATCAGCTCTTCTGTGATGACCTTGAATCTGATCTTCTG 4860  
Qy 4861 AAGAGAGAGCCCAAGTCAAGTGTGTGCAATACCAATCTCAACCTCTGATTTGA 4920  
Db 4861 AAGAGAGAGCCCAAGTCAAGTGTGTGCAATACCAATCTCAACCTCTGATTTGA 4920

Db 4861 AAGAGAGAGCCCAAGTCAAGTGTGTGCAATACCAATCTTCAACCTCTGATTTGA 4920  
Qy 4921 AAGTTCCTCAATTAAGATGTCAGAAATCTGCCAGGGTCCAGCTGTGCTCATACTG 4980  
Db 4921 AAGTTCCTCAATTAAGATGTCAGAAATCTGCCAGGGTCCAGCTGTGCTCATACTG 4980  
Qy 4981 ATACTGCGGGTATTAATGCAATGGAAGAAATGTGAGCAGGAGGAGCAGAAATTTGACAG 5040  
Db 4981 ATACTGCGGGTATTAATGCAATGGAAGAAATGTGAGCAGGAGGAGCAGAAATTTGACAG 5040  
Qy 5041 CTTCAACAGAAAGGGTCAACAAAGAAATGTCAGATGCTGTGCTGTGCTGTGAGCCAGAG 5100  
Db 5041 CTTCAACAGAAAGGGTCAACAAAGAAATGTCAGATGCTGTGCTGTGCTGTGAGCCAGAG 5100  
Qy 5101 AATTATGCTGTGTGACAGTTTGCAGAAACACACATCATCTTAACTTAATCTAATTA 5160  
Db 5101 AATTATGCTGTGTGACAGTTTGCAGAAACACACATCATCTTAACTTAATCTAATTA 5160  
Qy 5161 CTGAAGAGACTCACTCAGTGTGTATGAAACAGATGCTGAATTTGTGTGAGAGGACAC 5220  
Db 5161 CTGAAGAGACTCACTCAGTGTGTATGAAACAGATGCTGAATTTGTGTGAGAGGACAC 5220  
Qy 5221 TGAATATTTTCTAGAAATTCGGAGAGAAATGGGTAGTTAGCTAATTTCTGGGTGACCC 5280  
Db 5221 TGAATATTTTCTAGAAATTCGGAGAGAAATGGGTAGTTAGCTAATTTCTGGGTGACCC 5280  
Qy 5281 AGCTATTTAAAGAAAGAAATGCTGAATGACATGATTTTGAAGTCAAGAGAGATGG 5340  
Db 5281 AGCTATTTAAAGAAAGAAATGCTGAATGACATGATTTTGAAGTCAAGAGAGATGG 5340  
Qy 5341 TCAATGAAAGAAACCAACCAAGTCCAAAGCAAGAGAAAGATCCAGAGCAAGAAAGATCT 5400  
Db 5341 TCAATGAAAGAAACCAACCAAGTCCAAAGCAAGAGAAAGATCCAGAGCAAGAAAGATCT 5400  
Qy 5401 TCAGAGGCTGTAAGATCTGTGTATGAGGCTTCAACCAATGCTCCAGATCAACTG 5460  
Db 5401 TCAGAGGCTGTAAGATCTGTGTATGAGGCTTCAACCAATGCTCCAGATCAACTG 5460  
Qy 5461 AATGATGTAACAGTGTGTGTCTGTGTGAGAGAGCTTTCATCATTCACCTTG 5520  
Db 5461 AATGATGTAACAGTGTGTGTCTGTGTGAGAGAGCTTTCATCATTCACCTTG 5520  
Qy 5521 GCACAGGTCACCCCAATGTTGTGTGAGCCAGAGATGCTGACAGAGCAATGGCT 5580  
Db 5521 GCACAGGTCACCCCAATGTTGTGTGAGCCAGAGATGCTGACAGAGCAATGGCT 5580  
Qy 5581 TCATGCAATTTGGCAGATGTGTGAGGCACTGTGTGAGCCAGAGATGAGGAGTGTGAGCA 5640  
Db 5581 TCATGCAATTTGGCAGATGTGTGAGGCACTGTGTGAGCCAGAGATGAGGAGTGTGAGCA 5640  
Qy 5641 GTGTGACCTTACCAAGTCCAGAGGCTGACACCTTACTGATACCCAGATCCCCCA 5700  
Db 5641 GTGTGACCTTACCAAGTCCAGAGGCTGACACCTTACTGATACCCAGATCCCCCA 5700  
Qy 5701 GCCACTACTGA 5711  
Db 5701 GCCACTACTGA 5711

RESULT 10  
US-09-074-476-5  
; Sequence 5, Application US/09074476  
; Patent No. 6130322  
; GENERAL INFORMATION:  
; APPLICANT: Murphy, Patricia D.  
; APPLICANT: Allen, Antonette C.  
; APPLICANT: Alvares, Christopher P.  
; APPLICANT: Critz, Brenda S.  
; APPLICANT: Olson, Sheri J.  
; APPLICANT: Thurber, Denise  
; APPLICANT: Zeng, Bin  
; TITLE OF INVENTION: Coding Sequences of the Human  
; TITLE OF INVENTION: BRCA1 Gene

```

? NUMBER OF SEQUENCES: 72
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Howrey & Simon
? STREET: 1299 Pennsylvania Avenue N. W.
? CITY: Washington
? STATE: DC
? COUNTRY: USA
? ZIP: 20004
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/074,476
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 09/074,453
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Albert P. Halluin
? REGISTRATION NUMBER: 25,227
? REFERENCE/DOCKET NUMBER: 5371.34.US01
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 650-463-8109
? TELEFAX: 650-463-8400
? INFORMATION FOR SEQ ID NO: 5:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 5711 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: not relevant
? TOPOLOGY: linear
? MOLECULE TYPE: cdna
? ORIGINAL SOURCE:
? ORGANISM: Homo sapiens
? STRAIN: BRCA1 (om13)
? POSITION IN GENOME:
? CHROMOSOME/SEGMENT: 17
? MAP POSITION: 17q21
? US-09-074-476-5

Query March 99.8%; Score 5701.4; DB 3; Length 5711;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5705; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

```

QY 421 ATGCAAAAGCTATATTTTGCAGAAAAAGAAATTAATCTCTGTAACATCTAAAGATG 480
DB 421 ATGCAAAAGCTATATTTTGCAGAAAAAGAAATTAATCTCTGTAACATCTAAAGATG 480
QY 481 AAGTTTCTATCATCAAGATATGAGGCTTCAGAAAACCGTGCAAAAGACTTCTACAGATG 540
DB 481 AAGTTTCTATCATCAAGATATGAGGCTTCAGAAAACCGTGCAAAAGACTTCTACAGATG 540
QY 541 AACCCGAAAAATCCTTCCCTTGAGAGAAACCGATCTCAGTCCCACTCTCTAACCCTTGAA 600
DB 541 AACCCGAAAAATCCTTCCCTTGAGAGAAACCGATCTCAGTCCCACTCTCTAACCCTTGAA 600
QY 601 CTGTGAGAACTCTGAGGACAAAGCAGCGATACCACTCAAAAGACGTCTGTACATTTG 660
DB 601 CTGTGAGAACTCTGAGGACAAAGCAGCGATACCACTCAAAAGACGTCTGTGTACATTTG 660
QY 661 AATTGGATCTGATTTCTTGAGATACCGTTAATAAGCAATTAATTCAGTGTGGAG 720
DB 661 AATTGGATCTGATTTCTTGAGATACCGTTAATAAGCAATTAATTCAGTGTGGAG 720
QY 721 ATCAAGAAATTTTACAAATCACCCCTCAAGAACCAAGGATGAATTCAGTTTGTG 780
DB 721 ATCAAGAAATTTTACAAATCACCCCTCAAGAACCAAGGATGAATTCAGTTTGTG 780
QY 781 CAAAAAGGCTGCTTGGAATTTTCTGAGACGATGTATCAAAATATCTGAATCATCAAC 840
DB 781 CAAAAAGGCTGCTTGGAATTTTCTGAGACGATGTATCAAAATATCTGAATCATCAAC 840
QY 841 CCAGTAATATGATTTTGAACACCACTGAGAGCGTGCAGTGAAGGCGATCCAGAAAAGT 900
DB 841 CCAGTAATATGATTTTGAACACCACTGAGAGCGTGCAGTGAAGGCGATCCAGAAAAGT 900
QY 901 ATCAGGGATGTTCTGTTTCAAACTTGCATGTGAGGCCATGTGSCAAATCTCATGCCA 960
DB 901 ATCAGGGATGTTCTGTTTCAAACTTGCATGTGAGGCCATGTGSCAAATCTCATGCCA 960
QY 961 GCTCATTAACAGCAGAGAGACGAGTTTATTAACACATTAAGACAGATGAATGAGAAA 1020
DB 961 GCTCATTAACAGCAGAGAGACGAGTTTATTAACACATTAAGACAGATGAATGAGAAA 1020
QY 1021 AGGCTGAATTTCTGTAATTAAGCAAAACAGCTGCTTGAAGAGGCCAATTAACAGAT 1080
DB 1021 AGGCTGAATTTCTGTAATTAAGCAAAACAGCTGCTTGAAGAGGCCAATTAACAGAT 1080
QY 1081 GGGCTGGAATGAGAAAACATGTATGATGATGAGCGGACTCCAGACACAGAAAAAGGTAG 1140
DB 1081 GGGCTGGAATGAGAAAACATGTATGATGATGAGCGGACTCCAGACACAGAAAAAGGTAG 1140
QY 1141 ATCTGAATCTGATCCCTGTGTGAGAGAAAAGATGAATTAAGACAGAACTGGCATGCT 1200
DB 1141 ATCTGAATCTGATCCCTGTGTGAGAGAAAAGATGAATTAAGACAGAACTGGCATGCT 1200
QY 1201 CAGAGAAATCTAGAGATATCTGAAGATGTTCTTGATATACCTAAATAGCAGCATTCAGA 1260
DB 1201 CAGAGAAATCTAGAGATATCTGAAGATGTTCTTGATATACCTAAATAGCAGCATTCAGA 1260
QY 1261 AAGTTAATGATGTTTCCAGAGATGATGATGATGATGATGATGATGATGATGATGATG 1320
DB 1261 AAGTTAATGATGTTTCCAGAGATGATGATGATGATGATGATGATGATGATGATGATG 1320
QY 1321 GGGAGTCTGAATCAAAATGCCAAAGTATGATGATGATGATGATGATGATGATGATGATG 1380
DB 1321 GGGAGTCTGAATCAAAATGCCAAAGTATGATGATGATGATGATGATGATGATGATGATG 1380
QY 1381 AATATTTCTGTTCTTCAAGAGAAATAGACTTACTGAGCGCAGATGCTCATGAGGCTTAA 1440
DB 1381 AATATTTCTGTTCTTCAAGAGAAATAGACTTACTGAGCGCAGATGCTCATGAGGCTTAA 1440
QY 1441 TATGTAAGAGTGAAGAGATTCATCAATCAGTATGATGATGATGATGATGATGATGATGAT 1500
DB 1441 TATGTAAGAGTGAAGAGATTCATCAATCAGTATGATGATGATGATGATGATGATGATGAT 1500

```

QY	1501	TTGGGAAACCTATATGGAGGAAGGCAAGCCTCCCACTTAAAGCATGTAACTGAAATC	1560
Db	1501	TTGGGAAACCTATATGGAGGAAGGCAAGCCTCCCACTTAAAGCATGTAACTGAAATC	1560
QY	1561	TAAATATAGGAGCAATTGTTACTGAGGCAAGATTAATCAAGAGGCGTCCCTCAAAATA	1620
Db	1561	TAAATATAGGAGCAATTGTTACTGAGGCAAGATTAATCAAGAGGCGTCCCTCAAAATA	1620
QY	1621	AATTAAAGCGTAAAGAGAGACCTACATCAGGCTTTCATCTGAGGATTTTATCAAGAAAG	1680
Db	1621	AATTAAAGCGTAAAGAGAGACCTACATCAGGCTTTCATCTGAGGATTTTATCAAGAAAG	1680
QY	1661	CAGATTTTGGCAGCTTCAAAAAGACTCTGTAATGATTAATACAGGAACTTAACAAACGAGC	1740
Db	1661	CAGATTTTGGCAGCTTCAAAAAGACTCTGTAATGATTAATACAGGAACTTAACAAACGAGC	1740
QY	1741	AGAATGCTCAAGTGTATGAATATTACTAATAGTGGCATAGAGAAATPAAACAAAGGTGATT	1800
Db	1741	AGAATGCTCAAGTGTATGAATATTACTAATAGTGGCATAGAGAAATPAAACAAAGGTGATT	1800
QY	1801	CTATTTCAGAAATGAGAAAAATCTTAAACCAATAGATCACTCGAAAAGAAATCTGTGTTCA	1860
Db	1801	CTATTTCAGAAATGAGAAAAATCTTAAACCAATAGATCACTCGAAAAGAAATCTGTGTTCA	1860
QY	1861	AAAGCAAAAGCTGCAACTTAAAGCAGCAGTATAGCAATATGGAATCGAATTAATATCC	1920
Db	1861	AAAGCAAAAGCTGCAACTTAAAGCAGCAGTATAGCAATATGGAATCGAATTAATATATCC	1920
QY	1921	ACAAATTCAAAAGCAGCTTAAAAAGATATAGCGTAGGAGGAAGCTTCTACAGGCAATATTC	1980
Db	1921	ACAAATTCAAAAGCAGCTTAAAAAGATATAGCGTAGGAGGAAGCTTCTACAGGCAATATTC	1980
QY	1981	ATGCGCTTGAACCTAGTAGCTAGTAGAAATCTAAGCCCACTAATTTGTACTGAATTTGCATA	2040
Db	1981	ATGCGCTTGAACCTAGTAGCTAGTAGAAATCTAAGCCCACTAATTTGTACTGAATTTGCATA	2040
QY	2041	TTGATATAGTTGTTCTACGAGTGAAGAGATPAAAGAAAAAAGTACACCAATATGCCAGTCA	2100
Db	2041	TTGATATAGTTGTTCTACGAGTGAAGAGATPAAAGAAAAAAGTACACCAATATGCCAGTCA	2100
QY	2101	GGCACAAGCAAAACCTTACAACCTCAGTAAGGTAAAGAACTGGCAACTGGAGCAAGAAAGA	2160
Db	2101	GGCACAAGCAAAACCTTACAACCTCAGTAAGGTAAAGAACTGGCAACTGGAGCAAGAAAGA	2160
QY	2161	GTAAACAAGCCAAATGAAACAGACAAATAAAGACATGACAGATATCTTTCCAGAGCTGA	2220
Db	2161	GTAAACAAGCCAAATGAAACAGACAAATAAAGACATGACAGATATCTTTCCAGAGCTGA	2220
QY	2221	AGTTAACCAATGCACTCGGTGTTCTTTTACTAGTGTTCAAATACAGTAACTTAAAGAT	2280
Db	2221	AGTTAACCAATGCACTCGGTGTTCTTTTACTAGTGTTCAAATACAGTAACTTAAAGAT	2280
QY	2281	TTGTCAATCTCAGCCTTCCAAAGAGAAAAAGAGAGAAATCTGAAACAGTTAAAGGT	2340
Db	2281	TTGTCAATCTCAGCCTTCCAAAGAGAAAAAGAGAGAAATCTGAAACAGTTAAAGGT	2340
QY	2341	CTAATATATGCTGAAAGACCCCAAGATCTCATGTTAAGTGAAGGATTTTGGCAAATCG	2400
Db	2341	CTAATATATGCTGAAAGACCCCAAGATCTCATGTTAAGTGAAGGATTTTGGCAAATCG	2400
QY	2401	AAAGATCTGTAGAGATGACAGTATTTCTGTGATCTTGTACTGATTTATGCAACTCAGG	2460
Db	2401	AAAGATCTGTAGAGATGACAGTATTTCTGTGATCTTGTACTGATTTATGCAACTCAGG	2460
QY	2461	AAAGATCTCTGTTACTTGAAGTTAGCATCTTATGGAAGGCAAAACAAACCAATTAAT	2520
Db	2461	AAAGATCTCTGTTACTTGAAGTTAGCATCTTATGGAAGGCAAAACAAACCAATTAAT	2520
QY	2521	GTGTAGTCAGTGTGACAGATTTGAAACCCCAAGGACATATTAATGATGTTGTTCCAAAG	2580
Db	2521	GTGTAGTCAGTGTGACAGATTTGAAACCCCAAGGACATATTAATGATGTTGTTCCAAAG	2580
QY	2581	ATTAAATGAATGACACAGAGGCTTTAAATATCACTTGGGACATGAGATTAAACAACATCTC	2640

Dp	2561	ATATATGAAATGACACAGAGGCTTTAAGTATCCATTGGGACATGAAATTACACAGCTC	2640
Oy	2641	GGGAAAACAGATATGAATGGAAGAAGTGAATGCTACAGTATTTGGACAATACAT	2700
Dp	2641	GGGAAACAGCATATGAATGGAAGAAGTGAATGCTATGATTCCTCAATTTTGCAGAAATCAT	2700
Oy	2701	TCAGGTTTCAAAGGCCAGTCATTTGCTCTGTTTCAATCCAGAAATGCAGAGAG	2760
Dp	2701	TCAGGTTTCAAAGGCCAGTCATTTGCTCTGTTTCAATCCAGAAATGCAGAGAG	2760
Oy	2761	AATGGCAACATTCCTGCGCCACTCTGGGTCCTTAAAGAAACAAGTCCAAAGTCATT	2820
Dp	2761	AATGGCAACATTCCTGCGCCACTCTGGGTCCTTAAAGAAACAAGTCCAAAGTCATT	2820
Oy	2821	TTGATATGGAACAAAAGGAGMAAAATCAAGAAAGAATGAGTCTATATCAAGCTGTAC	2880
Dp	2821	TTGATATGGAACAAAAGGAGMAAAATCAAGAAAGAATGAGTCTATATCAAGCTGTAC	2880
Oy	2881	AGACGTTTAATATCATCTGCAGGCTTTCTCTGTGTTGTCAGAAAGATATGCGAGTTGATA	2940
Dp	2881	AGACGTTTAATATCATCTGCAGGCTTTCTCTGTGTTGTCAGAAAGATATGCGAGTTGATA	2940
Oy	2941	ATGCCAAATGTATATCAAAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCCAGAGCA	3000
Dp	2941	ATGCCAAATGTATATCAAAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCCAGAGCA	3000
Oy	3001	ACGAAATCTGACCTCACTACTCCAAATAAACATGAGACTTTTCAAAACCCTATGCTATAC	3060
Dp	3001	ACGAAATCTGACCTCACTACTCCAAATAAACATGAGACTTTTCAAAACCCTATGCTATAC	3060
Oy	3061	CACCACTTTTTCCCATCAAGTCATTTGTTAAACCTAAATGTAGAAAAATCTGCTAGAG	3120
Dp	3061	CACCACTTTTTCCCATCAAGTCATTTGTTAAACCTAAATGTAGAAAAATCTGCTAGAG	3120
Oy	3121	AAAACTTTGAGGAACATTCATATGTCACCTGAAAGAGAAATGGGAAATGAGAAACATTCOA	3180
Dp	3121	AAAACTTTGAGGAACATTCATATGTCACCTGAAAGAGAAATGGGAAATGAGAAACATTCOA	3180
Oy	3181	GTACAGTGAACAATTTAGCCGTATATACATTAAGAAATGTTTTTAAAGAGCAGCT	3240
Dp	3181	GTACAGTGAACAATTTAGCCGTATATACATTAAGAAATGTTTTTAAAGAGCAGCT	3240
Oy	3241	CAAGCAATATTTAATGAAGTAGGTCCTCACTACTAATGAATGGGGCTCCAGTATTAATGAA	3300
Dp	3241	CAAGCAATATTTAATGAAGTAGGTCCTCACTACTAATGAATGGGGCTCCAGTATTAATGAA	3300
Oy	3301	TAGGTTCCAGATGAGAAAACATTCAGAGAACTAGATGAGAAACAGAGGCCAAATATGA	3360
Dp	3301	TAGGTTCCAGATGAGAAAACATTCAGAGAACTAGATGAGAAACAGAGGCCAAATATGA	3360
Oy	3361	ATGCTATCTTAGATTTAGGGGTTTTTGGCAACTGAGGTCATATPAAACAAGTCTTCTCGAA	3420
Dp	3361	ATGCTATCTTAGATTTAGGGGTTTTTGGCAACTGAGGTCATATPAAACAAGTCTTCTCGAA	3420
Oy	3421	GTAATTTGAAGCATCTGAAATTAATAAAGCAAGATATGAAAGAAATGATCAGACTGTTA	3480
Dp	3421	GTAATTTGAAGCATCTGAAATTAATAAAGCAAGATATGAAAGAAATGATCAGACTGTTA	3480
Oy	3481	ATACAGATTTTCTCTCATATCTGATTTAGATTAATTAGAACAGCTATGGGAAGTATGC	3540
Dp	3481	ATACAGATTTTCTCTCATATCTGATTTAGATTAATTAGAACAGCTATGGGAAGTATGC	3540
Oy	3541	ATGCATCTCAGGTTTGTCTGAGACACTGATGACCTGTTAGATGATGGTAAATTAAGG	3600
Dp	3541	ATGCATCTCAGGTTTGTCTGAGACACTGATGACCTGTTAGATGATGGTAAATTAAGG	3600
Oy	3601	AAGATACTAGTTTGTCTGAAAAATGACATTAAGAAAGTTCTGCTGTTTTTGAACAAACG	3660
Dp	3601	AAGATACTAGTTTGTCTGAAAAATGACATTAAGAAAGTTCTGCTGTTTTTGAACAAACG	3660
Oy	3661	TCACAGAGAGAGCTTAGCAGAGGCTCTAGCCCTTTACCCCATATCACATTTGGCTCAGG	3720
Dp	3661	TCACAGAGAGAGCTTAGCAGAGGCTCTAGCCCTTTACCCCATATCACATTTGGCTCAGG	3720



TITLE OF INVENTION: Identifying Mutations In Targeted Polynucleotide Strands  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESSES: 13  
ADDRESSES: Dann, Dorfman, Herrell and Skillman, P.C.  
STREET: 1601 Market Street, Suite 720  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103-2307  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/658,322  
FILING DATE: 05-JUN-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Hagan, Patrick J.  
REGISTRATION NUMBER: 27,643  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 563-4100  
TELEFAX: (215) 563-4044  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5711 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: not relevant  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-658-322-1

Query Match 99.8%; Score 5699.8; DB 2; Length 5711;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 5704; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 AGCTCGCTGAGACCTTCCGACCCCGACACAGGCTGTGGGTTCTCAGATTACTGGGCC 60  
DB 1 AGCTCGCTGAGACCTTCCGACCCCGACACAGGCTGTGGGTTCTCAGATTACTGGGCC 60  
QY 61 CCTGGCTCAGAGAGGCTTCAACCTCTGCTGTGGGTAAGTTCAATGGAGAGAA 120  
DB 61 CCTGGCTCAGAGAGGCTTCAACCTCTGCTGTGGGTAAGTTCAATGGAGAGAA 120  
QY 121 TGGATTATCTGCTCTTGGCGTTGAAGAGTCAAAATGCTAATGCTATGCAAGAAA 180  
DB 121 TGGATTATCTGCTCTTGGCGTTGAAGAGTCAAAATGCTAATGCTATGCAAGAAA 180  
QY 181 TCTTAGAGTGTCCATCTGTCTGAGTGTATCAAGAACTGTCTCCCAAAAGTGTGACC 240  
DB 181 TCTTAGAGTGTCCATCTGTCTGAGTGTATCAAGAACTGTCTCCCAAAAGTGTGACC 240  
QY 241 ACATATTTTGGAAATTTTGCATGCTGAATCTTCAACCAAGAGAGAGGCTTCAAGT 300  
DB 241 ACATATTTTGGAAATTTTGCATGCTGAATCTTCAACCAAGAGAGAGGCTTCAAGT 300  
QY 301 GTCTTTATGTGAAGATGATATACCAAAAGAGGCTTCAAGAAAGTACGAGATTAGTC 360  
DB 301 GTCTTTATGTGAAGATGATATACCAAAAGAGGCTTCAAGAAAGTACGAGATTAGTC 360  
QY 361 AACTGTTGAAGAGTATGAAAAATCATTTGTGCTTTACAGTTGACACAGGTTGGAGT 420  
DB 361 AACTGTTGAAGAGTATGAAAAATCATTTGTGCTTTACAGTTGACACAGGTTGGAGT 420  
QY 421 ATGCAAAAGAGCTATATTTTGCAGAAAAAGAAATTAATCTCTGTAAGATCTAAAGATG 480  
DB 421 ATGCAAAAGAGCTATATTTTGCAGAAAAAGAAATTAATCTCTGTAAGATCTAAAGATG 480  
QY 481 AAGTTTATCATCCAAAGTATGGGCTACAGAAACGTCGCAAAAGACTTTCACAGAGTG 540  
DB 481 AAGTTTATCATCCAAAGTATGGGCTACAGAAACGTCGCAAAAGACTTTCACAGAGTG 540

DB 481 AAGTTTATCATCCAAAGTATGGGCTACAGAAACGTCGCAAAAGACTTTCACAGAGTG 540  
QY 541 AACCAGAAATCTTCCCTTGAGAGAAACCACTCAGTGCATCCATCTTAACCTTGGAA 600  
DB 541 AACCAGAAATCTTCCCTTGAGAGAAACCACTCAGTGCATCCATCTTAACCTTGGAA 600  
QY 601 CTGTGAGAACTCTGAGGACAAAGCAGGATACCACTCAAAAGACGTCTGTCTACATG 660  
DB 601 CTGTGAGAACTCTGAGGACAAAGCAGGATACCACTCAAAAGACGTCTGTCTACATG 660  
QY 661 AATTGGATCTGATTTCTTCTGAAGATACCGTTAATTAAGCACTTATTTGAGTGGAG 720  
DB 661 AATTGGATCTGATTTCTTCTGAAGATACCGTTAATTAAGCACTTATTTGAGTGGAG 720  
QY 721 ATCAAGATGTTCAAATCAACCCCTCAAGGACAGGATGAATCAGTTTGGATTCTG 780  
DB 721 ATCAAGATGTTCAAATCAACCCCTCAAGGACAGGATGAATCAGTTTGGATTCTG 780  
QY 781 CAAAAAGGCTCTTGAAATTTTCTGAGCGATGTAAACAAATACCTGAACATCAAC 840  
DB 781 CAAAAAGGCTCTTGAAATTTTCTGAGCGATGTAAACAAATACCTGAACATCAAC 840  
QY 841 CCAATTAATATGATTTTGAACCACTGAGAAAGCGTGCAGTGAAGGCTACAGAAAGT 900  
DB 841 CCAATTAATATGATTTTGAACCACTGAGAAAGCGTGCAGTGAAGGCTACAGAAAGT 900  
QY 901 ATCAGGGATGTTCTGTTCAACTGATGAGGATGAGGCAATGAGCAAAATCTATGCCA 960  
DB 901 ATCAGGGATGTTCTGTTCAACTGATGAGGATGAGGCAATGAGCAAAATCTATGCCA 960  
QY 961 GCTCATTTACAGCATGAGAACGACAGTTTACTCACTAAAGACAGATGATAGAAA 1020  
DB 961 GCTCATTTACAGCATGAGAACGACAGTTTACTCACTAAAGACAGATGATAGAAA 1020  
QY 1021 AGGCTGAATTTGTAAATTAAGCAACAGCTGTGCTTAAGCAGAGGCCAATTAACAT 1080  
DB 1021 AGGCTGAATTTGTAAATTAAGCAACAGCTGTGCTTAAGCAGAGGCCAATTAACAT 1080  
QY 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGCGGAGCTCCAGACAGAAAAAGTAG 1140  
DB 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGCGGAGCTCCAGACAGAAAAAGTAG 1140  
QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGAAATACAGAACTGCATGCT 1200  
DB 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGAAATACAGAACTGCATGCT 1200  
QY 1201 CAGAGATCTTGAAGATCTGAAGATGTTCTTGGATTAACCTTAATGACGATTCAGA 1260  
DB 1201 CAGAGATCTTGAAGATCTGAAGATGTTCTTGGATTAACCTTAATGACGATTCAGA 1260  
QY 1261 AAGTTAATGAGTGTTCAGAGATGATGAACGTTAGTTCATGATGACTCAATGATG 1320  
DB 1261 AAGTTAATGAGTGTTCAGAGATGATGAACGTTAGTTCATGATGACTCAATGATG 1320  
QY 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGTGAATGATGAGAGCTTAAATAGGATAGT 1380  
DB 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGTGAATGATGAGAGCTTAAATAGGATAGT 1380  
QY 1381 AATATTCGTGTTCTTCAAGAGAAATTAAGCTTACGCGCAGTATCTCATAGGCTTTAA 1440  
DB 1381 AATATTCGTGTTCTTCAAGAGAAATTAAGCTTACGCGCAGTATCTCATAGGCTTTAA 1440  
QY 1441 TATGTAAGAGTGAAGGTTCACTCCAAATCAGTAGAGATTAATGAAACAAATAT 1500  
DB 1441 TATGTAAGAGTGAAGGTTCACTCCAAATCAGTAGAGATTAATGAAACAAATAT 1500  
QY 1501 TTGGGAAAACTATCGAAGAGGCAAGCTCCCAACTTAAGCATATGTAAGTAAATC 1560  
DB 1501 TTGGGAAAACTATCGAAGAGGCAAGCTCCCAACTTAAGCATATGTAAGTAAATC 1560  
QY 1561 TAAATTAAGAGCAATTTGTTACTGAGCCACAGATTAATCAAGAGCGTCCCTCAAAATA 1620  
DB 1561 TAAATTAAGAGCAATTTGTTACTGAGCCACAGATTAATCAAGAGCGTCCCTCAAAATA 1620



QY 1621 AATTAAAGCTTAAAGAGACCTTACATCAGGCTTCATCTGAGATTTTATCAAGAAAG 1680  
Db 1621 AATTAAAGCTTAAAGAGACCTTACATCAGGCTTCATCTGAGATTTTATCAAGAAAG 1680  
QY 1681 CAGATTTGGCAGTTCAAAAGACTCCTGAAATGATTAATCAAGGAACTAAACCAAGCGAGC 1740  
Db 1681 CAGATTTGGCAGTTCAAAAGACTCCTGAAATGATTAATCAAGGAACTAAACCAAGCGAGC 1740  
QY 1741 AGAATGCTGAGTGAATTAATTAATGATGCTGATGAGAAATTAACCAAGAGTGAAT 1800  
Db 1741 AGAATGCTGAGTGAATTAATTAATGATGCTGATGAGAAATTAACCAAGAGTGAAT 1800  
QY 1801 CTATTCAGATGAGAAAATCCTTAACCAATAGATCACTCGAAAAGATCTGCTTCA 1860  
Db 1801 CTATTCAGATGAGAAAATCCTTAACCAATAGATCACTCGAAAAGATCTGCTTCA 1860  
QY 1861 AAACGAAAGCTGAACCTTAATAGCAGCAGTATTAAGCAATATGGAATCTCGAATTAATATCC 1920  
Db 1861 AAACGAAAGCTGAACCTTAATAGCAGCAGTATTAAGCAATATGGAATCTCGAATTAATATCC 1920  
QY 1921 ACAATTCAAAAGCACTTAAAGCAATAGCTGAGAGAAAGTCTTCTACAGGCAATATTC 1980  
Db 1921 ACAATTCAAAAGCACTTAAAGCAATAGCTGAGAGAAAGTCTTCTACAGGCAATATTC 1980  
QY 1981 ATGCGCTTGAACCTAGTAGCTAGTAAATCTTAAGCCCACTTAATTTGTAATTTGCAAA 2040  
Db 1981 ATGCGCTTGAACCTAGTAGCTAGTAAATCTTAAGCCCACTTAATTTGTAATTTGCAAA 2040  
QY 2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAGAAAGTCAACCAATGCGCATCA 2100  
Db 2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAGAAAGTCAACCAATGCGCATCA 2100  
QY 2101 GGCACAGCAAGAACTTACATCTATGAAAGTAAAGAACTGCAACTGAGCCCAAGAAAG 2160  
Db 2101 GGCACAGCAAGAACTTACATCTATGAAAGTAAAGAACTGCAACTGAGCCCAAGAAAG 2160  
QY 2161 GTAAACAAGCCAAATGAACAGACAACTAAAGCATGACAGTGAATCTTTCCAGAGCTGA 2220  
Db 2161 GTAAACAAGCCAAATGAACAGACAACTAAAGCATGACAGTGAATCTTTCCAGAGCTGA 2220  
QY 2221 AGTTAAACAATGCACTGCTTCTTTTACTTAAGTTCCTAAATACAGTGAATCTTAAGAAAT 2280  
Db 2221 AGTTAAACAATGCACTGCTTCTTTTACTTAAGTTCCTAAATACAGTGAATCTTAAGAAAT 2280  
QY 2281 TTGTCAATCTTAGCTTCCAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGTGT 2340  
Db 2281 TTGTCAATCTTAGCTTCCAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGTGT 2340  
QY 2341 CTAATTAATGCTGAAGACCCCAAGATCTCAGTTAAGTGAAGAAAGGTTTGGCAACCTG 2400  
Db 2341 CTAATTAATGCTGAAGACCCCAAGATCTCAGTTAAGTGAAGAAAGGTTTGGCAACCTG 2400  
QY 2401 AAAAGATCTGTAGAGAGTATTTTCACTGCTGATCTGATTAATGAGCACTCAGG 2460  
Db 2401 AAAAGATCTGTAGAGAGTATTTTCACTGCTGATCTGATTAATGAGCACTCAGG 2460  
QY 2461 AAAAGATCTGTAGAGAGTATTTTCACTGCTGATCTGATTAATGAGCACTCAGG 2520  
Db 2461 AAAAGATCTGTAGAGAGTATTTTCACTGCTGATCTGATTAATGAGCACTCAGG 2520  
QY 2521 GTGTGAGTCACTGTGACAGTATTTGAAACCCCAAGGACTAATTTAGTGTTCCTCAAG 2580  
Db 2521 GTGTGAGTCACTGTGACAGTATTTGAAACCCCAAGGACTAATTTAGTGTTCCTCAAG 2580  
QY 2581 ATTAATGAATGAACAGAGGCTTTAAGTATCTAATGAGGACATGAAGTTAAACCAAGTC 2640  
Db 2581 ATTAATGAATGAACAGAGGCTTTAAGTATCTAATGAGGACATGAAGTTAAACCAAGTC 2640  
QY 2641 GGGAAACAAGCATAGAAATGAAAGAAAGTGAATCTGATCTCAGATATTTGGCAAGTACAT 2700  
Db 2641 GGGAAACAAGCATAGAAATGAAAGAAAGTGAATCTGATCTCAGATATTTGGCAAGTACAT 2700

QY 2701 TCAAGTTTCAAGGCGCAGTCATTTGCTGTGTTTCAATTCAGAGAAATGCAAGAGG 2760  
Db 2701 TCAAGTTTCAAGGCGCAGTCATTTGCTGTGTTTCAATTCAGAGAAATGCAAGAGG 2760  
QY 2761 AATGTGCAACATTTCTGCTCCACTGCTGGTCTTTAAGAAACAAAGTCCAAAGTCACTT 2820  
Db 2761 AATGTGCAACATTTCTGCTCCACTGCTGGTCTTTAAGAAACAAAGTCCAAAGTCACTT 2820  
QY 2821 TTGAATGGAACAAAGAGAAATCAAGGAAAGATGAGTCTAATATCAAGCCTGTAC 2880  
Db 2821 TTGAATGGAACAAAGAGAAATCAAGGAAAGATGAGTCTAATATCAAGCCTGTAC 2880  
QY 2881 AGACAGTTAATATCACTGACAGCTTTCCGTGTGTGTGTCAGAAAGATTAAGCCAGTTGATA 2940  
Db 2881 AGACAGTTAATATCACTGACAGCTTTCCGTGTGTGTGTCAGAAAGATTAAGCCAGTTGATA 2940  
QY 2941 ATGCCAAATGTAATCAAGAGAGGCTTGAAGTTTGTCTATCATCTCAGATTCAGAGCA 3000  
Db 2941 ATGCCAAATGTAATCAAGAGAGGCTTGAAGTTTGTCTATCATCTCAGATTCAGAGCA 3000  
QY 3001 AGCAACTGAGCTCATTAATCAATTAACATGACCTTTTCAAAACCATATGCTATAC 3060  
Db 3001 AGCAACTGAGCTCATTAATCAATTAACATGACCTTTTCAAAACCATATGCTATAC 3060  
QY 3061 CACCACTTTTCCCATCAAGTCATTTGTTAAACATTAATGTAAGAAATCTGCTAGAG 3120  
Db 3061 CACCACTTTTCCCATCAAGTCATTTGTTAAACATTAATGTAAGAAATCTGCTAGAG 3120  
QY 3121 AAAACCTTTGAGAACATTCATGTCACCTGAAAGAAATGGGAAATGAAACATTCGA 3180  
Db 3121 AAAACCTTTGAGAACATTCATGTCACCTGAAAGAAATGGGAAATGAAACATTCGA 3180  
QY 3181 GTACAGTGAACCAATTTGACCGCTAATTAATTAAGAAATCTTTTAAAGAGCAGCT 3240  
Db 3181 GTACAGTGAACCAATTTGACCGCTAATTAATTAAGAAATCTTTTAAAGAGCAGCT 3240  
QY 3241 CAAGCAATATTAATGAAGTTCAGATCTTAATGAAGTGGGCTCCAGTATTAATGAAG 3300  
Db 3241 CAAGCAATATTAATGAAGTTCAGATCTTAATGAAGTGGGCTCCAGTATTAATGAAG 3300  
QY 3301 TAGGTTCCAGTATGAAGAAATTCAGAGCAACCTAGTGAAGAAACAGAGGCCAAATTTGA 3360  
Db 3301 TAGGTTCCAGTATGAAGAAATTCAGAGCAACCTAGTGAAGAAACAGAGGCCAAATTTGA 3360  
QY 3361 ATGCTATGCTTAAGTATGAGGTTTGGCACTGAGGCTTAATTAACAAAGTCTTCTGGA 3420  
Db 3361 ATGCTATGCTTAAGTATGAGGTTTGGCACTGAGGCTTAATTAACAAAGTCTTCTGGA 3420  
QY 3421 GTAATTTGAAGATCTGAATTAAGAAAGCAAGATTAAGAAAGTATGAGTTCAGCTGTA 3480  
Db 3421 GTAATTTGAAGATCTGAATTAAGAAAGCAAGATTAAGAAAGTATGAGTTCAGCTGTA 3480  
QY 3481 ATACAGATTTTCTCCATATCTGATTTCAATTAAGTGAACAGCTATGGAAGTATGTC 3540  
Db 3481 ATACAGATTTTCTCCATATCTGATTTCAATTAAGTGAACAGCTATGGAAGTATGTC 3540  
QY 3541 ATGCACTCAGGTTGTTCTGAGACCTGATGACCTGTTAGATGATGTTGAATTAAGG 3600  
Db 3541 ATGCACTCAGGTTGTTCTGAGACCTGATGACCTGTTAGATGATGTTGAATTAAGG 3600  
QY 3601 AAGATACAGTTTGTCTGAGACCTGATGACCTGTTAGATGATGTTGAATTAAGG 3660  
Db 3601 AAGATACAGTTTGTCTGAGACCTGATGACCTGTTAGATGATGTTGAATTAAGG 3660  
QY 3661 TCCAGAGAGAGAGCTTGAAGAGTCTAGCCCTTTGACCCATACAGATTTGGCTCAGG 3720  
Db 3661 TCCAGAGAGAGAGCTTGAAGAGTCTAGCCCTTTGACCCATACAGATTTGGCTCAGG 3720  
QY 3721 GTTACCGAAGAGGCGCAAGAAATTAAGTCTCAGAAAGAGAACTTATCTAGTGAGATG 3780  
Db 3721 GTTACCGAAGAGGCGCAAGAAATTAAGTCTCAGAAAGAGAACTTATCTAGTGAGATG 3780  
QY 3781 AAGAGCTTCCCTGCTCAGACCTTTGTAATTTGTAAGTAAACAAATATCTCTCAGT 3840





TITLE OF INVENTION: PROTEINS AND SCREENING AND THERAPEUTIC METHODS BASED ON  
NUMBER OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2 PROTEINS.  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ARLES A. TAYLOR, JR.  
STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER  
CITY: DURHAM  
STATE: NORTH CAROLINA  
COUNTRY: USA  
ZIP: 27707  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage  
COMPUTER: IBM PC/XT/AT compatible  
OPERATING SYSTEM: Windows 3.1  
SOFTWARE: WORD PERFECT 6.1 and ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/603,753D  
FILING DATE: 20 FEB 1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/373,799  
FILING DATE: 17 JAN 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: ARLES A. TAYLOR, JR.  
REGISTRATION NUMBER: 39,395  
REFERENCE/DOCKET NUMBER: 1242/2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 493-8000  
TELEFAX: (919) 419-0383  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5712  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: no  
ANTI-SENSE: no  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE: adult  
TISSUE TYPE: female breast  
CELL TYPE: ductal carcinoma in situ, invasive  
CELL LINE: breast cancer and normal breast tissue  
CELL LINE: not derived from a cell line  
ORGANELLE: no  
IMMEDIATE SOURCE:  
LIBRARY: cDNA library derived from human  
CLONE: obtained using published sequence  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: unknown  
MAP POSITION: unknown  
UNITS: unknown  
FEATURE:  
NAME/KEY: BRCA1  
LOCATION: Genbank accession no. U14680  
IDENTIFICATION METHOD: microscopically directed  
IDENTIFICATION METHOD: sampling and nuclease protection assay  
OTHER INFORMATION: gene encoding BRCA1 protein  
PUBLICATION INFORMATION:  
AUTHORS: Miki, Y., et. al.  
TITLE: A strong candidate gene for the breast and  
TITLE: ovarian cancer susceptibility gene BRCA1.  
JOURNAL: Science  
VOLUME: 266  
PAGES: 66-71  
DATE: 1994  
RELEVANT RESIDUES IN SEQ ID NO: 1:  
US-08-603-753D-1

Query Match 99.8%; Score 5699.8; DB 2; Length 5712;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 5704; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
QY 1 AGCTGCTGAGACCTTCTGAGACCCCGACACAGGCTGTGGGTTTCTCAGATTAACGTGGCC 60  
DB 1 AGCTGCTGAGACCTTCTGAGACCCCGACACAGGCTGTGGGTTTCTCAGATTAACGTGGCC 60  
QY 61 CTTGGGCTCAGAGGCTTCAACCTCTGCTGAGGTTAAAGTTCATTTGAAAGAGAA 120  
DB 61 CTTGGGCTCAGAGGCTTCAACCTCTGCTGAGGTTAAAGTTCATTTGAAAGAGAA 120  
QY 121 TGGATTATCTGCTCTTCTGAGGAGTGAAGAGTAACTATTAATGATGACAGAAA 180  
DB 121 TGGATTATCTGCTCTTCTGAGGAGTGAAGAGTAACTATTAATGATGACAGAAA 180  
QY 181 TCTTAGAGTGTCCATCTGTCTGAGGTTGATCAAGAACTGTCTCCACAAAGTGTACC 240  
DB 181 TCTTAGAGTGTCCATCTGTCTGAGGTTGATCAAGAACTGTCTCCACAAAGTGTACC 240  
QY 241 ACATATTTTGCAGAAATTTTGCAGTGAAGACTTCAACCAAGAGAGGCTTCAAGT 300  
DB 241 ACATATTTTGCAGAAATTTTGCAGTGAAGACTTCAACCAAGAGAGGCTTCAAGT 300  
QY 301 GTCTTTATGTAAGATGATATTAACCAAGAGGCTTCAAGAAAGTACGAGATTAGTC 360  
DB 301 GTCTTTATGTAAGATGATATTAACCAAGAGGCTTCAAGAAAGTACGAGATTAGTC 360  
QY 361 AACTGTTGAAGAGCTATTGAAATCAATTTGTGCTTTTCAAGTTGACACAGGTTGGAGT 420  
DB 361 AACTGTTGAAGAGCTATTGAAATCAATTTGTGCTTTTCAAGTTGACACAGGTTGGAGT 420  
QY 421 ATGCAAGAGCTATATTTTGCAGAAAGAAATTAATCTTCCGTAACATCAAAAGATG 480  
DB 421 ATGCAAGAGCTATATTTTGCAGAAAGAAATTAATCTTCCGTAACATCAAAAGATG 480  
QY 481 AAGTTTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAGACTTCTACAGAGTG 540  
DB 481 AAGTTTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAGACTTCTACAGAGTG 540  
QY 541 AACCGGAAATCTTCTTGGAGAAACCAAGTCTCAGTGTCCAACTCTTCAACCTTGGAA 600  
DB 541 AACCGGAAATCTTCTTGGAGAAACCAAGTCTCAGTGTCCAACTCTTCAACCTTGGAA 600  
QY 601 CTGTGAGAACTGTGAGCAAAAGCGGATACCACTTCAAAAGAGCTGTCTCATTTG 660  
DB 601 CTGTGAGAACTGTGAGCAAAAGCGGATACCACTTCAAAAGAGCTGTCTCATTTG 660  
QY 661 AATTGGATCTGATCTTCTGAGAGTACCGTTAATAGGCACTTAATGACAGTGGAG 720  
DB 661 AATTGGATCTGATCTTCTGAGAGTACCGTTAATAGGCACTTAATGACAGTGGAG 720  
QY 721 ATCAAGAAATGTTCAAAATCAACCTCTCAAGAACCGAGATGAATCAATTGATCTG 780  
DB 721 ATCAAGAAATGTTCAAAATCAACCTCTCAAGAACCGAGATGAATCAATTGATCTG 780  
QY 781 CAAAAAAGGCTGCTGTGAATTTTCTGAGCGGATGTAACTGAACATCATCAAC 840  
DB 781 CAAAAAAGGCTGCTGTGAATTTTCTGAGCGGATGTAACTGAACATCATCAAC 840  
QY 841 CCAATATATATGATTTGAACACCACTGAGAGCGGAGCTGAGAGGATCCAGAAAAGT 900  
DB 841 CCAATATATATGATTTGAACACCACTGAGAGCGGAGCTGAGAGGATCCAGAAAAGT 900  
QY 901 ATCAGGATAGTCTGTTTCAAACTTGCATGTGAGCCATGTGGCAAAATATCTATGCCA 960  
DB 901 ATCAGGATAGTCTGTTTCAAACTTGCATGTGAGCCATGTGGCAAAATATCTATGCCA 960  
QY 961 GCTCATTAAGATGAGAAACAGAGCTTTATTAATCACTAAAGACGAATGATGAGAA 1020  
DB 961 GCTCATTAAGATGAGAAACAGAGCTTTATTAATCACTAAAGACGAATGATGAGAA 1020  
QY 1021 AGCTGAATTTCTGTAATAAAGCAAGGCTGCTTGAAGAGCCAACTAATCAGAT 1080

Db 1021 AGCGTAATTCGTATATAAAGCAACAGCCCTGCGTTAGCAAGAGCCACATACAT 1080  
Qy 1081 GGGCTGAAAGTAGAAAACATGTAAATGATAGCGGCACTCCAGCAACAAAAAGTAG 1140  
Db 1081 GGGCTGAAAGTAGAAAACATGTAAATGATAGCGGCACTCCAGCAACAAAAAGTAG 1140  
Qy 1141 ATCTGAAGCTGATCCCGTGTGTGAGAAAAGATGAAATGAGCAAGAACTGCCATGCT 1200  
Db 1141 ATCTGAAGCTGATCCCGTGTGTGAGAAAAGATGAAATGAGCAAGAACTGCCATGCT 1200  
Qy 1201 CAGAGAACTCTAGAGATCTGAAGATGTTCTTGATTAACATAATAGCAGCATTCAGA 1260  
Db 1201 CAGAGAACTCTAGAGATCTGAAGATGTTCTTGATTAACATAATAGCAGCATTCAGA 1260  
Qy 1261 AAGTTAATGAGGTGTTTCCAGAAAGTGAATCTGTAGTTCATGATGCTCACATGATG 1320  
Db 1261 AAGTTAATGAGGTGTTTCCAGAAAGTGAATCTGTAGTTCATGATGCTCACATGATG 1320  
Qy 1321 GGGAGCTGAATCAATGCAAAAGTAGAGTGAATGATGAGTTCATAATAGGTAGATG 1380  
Db 1321 GGGAGCTGAATCAATGCAAAAGTAGAGTGAATGATGAGTTCATAATAGGTAGATG 1380  
Qy 1381 AATATTCGTCTCTCAGAGAAAATGACTTACTGCGCAGTATCTGATGAGGCTTTAA 1440  
Db 1381 AATATTCGTCTCTCAGAGAAAATGACTTACTGCGCAGTATCTGATGAGGCTTTAA 1440  
Qy 1441 TATGTAAAAGTGAAGAGTTCCTCCAAATCAGTGAAGATATTTTGAAGCAAAATAT 1500  
Db 1441 TATGTAAAAGTGAAGAGTTCCTCCAAATCAGTGAAGATATTTTGAAGCAAAATAT 1500  
Qy 1501 TTGGGAAAACCTATGGAAGAAAGGAGGCTCCCACTTAAGCATGATGAATGAAATTC 1560  
Db 1501 TTGGGAAAACCTATGGAAGAAAGGAGGCTCCCACTTAAGCATGATGAATGAAATTC 1560  
Qy 1561 TAAATATAGAGACATTTGTTACTGAGCAACAGATATTAACAAGAGGCTCCCTCAGAAATA 1620  
Db 1561 TAAATATAGAGACATTTGTTACTGAGCAACAGATATTAACAAGAGGCTCCCTCAGAAATA 1620  
Qy 1621 AATTAAGCGTAAAGAGACCTATCATAGGCTTCATCTGAGATTTTATCAAGAAAG 1680  
Db 1621 AATTAAGCGTAAAGAGACCTATCATAGGCTTCATCTGAGATTTTATCAAGAAAG 1680  
Qy 1681 CAGATTTGGCAGTTGTAAGAAAGCTCCTGAATGATTAATCAGGAACTAAACCAAGGAGC 1740  
Db 1681 CAGATTTGGCAGTTGTAAGAAAGCTCCTGAATGATTAATCAGGAACTAAACCAAGGAGC 1740  
Qy 1741 AGAATGCTCAAGTATGATATTTACTAATAGTGTCTATGAGATTAACCAAAAGGTGAT 1800  
Db 1741 AGAATGCTCAAGTATGATATTTACTAATAGTGTCTATGAGATTAACCAAAAGGTGAT 1800  
Qy 1801 CTATTCAGATAGAGAAAAATCTTAACCAATGAAATCACTCGAAAAAGATCTGCTTTCA 1860  
Db 1801 CTATTCAGATAGAGAAAAATCTTAACCAATGAAATCACTCGAAAAAGATCTGCTTTCA 1860  
Qy 1861 AAACGAAGCTGAACCTATAGCAGCAGATATAGCAATATGSACTCGAATTAATATCC 1920  
Db 1861 AAACGAAGCTGAACCTATAGCAGCAGATATAGCAATATGSACTCGAATTAATATCC 1920  
Qy 1921 ACAATTTCAAAAGCACTTAAGAAAGATAGGCTGAGAGGAGTCTTCTACAGAGCATATTC 1980  
Db 1921 ACAATTTCAAAAGCACTTAAGAAAGATAGGCTGAGAGGAGTCTTCTACAGAGCATATTC 1980  
Qy 1981 ATGCGCTTGAATAGTACTAGTAGAATCTAAGCCCACTAATTTGATCTGAATTCGAAA 2040  
Db 1981 ATGCGCTTGAATAGTACTAGTAGAATCTAAGCCCACTAATTTGATCTGAATTCGAAA 2040  
Qy 2041 TTGATAGTGTCTTCTGAGTGAAGATTAAGAAAAAGTGAACCAACCAAGTCCAGTCA 2100  
Db 2041 TTGATAGTGTCTTCTGAGTGAAGATTAAGAAAAAGTGAACCAACCAAGTCCAGTCA 2100  
Qy 2101 GGCACAGCAAGAAACCTAACATCTAGGAAGGTAAAGAACTGCAACTGAGCCAAAGAGA 2160  
Db 2101 GGCACAGCAAGAAACCTAACATCTAGGAAGGTAAAGAACTGCAACTGAGCCAAAGAGA 2160

Db 2101 GGCACAGCAAGAAACCTAACATCTAGGAAGGTAAAGAACTGCAACTGAGCCAAAGAGA 2160  
Qy 2161 GTAACAGCCAAATGAACAGACAGTAAAGACATGACAGATATCTTTCCAGAGCTGA 2220  
Db 2161 GTAACAGCCAAATGAACAGACAGTAAAGACATGACAGAGATATCTTTCCAGAGCTGA 2220  
Qy 2221 AGTTAACAAATGACACTGTTCTTTTACTAAGTGTTCAAATACAGTAACTTAAGAAAT 2280  
Db 2221 AGTTAACAAATGACACTGTTCTTTTACTAAGTGTTCAAATACAGTAACTTAAGAAAT 2280  
Qy 2281 TTGTCAATCTAGCCCTTCCAAAGAGAAAGAAAGAAACCTAAGAAACAGTTAAAGTGT 2340  
Db 2281 TTGTCAATCTAGCCCTTCCAAAGAGAAAGAAAGAAACCTAAGAAACAGTTAAAGTGT 2340  
Qy 2341 CTAATTAATGCTGAAGACCCCAAGATCTCAAGTTAAGTGAAGAAAGGTTTGGCAACTG 2400  
Db 2341 CTAATTAATGCTGAAGACCCCAAGATCTCAAGTTAAGTGAAGAAAGGTTTGGCAACTG 2400  
Qy 2401 AAAAGTCTGTAGAGAGTAGAGTATTTTCACTGTGTAACCTGTACTGATTAATGSCACTCAG 2460  
Db 2401 AAAAGTCTGTAGAGAGTAGAGTATTTTCACTGTGTAACCTGTACTGATTAATGSCACTCAG 2460  
Qy 2461 AAAGTATCTGTTACTGGAAGTTAGCACTTAGGAAAGGCAAAAACAGAACCAATTAAT 2520  
Db 2461 AAAGTATCTGTTACTGGAAGTTAGCACTTAGGAAAGGCAAAAACAGAACCAATTAAT 2520  
Qy 2521 GTGTGAGTCACTGTGAGCACTTTTGAAAACCCCAAGGACCTAATTCATGTTTCCAAAG 2580  
Db 2521 GTGTGAGTCACTGTGAGCACTTTTGAAAACCCCAAGGACCTAATTCATGTTTCCAAAG 2580  
Qy 2581 AATAATGAATATGACACAGAAAGCTTTAAGTATCCATTGGACATGAAATTAACCAAGTC 2640  
Db 2581 AATAATGAATATGACACAGAAAGCTTTAAGTATCCATTGGACATGAAATTAACCAAGTC 2640  
Qy 2641 GGGAAAACAGATAGAAATGGAAGAAAGTGAATGATGCTCAGTATTTGCAAAATCAT 2700  
Db 2641 GGGAAAACAGATAGAAATGGAAGAAAGTGAATGATGCTCAGTATTTGCAAAATCAT 2700  
Qy 2701 TCAAGTTTCAAAAGGCGCAGTATTTGCTGTTTCAAAATCCAGGAAATGCAAGAGG 2760  
Db 2701 TCAAGTTTCAAAAGGCGCAGTATTTGCTGTTTCAAAATCCAGGAAATGCAAGAGG 2760  
Qy 2761 AATGTGCAACATTCCTGCGCAGTCTGAGGCTCTTAAGAAACCAAGTCCAAAGTCACT 2820  
Db 2761 AATGTGCAACATTCCTGCGCAGTCTGAGGCTCTTAAGAAACCAAGTCCAAAGTCACT 2820  
Qy 2821 TTGAATGTGAACAAAAGGAAAGAAATCAAGGAAAGATGAGTCTAATCAAGCCTGTAC 2880  
Db 2821 TTGAATGTGAACAAAAGGAAAGAAATCAAGGAAAGATGAGTCTAATCAAGCCTGTAC 2880  
Qy 2881 AGACAGTTAATATCACTGCAAGCTTCTGTGTGTGTGTCAGAAAGATTAAGCAGTTGATA 2940  
Db 2881 AGACAGTTAATATCACTGCAAGCTTCTGTGTGTGTGTCAGAAAGATTAAGCAGTTGATA 2940  
Qy 2941 ATGCCAAATGTATATCACTGCAAGGCTCTAGGTTTGTCTATCATCTGATTCAGAGGCA 3000  
Db 2941 ATGCCAAATGTATATCACTGCAAGGCTCTAGGTTTGTCTATCATCTGATTCAGAGGCA 3000  
Qy 3001 ACGAAATCTGAACCTATTACTCAAAATTAACATGAGCTTTTCAAAAACCATATGCTATAC 3060  
Db 3001 ACGAAATCTGAACCTATTACTCAAAATTAACATGAGCTTTTCAAAAACCATATGCTATAC 3060  
Qy 3061 CACCACTTTTCCATCAAGTCAATTTGTTAAACCTAATGTAAGAAAAATCTGCTAGAGG 3120  
Db 3061 CACCACTTTTCCATCAAGTCAATTTGTTAAACCTAATGTAAGAAAAATCTGCTAGAGG 3120  
Qy 3121 AAAAATTGAGAGAACATTCATGCACTGAAAGGAAATGGAATGGAACATTCGAA 3180  
Db 3121 AAAAATTGAGAGAACATTCATGCACTGAAAGGAAATGGAATGGAACATTCGAA 3180  
Qy 3181 GTACAGTAGACCAATTAAGCCGTATTAACATTTAGAGAAATGTTTTTAAAGAGCAGCT 3240  
Db 3181 GTACAGTAGACCAATTAAGCCGTATTAACATTTAGAGAAATGTTTTTAAAGAGCAGCT 3240

QY 3241 CAAGCAATATTAAATGAAGTTCAGTAATAATGAAGTGGCTCCAGTATTATGA 3300  
| | | | |  
Db 3241 CAAGCAATATTAAATGAAGTTCAGTAATAATGAAGTGGCTCCAGTATTATGA 3300  
| | | | |  
QY 3301 TAGGTTCCAGTATGAATAAATTCAGAGCAATAGTGAACAGAGGCGCAAAATGA 3360  
| | | | |  
Db 3301 TAGGTTCCAGTATGAATAAATTCAGAGCAATAGTGAACAGAGGCGCAAAATGA 3360  
| | | | |  
QY 3361 ATGCTAATGCTTAATGAAGGCTTTTGGCACTGAGAGTCTATTAACAAGTCTTCTGGA 3420  
| | | | |  
Db 3361 ATGCTAATGCTTAATGAAGGCTTTTGGCACTGAGAGTCTATTAACAAGTCTTCTGGA 3420  
| | | | |  
QY 3421 GTAATTTGAAGCATCTGTAATAAATAAAGCAAGATATGAAGATGTTGAGCTGTTA 3480  
| | | | |  
Db 3421 GTAATTTGAAGCATCTGTAATAAATAAAGCAAGATATGAAGATGTTGAGCTGTTA 3480  
| | | | |  
QY 3481 ATACAGATTTCTCTCATATCTGATTTTCAATTAAGTGAACAGGCTATGGGAAGTATC 3540  
| | | | |  
Db 3481 ATACAGATTTCTCTCATATCTGATTTTCAATTAAGTGAACAGGCTATGGGAAGTATC 3540  
| | | | |  
QY 3541 ATGCTATCAAGTGTGTTCTGAGACCTGATGACCTGTTAATGATGTGAATAAAG 3600  
| | | | |  
Db 3541 ATGCTATCAAGTGTGTTCTGAGACCTGATGACCTGTTAATGATGTGAATAAAG 3600  
| | | | |  
QY 3601 AAGACTAGTGTGCTGTAATAATGAATTAAGAAAGTTCTGCTGTTTTCAGAAAGCG 3660  
| | | | |  
Db 3601 AAGACTAGTGTGCTGTAATAATGAATTAAGAAAGTTCTGCTGTTTTCAGAAAGCG 3660  
| | | | |  
QY 3661 TCCAGAGAGAGGCTTAGCAGAGTCTTAGGCTTTTCAACCTATACATTTGCTCAG 3720  
| | | | |  
Db 3661 TCCAGAGAGAGGCTTAGCAGAGTCTTAGGCTTTTCAACCTATACATTTGCTCAG 3720  
| | | | |  
QY 3721 GTTACCGAAGAGGCGCAAGAAATTAGAGTCTCAGAGAGAACTTATCTAGTGAAGATG 3780  
| | | | |  
Db 3721 GTTACCGAAGAGGCGCAAGAAATTAGAGTCTCAGAGAGAACTTATCTAGTGAAGATG 3780  
| | | | |  
QY 3781 AAGAGCTTCCCTGCTTCCAAACCTGTAATTTGTAAGTAAACAATATACCTTCTCAGT 3840  
| | | | |  
Db 3781 AAGAGCTTCCCTGCTTCCAAACCTGTAATTTGTAAGTAAACAATATACCTTCTCAGT 3840  
| | | | |  
QY 3841 CTACTAGGCAATAGACCGTGTGCTACCGAGTCTGCTTAAGAAACAGAGAGAAATTTAT 3900  
| | | | |  
Db 3841 CTACTAGGCAATAGACCGTGTGCTACCGAGTCTGCTTAAGAAACAGAGAGAAATTTAT 3900  
| | | | |  
QY 3901 TATCATTTGAAGAAATGCTTAAATGAATGACGTACCAAGTAAATTTGGCAAGGCAATCTC 3960  
| | | | |  
Db 3901 TATCATTTGAAGAAATGCTTAAATGAATGACGTACCAAGTAAATTTGGCAAGGCAATCTC 3960  
| | | | |  
QY 3961 AGGAACATCACCTTAGTGAAGAAACAAATGTTCTGCTAGCTTTTCTTCAAGTGA 4020  
| | | | |  
Db 3961 AGGAACATCACCTTAGTGAAGAAACAAATGTTCTGCTAGCTTTTCTTCAAGTGA 4020  
| | | | |  
QY 4021 GTGAATTTGAAGACTTGAATGCAAAATACCAAGGATCTTCTGATTTGTTCTT 4080  
| | | | |  
Db 4021 GTGAATTTGAAGACTTGAATGCAAAATACCAAGGATCTTCTGATTTGTTCTT 4080  
| | | | |  
QY 4081 CCAAAACAATGAGCATCAGTCTGAAGCCAGAGGAGTTGCTGAGTGAACAAGAAATGG 4140  
| | | | |  
Db 4081 CCAAAACAATGAGCATCAGTCTGAAGCCAGAGGAGTTGCTGAGTGAACAAGAAATGG 4140  
| | | | |  
QY 4141 TTTTCAGATGATGAAGAAAGAGACGGGCTTGGAAAGAAATATCAAGAGAGCAAGGA 4200  
| | | | |  
Db 4141 TTTTCAGATGATGAAGAAAGAGACGGGCTTGGAAAGAAATATCAAGAGAGCAAGGA 4200  
| | | | |  
QY 4201 TGGATTTCAAACCTTAGAGTGAAGACATCTGGGTGAGAGTGAACCAAGCTCTCTGAAG 4260  
| | | | |  
Db 4201 TGGATTTCAAACCTTAGAGTGAAGACATCTGGGTGAGAGTGAACCAAGCTCTCTGAAG 4260  
| | | | |  
QY 4261 ACTGCTCAGGGCTATCTCTCAGAGTGAATTTTAAACAATGAGAGAGGATACCATGC 4320  
| | | | |  
Db 4261 ACTGCTCAGGGCTATCTCTCAGAGTGAATTTTAAACAATGAGAGAGGATACCATGC 4320  
| | | | |

QY 4321 AACATTAACCTGATTAAGCTCCAGAGAGAAATGGCTGAATAGAAAGCTGTGTAGAACGC 4380  
| | | | |  
Db 4321 AACATTAACCTGATTAAGCTCCAGAGAGAAATGGCTGAATAGAAAGCTGTGTAGAACGC 4380  
| | | | |  
QY 4381 ATGGAGCCAGCTTCTTAACAGCTACCTTCAATATATAGTACTCTCTGCTTGAAG 4440  
| | | | |  
Db 4381 ATGGAGCCAGCTTCTTAACAGCTACCTTCAATATATAGTACTCTCTGCTTGAAG 4440  
| | | | |  
QY 4441 ACCTCGAAATCCAGAAACAAAGACATGAGAAAGAGATTAATCTTCAAGAAAGTA 4500  
| | | | |  
Db 4441 ACCTCGAAATCCAGAAACAAAGACATGAGAAAGAGATTAATCTTCAAGAAAGTA 4500  
| | | | |  
QY 4501 GTGAATTAACCTTAAGCCAGAAATCCAGAGGCTTTCTGCTGACAGATTTGAGTGTCTG 4560  
| | | | |  
Db 4501 GTGAATTAACCTTAAGCCAGAAATCCAGAGGCTTTCTGCTGACAGATTTGAGTGTCTG 4560  
| | | | |  
QY 4561 CAGATAGTCTTCAACAGTAAATAAAGAACAGAGAGTGAAGGTCATCCCTTTTAAT 4620  
| | | | |  
Db 4561 CAGATAGTCTTCAACAGTAAATAAAGAACAGAGAGTGAAGGTCATCCCTTTTAAT 4620  
| | | | |  
QY 4621 GCCCATCATTTGATGATAGTGGGTATCATGCAAGTGGCTGGGAGTCTTCAGAAATAGA 4680  
| | | | |  
Db 4621 GCCCATCATTTGATGATAGTGGGTATCATGCAAGTGGCTGGGAGTCTTCAGAAATAGA 4680  
| | | | |  
QY 4681 ACTACCCATCTCAAGAGAGCTCATTAAGTGTGATGAGAGAGCAACAGCTGGAAG 4740  
| | | | |  
Db 4681 ACTACCCATCTCAAGAGAGCTCATTAAGTGTGATGAGAGAGCAACAGCTGGAAG 4740  
| | | | |  
QY 4741 AGTCTGGGCCACAGATTTGACGGAACATCTTACCTGCAAGGCAAGATCTTAGAGGAA 4800  
| | | | |  
Db 4741 AGTCTGGGCCACAGATTTGACGGAACATCTTACCTGCAAGGCAAGATCTTAGAGGAA 4800  
| | | | |  
QY 4801 CCCCTTACCTGGAATCTGGAATCAAGCTCTTCTGATGACCTGTAATCTGATCTCTG 4860  
| | | | |  
Db 4801 CCCCTTACCTGGAATCTGGAATCAAGCTCTTCTGATGACCTGTAATCTGATCTCTG 4860  
| | | | |  
QY 4861 AAGACAGAGGCCAGAGTCAAGTCTGTTGGCAATACATCACTTCAACTCTGCAATGA 4920  
| | | | |  
Db 4861 AAGACAGAGGCCAGAGTCAAGTCTGTTGGCAATACATCACTTCAACTCTGCAATGA 4920  
| | | | |  
QY 4921 AAGTTCGCCAATGGAAGTTGAGAGATCTGCCAGAGTCCAGCTGCTGCTACTACTG 4980  
| | | | |  
Db 4921 AAGTTCGCCAATGGAAGTTGAGAGATCTGCCAGAGTCCAGCTGCTGCTACTACTG 4980  
| | | | |  
QY 4981 ATACTGCTGGGTATATGATCAATGAAAGAGTGTGAGAGAGGAGCAAGATTTGACAG 5040  
| | | | |  
Db 4981 ATACTGCTGGGTATATGATCAATGAAAGAGTGTGAGAGAGGAGCAAGATTTGACAG 5040  
| | | | |  
QY 5041 CTTCAACGAAAGGCTCAACAAAGATGTCATGAGTGTGCTGAGCTGAGCCAGAG 5100  
| | | | |  
Db 5041 CTTCAACGAAAGGCTCAACAAAGATGTCATGAGTGTGCTGAGCTGAGCCAGAG 5100  
| | | | |  
QY 5101 AATTTATGCTGTGTATACAGTGTGCGAGAAACACACATCACTTAACTTAATTA 5160  
| | | | |  
Db 5101 AATTTATGCTGTGTATACAGTGTGCGAGAAACACACATCACTTAACTTAATTA 5160  
| | | | |  
QY 5161 CTGAAGAGACTATGATGTTGTTATGAACAGATGCTGAGTGTGTGTGAACGACAC 5220  
| | | | |  
Db 5161 CTGAAGAGACTATGATGTTGTTATGAACAGATGCTGAGTGTGTGTGAACGACAC 5220  
| | | | |  
QY 5221 TGAATATTTTCTAGAAATGCGGAGGAGAAATGGGTGTTAGCTATTTCTGGGTGACCC 5280  
| | | | |  
Db 5221 TGAATATTTTCTAGAAATGCGGAGGAGAAATGGGTGTTAGCTATTTCTGGGTGACCC 5280  
| | | | |  
QY 5281 AGCTATTTTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGAGATGG 5340  
| | | | |  
Db 5281 AGCTATTTTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGAGATGG 5340  
| | | | |  
QY 5341 TCAATGAAAGAAACCAAGAGTCCAAAGCGAGCAAGAGATCCAGAGCAGAAAGATCT 5400  
| | | | |  
Db 5341 TCAATGAAAGAAACCAAGAGTCCAAAGCGAGCAAGAGATCCAGAGCAGAAAGATCT 5400  
| | | | |  
QY 5401 TCAAGGGGCTAGAAATCTGTTGCTATGGGCCCTTACCAACAATGCCAGATCAACTGG 5460  
| | | | |

Db	5461	TCAGGGGGCTGAGAAATCTGTTCCTATGGGCCCTTACCAACATGCCCAAGATCAACTCG	5466
QY	5461	AATGATATGTAACAGCTGTGTGTGCTTCTGTGTGAAGAGCTTTCATCATTCACCTTGG	5522
Db	5461	AATGATATGTAACAGCTGTGTGTGCTTCTGTGTGAAGAGCTTTCATCATTCACCTTGG	5522
QY	5521	GCACAGGTGCACCAACCAATTGTGTGTGTGTGCAGCCAGATGCCCTGTGCACAGAGCATATGCT	5588
Db	5521	GCACAGGTGCACCAACCAATTGTGTGTGTGTGCAGCCAGATGCCCTGTGCACAGAGCAATATGCT	5588
QY	5581	TCCATGCAATTTGGGCGAGATGTGTGTGAGGACCTGTGTGTACCCGAGAGTGTGTGTGACA	5640
Db	5581	TCCATGCAATTTGGGCGAGATGTGTGTGAGGACCTGTGTGTACCCGAGAGTGTGTGTGACA	5640
QY	5641	GTTGTGCACTCTACCAAGTGCAGAGAGCTGTGACACTTACTGTATACCCAGATCCCCACA	5700
Db	5641	GTTGTGCACTCTACCAAGTGCAGAGAGCTGTGACACTTACTGTATACCCAGATCCCCACA	5700
QY	5701	GCCACTACTGA 5711	
Db	5701	GCCACTACTGA 5711	

RESULT 13  
 US-09-099-753-1  
 Sequence 1, Application US/09099753  
 Patent No. 6149903  
 GENERAL INFORMATION:  
 APPLICANT: HOLT, JEFFREY T.  
 APPLICANT: JENSEN, ROY A.  
 APPLICANT: PAGE, DAVID L.  
 APPLICANT: KING, MARY-CLAIRE  
 APPLICANT: SZABO, CSILLA I.  
 APPLICANT: JETTON, THOMAS L.  
 APPLICANT: ROBINSON-BENION, CHERYL L.  
 APPLICANT: THOMPSON, MARILYN E.  
 TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2  
 TITLE OF INVENTION: PROTEINS AND SCREENING AND THERAPEUTIC METHODS BASED ON  
 TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2 PROTEINS.  
 NUMBER OF SEQUENCES: 29  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: ARLES A. TAYLOR, JR.  
 STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER  
 STREET: BOULEVARD  
 CITY: DURHAM  
 STATE: NORTH CAROLINA  
 COUNTRY: USA  
 ZIP: 27707  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.50 inch, 800 KB storage  
 COMPUTER: IBM PC/XT/AT compatible  
 OPERATING SYSTEM: Windows 3.1  
 SOFTWARE: WORD PERFECT 6.1 and ASCII  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/099,753  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/603,753  
 FILING DATE: 20 FEB 1996  
 APPLICATION NUMBER: U.S. 08/373,799  
 FILING DATE: 17 JAN 1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: ARLES A. TAYLOR, JR.  
 REGISTRATION NUMBER: 39,395  
 REFERENCE/DOCKET NUMBER: 1242/2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (919) 493-8000  
 TELEFAX: (919) 419-0383  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:

Query Match	Best Local Similarity	Score	DB	Length
Matches 5704; Conservative	99.8%; Pred. No. 0; Mismatches 7; Indels 0; Gaps 0	5699.8; DB 3; Length 5712;		
1	AGCTGCTGAGACTCTCTGGAACCCGACACAGGCTGTGGGTTTCTCAGATTAATCGGCC	60		
1	AGCTGCTGAGACTCTCTGGAACCCGACACAGGCTGTGGGTTTCTCAGATTAATCGGCC	60		
61	CCTGGGCTCAGAGAGGCTTCAACCTCTGCTCTGGTAAAGTTTCATTGGAACAGAAAGAA	120		
61	CCTGGGCTCAGAGAGGCTTCAACCTCTGCTCTGGTAAAGTTTCATTGGAACAGAAAGAA	120		
121	TGGAATTATCGCTCTTCGCGGTGAAGAAGTACAAATGTCAATTAATGCTATGCAAGAA	180		
121	TGGAATTATCGCTCTTCGCGGTGAAGAAGTACAAATGTCAATTAATGCTATGCAAGAA	180		
181	TCTTGAAGTGTCCATCTGTCTGAGAGTTGATCAAGAACTGTCTCCACAAAGTGTGACC	240		
181	TCTTGAAGTGTCCATCTGTCTGAGAGTTGATCAAGAACTGTCTCCACAAAGTGTGACC	240		
241	ACATATTTTGGAAATTTTGGATGCTGAAACTTCTCAACAGAGAAAGGCTTTCACAGT	300		
241	ACATATTTTGGAAATTTTGGATGCTGAAACTTCTCAACAGAGAAAGGCTTTCACAGT	300		
301	GTCCTTATATGTAAGATATTAACCAAAAGAGCTTCAAGAAAGTACGAGATTAGTC	360		
301	GTCCTTATATGTAAGATATTAACCAAAAGAGCTTCAAGAAAGTACGAGATTAGTC	360		
361	AACCTGTGAAGAGCTATGTAAGAAATCATTTGTGCTTTCACTTGACACAGGTTTGAGT	420		
361	AACCTGTGAAGAGCTATGTAAGAAATCATTTGTGCTTTCACTTGACACAGGTTTGAGT	420		
421	ATGGAACAGCTATATTTTGGCAAAAGAAATTAATCTCTCGAATCTAAAGATG	480		

Db 421 ATGCAACAGCTATATTTTGCAGAAAAGAAATTACTCTGAAACATCTAAAGATG 480  
Qy 481 AAGTTTCTATATCCAAAGTATGGCTTCAGAAAACCGGCCAAAGACTTCTACAGATG 540  
Db 481 AAGTTTCTATATCCAAAGTATGGCTTCAGAAAACCGGCCAAAGACTTCTACAGATG 540  
Qy 541 AACCCGAAATCTCTTCTGAGGAAACAGCTCAGTGTCAACTCTTAACCTTGA 600  
Db 541 AACCCGAAATCTCTTCTGAGGAAACAGCTCAGTGTCAACTCTTAACCTTGA 600  
Qy 601 CTGTGAGAACTCTGAGCAAAAGCAGCGATCAACTCAAAAGACGTCTGTCTACATG 660  
Db 601 CTGTGAGAACTCTGAGCAAAAGCAGCGATCAACTCAAAAGACGTCTGTCTACATG 660  
Qy 661 AATTGGATCTGATTTCTTCTGAGATACCTGTTAATAGGCACTTATTGCGTGGAG 720  
Db 661 AATTGGATCTGATTTCTTCTGAGATACCTGTTAATAGGCACTTATTGCGTGGAG 720  
Qy 721 ATCAAGATTTGTTCAATCAACCCCTCAAGAACCGGATGAAATCACTTGTGATTCG 780  
Db 721 ATCAAGATTTGTTCAATCAACCCCTCAAGAACCGGATGAAATCACTTGTGATTCG 780  
Qy 781 CAAAAAGGCTGCTGTGAAATTTTCTGAGAGGATGTAACTAATCTGACATCATCAC 840  
Db 781 CAAAAAGGCTGCTGTGAAATTTTCTGAGAGGATGTAACTAATCTGACATCATCAC 840  
Qy 841 CCAAGTAAATGATTTTGAACACCACTGAGAACCGTGCAGCTGAGAGGATCCAGAAAGT 900  
Db 841 CCAAGTAAATGATTTTGAACACCACTGAGAACCGTGCAGCTGAGAGGATCCAGAAAGT 900  
Qy 901 ATCGAGGATTTCTGTTCAAACTTGCATGTGAGACCACTGAGCAAAATCTCATGCA 960  
Db 901 ATCGAGGATTTCTGTTCAAACTTGCATGTGAGACCACTGAGCAAAATCTCATGCA 960  
Qy 961 GCTCATTCACAGATGAGAAACAGAGTTTATTACTCACTAAAGACAGATGTAGAAA 1020  
Db 961 GCTCATTCACAGATGAGAAACAGAGTTTATTACTCACTAAAGACAGATGTAGAAA 1020  
Qy 1021 AGGCTGAATTTCTGTAAATAAAGCAACAGCTGCTGCTGAGCAAGGACCACTAACAT 1080  
Db 1021 AGGCTGAATTTCTGTAAATAAAGCAACAGCTGCTGCTGAGCAAGGACCACTAACAT 1080  
Qy 1081 GGGCTGGAATGAGAAACATGTATGTATGGCGGACTCCAGCAACAGAAAAAGGATG 1140  
Db 1081 GGGCTGGAATGAGAAACATGTATGTATGGCGGACTCCAGCAACAGAAAAAGGATG 1140  
Qy 1141 ATCTGAATGCTGATCCCTGTGTGTGAGAGAAAGATGGAATGAAATGCAATGCT 1200  
Db 1141 ATCTGAATGCTGATCCCTGTGTGTGAGAGAAAGATGGAATGAAATGCAATGCT 1200  
Qy 1201 CAGAGAAATCTTAAGATATCTGAAGATGTTCTTGATTAACATAATAGCAGCATTCGA 1260  
Db 1201 CAGAGAAATCTTAAGATATCTGAAGATGTTCTTGATTAACATAATAGCAGCATTCGA 1260  
Qy 1261 AAGTTAATGAGTGGTTTCCAGAAATGATGAACTGTAGTTCATGATGCTCACTCATG 1320  
Db 1261 AAGTTAATGAGTGGTTTCCAGAAATGATGAACTGTAGTTCATGATGCTCACTCATG 1320  
Qy 1321 GGGAGTCTGAATCAAAATGCAAAAGTATGATGTTGGAAGTCTTAATAGAGTATG 1380  
Db 1321 GGGAGTCTGAATCAAAATGCAAAAGTATGATGTTGGAAGTCTTAATAGAGTATG 1380  
Qy 1381 AATATTTCTGTTCTTCAAGAAAATAGACTTACTGCGCAGTGTCTCTAGGGCTTTAA 1440  
Db 1381 AATATTTCTGTTCTTCAAGAAAATAGACTTACTGCGCAGTGTCTCTAGGGCTTTAA 1440  
Qy 1441 TATGTAAAGTGAAGAGTTCTCACTCAATCAGTGAAGATTAATGGAAGCAAAATAT 1500  
Db 1441 TATGTAAAGTGAAGAGTTCTCACTCAATCAGTGAAGATTAATGGAAGCAAAATAT 1500  
Qy 1501 TTGGGAAACCTATCGGAAGAGGCAAGCTCCCAACTTAAGCATGTAATGAAAAATC 1560  
Db 1501 TTGGGAAACCTATCGGAAGAGGCAAGCTCCCAACTTAAGCATGTAATGAAAAATC 1560

Db 1501 TTGGGAAACCTATCGGAAGAGGCAAGCTCCCAACTTAAGCATGTAATGAAAAATC 1560  
Qy 1561 TAATTATAGAGATTTGTTAGGCAAGATTAATCAAGAGAGTCCCTGCAAAATA 1620  
Db 1561 TAATTATAGAGATTTGTTAGGCAAGATTAATCAAGAGAGTCCCTGCAAAATA 1620  
Qy 1621 AATTAAAGCGTAAAGAGACCTTACATCAGGCTTCACTCTGAGATTTTATCAAGAAAG 1680  
Db 1621 AATTAAAGCGTAAAGAGACCTTACATCAGGCTTCACTCTGAGATTTTATCAAGAAAG 1680  
Qy 1681 CAGATTTGGCAGTTCAAAAGACTCCTGATTAATGATTAATCAGGAACTTAACCAAGAGC 1740  
Db 1681 CAGATTTGGCAGTTCAAAAGACTCCTGATTAATGATTAATCAGGAACTTAACCAAGAGC 1740  
Qy 1741 AGAATGGTCAAGTATGATTAATTAATGATGATGATGATGATGATGATGATGATGAT 1800  
Db 1741 AGAATGGTCAAGTATGATTAATTAATGATGATGATGATGATGATGATGATGATGAT 1800  
Qy 1801 CTATTCAGATGAGAAAAATCTTAACCAATAGATCACTGAAAAAGAAATCTGCTTCA 1860  
Db 1801 CTATTCAGATGAGAAAAATCTTAACCAATAGATCACTGAAAAAGAAATCTGCTTCA 1860  
Qy 1861 AAACGAAAGCTGAACCTTAAGCAGAGTATTAAGCAATATGAACTCGAATTAATATCC 1920  
Db 1861 AAACGAAAGCTGAACCTTAAGCAGAGTATTAAGCAATATGAACTCGAATTAATATCC 1920  
Qy 1921 ACAATTCAAAAGCACTTAAAGAAATAGCTGAGAGAAATCTTCTTACCGAGATATTC 1980  
Db 1921 ACAATTCAAAAGCACTTAAAGAAATAGCTGAGAGAAATCTTCTTACCGAGATATTC 1980  
Qy 1981 ATGGCTTGAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2040  
Db 1981 ATGGCTTGAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2040  
Qy 2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAAGATGACCAACCAATGCCAGTCA 2100  
Db 2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAAGATGACCAACCAATGCCAGTCA 2100  
Qy 2101 GGCACAGCAAAACCTTACATCTGAGAAAGTAAAGAACTTGCACCTGGAACCAAGAAAG 2160  
Db 2101 GGCACAGCAAAACCTTACATCTGAGAAAGTAAAGAACTTGCACCTGGAACCAAGAAAG 2160  
Qy 2161 GTAACCAAGCAAAATGAACAGCAAGTAAAGACATGACATGATTAATCTTCCAGAGCTGA 2220  
Db 2161 GTAACCAAGCAAAATGAACAGCAAGTAAAGACATGACATGATTAATCTTCCAGAGCTGA 2220  
Qy 2221 AGTTAACAAATGCACTGCTGTTCTTTACTTAAGTGTTCATTAACAGTGAACCTTAAGAT 2280  
Db 2221 AGTTAACAAATGCACTGCTGTTCTTTACTTAAGTGTTCATTAACAGTGAACCTTAAGAT 2280  
Qy 2281 TTGTCAATCTTACGCTTCCAGAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 2340  
Db 2281 TTGTCAATCTTACGCTTCCAGAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 2340  
Qy 2341 CTAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTCAGAACTG 2400  
Db 2341 CTAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTCAGAACTG 2400  
Qy 2401 AAAGATCTGTAGAGATGAGATTTTCACTGATGCTGATGATGATGATGATGATGATG 2460  
Db 2401 AAAGATCTGTAGAGATGAGATTTTCACTGATGCTGATGATGATGATGATGATGATG 2460  
Qy 2461 AAAGATCTGTAGAGATGAGATTTTCACTGATGCTGATGATGATGATGATGATGATG 2520  
Db 2461 AAAGATCTGTAGAGATGAGATTTTCACTGATGCTGATGATGATGATGATGATGATG 2520  
Qy 2521 GTGTAGTCAAGTGAAGATTTTGAAGACCCCAAGAGCTTAATCAAGTGTTCAGAAAG 2580  
Db 2521 GTGTAGTCAAGTGAAGATTTTGAAGACCCCAAGAGCTTAATCAAGTGTTCAGAAAG 2580  
Qy 2581 ATTAATGAATGACACAGAAAGCTTTTAATGATTCATTTGGGACATGAAGTTAACCAAGTC 2640  
Db 2581 ATTAATGAATGACACAGAAAGCTTTTAATGATTCATTTGGGACATGAAGTTAACCAAGTC 2640

2641 GGGAAACAAGCATAGAAATGGAAGAGAACTTATGCTCAGTATTTGAGATAATCAT 2700  
2641 GGGAAACAAGCATAGAAATGGAAGAGAACTTATGCTCAGTATTTGAGATAATCAT 2700  
2701 TCAAGTTTCAAAAGCGCCAGTCAATTTGCTGTGTTTCAATTCAGAAATCAGAAAGAG 2760  
2701 TCAAGTTTCAAAAGCGCCAGTCAATTTGCTGTGTTTCAATTCAGAAATCAGAAAGAG 2760  
2761 AATGTCACATCTCTGCCCCACTGTGGCTCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
2761 AATGTCACATCTCTGCCCCACTGTGGCTCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
2821 TTGAATGTGAACAAAGAGAAATCAAGAGAAAGATGATCTAATATCAAGCTGTAC 2880  
2821 TTGAATGTGAACAAAGAGAAATCAAGAGAAAGATGATCTAATATCAAGCTGTAC 2880  
2881 AGACATTAATATCATCTGACAGCTTTCTGTGTGTGTCAAGAAAGATAGCCAGTTGATA 2940  
2881 AGACATTAATATCATCTGACAGCTTTCTGTGTGTGTCAAGAAAGATAGCCAGTTGATA 2940  
2941 ATGCCAAATGTAATATCAAAAGAGCTTAGGTTTGTCTATCATCTGATTCAGAGCA 3000  
2941 ATGCCAAATGTAATATCAAAAGAGCTTAGGTTTGTCTATCATCTGATTCAGAGCA 3000  
3001 ACGAACTGGACTGATTAATCAAAATTAACATGAGCTTTTCAAAACCCATATGCTATAC 3060  
3001 ACGAACTGGACTGATTAATCAAAATTAACATGAGCTTTTCAAAACCCATATGCTATAC 3060  
3061 CACCACTTTTCCATCAAGTCAATTTGTTAAACCTAAATGTAGAAATATCTGCTAGAG 3120  
3061 CACCACTTTTCCATCAAGTCAATTTGTTAAACCTAAATGTAGAAATATCTGCTAGAG 3120  
3121 AAAAATTGAGGAACATTCATGTAATGTAAGAAAGAAATGGAATATGAAACATTTCAA 3180  
3121 AAAAATTGAGGAACATTCATGTAATGTAAGAAAGAAATGGAATATGAAACATTTCAA 3180  
3181 GTACAGTGAACATTAAGCTGTAATTAACATTAAGAAATGTTTAAAGAGCAGCT 3240  
3181 GTACAGTGAACATTAAGCTGTAATTAACATTAAGAAATGTTTAAAGAGCAGCT 3240  
3241 CAAGCAATTAATTAAGTGAAGTTCAGTACTAATGAAGTGGGCTCCAGTATTAATGAA 3300  
3241 CAAGCAATTAATTAAGTGAAGTTCAGTACTAATGAAGTGGGCTCCAGTATTAATGAA 3300  
3301 TAGGTTCCAGTGAAGAAACATTCAGAGCAAACTAGTGAAGAAAGAGGCGCAAAATTGA 3360  
3301 TAGGTTCCAGTGAAGAAACATTCAGAGCAAACTAGTGAAGAAAGAGGCGCAAAATTGA 3360  
3361 ATGCTATGCTTAAGTGAAGGTTTGAACCTGAGAGCTATTAACAAAGCTTCTGCGAA 3420  
3361 ATGCTATGCTTAAGTGAAGGTTTGAACCTGAGAGCTATTAACAAAGCTTCTGCGAA 3420  
3421 GTAATTTGAACATCTGAAATTAATAAGCAAGATATGAAGAGTATGTTCAAGCTGTA 3480  
3421 GTAATTTGAACATCTGAAATTAATAAGCAAGATATGAAGAGTATGTTCAAGCTGTA 3480  
3481 ATACAGATTTCTTCATATCTGATTTAGTAACTTAAGAACAGCTATGGAAGTATGTC 3540  
3481 ATACAGATTTCTTCATATCTGATTTAGTAACTTAAGAACAGCTATGGAAGTATGTC 3540  
3481 ATACAGATTTCTTCATATCTGATTTAGTAACTTAAGAACAGCTATGGAAGTATGTC 3540  
3541 ATGCTATGCTTAAGTGAAGGTTTGAACCTGAGAGCTATTAACAAAGCTTCTGCGAA 3600  
3541 ATGCTATGCTTAAGTGAAGGTTTGAACCTGAGAGCTATTAACAAAGCTTCTGCGAA 3600  
3601 AAGATTAAGTGAAGGTTTGAACCTGAGAGCTATTAACAAAGCTTCTGCGAA 3660  
3601 AAGATTAAGTGAAGGTTTGAACCTGAGAGCTATTAACAAAGCTTCTGCGAA 3660  
3661 TCAGAGAGAGAGCTTGAAGAGTCTAGAGCTTCAAGCTATACATTTGCTGAG 3720  
3661 TCAGAGAGAGAGCTTGAAGAGTCTAGAGCTTCAAGCTATACATTTGCTGAG 3720  
3661 TCAGAGAGAGAGCTTGAAGAGTCTAGAGCTTCAAGCTATACATTTGCTGAG 3720

3721 GTTACCGAAGAGGGCCAGAAATTAAGTCTCAGAGAGACTTAATCTAGAGAGATG 3780  
3721 GTTACCGAAGAGGGCCAGAAATTAAGTCTCAGAGAGACTTAATCTAGAGAGATG 3780  
3781 AAGAGCTTCCCTGCTTCCAAACATTTGTTTGGTAAAGTAAACATATATACCTTCAGT 3840  
3781 AAGAGCTTCCCTGCTTCCAAACATTTGTTTGGTAAAGTAAACATATATACCTTCAGT 3840  
3841 CTACTAGGATAGACACCGTGTCTACCGAGTCTCTGTCTAGAAACACAGAGAAATTTAT 3900  
3841 CTACTAGGATAGACACCGTGTCTACCGAGTCTCTGTCTAGAAACACAGAGAAATTTAT 3900  
3901 TATCATTAAGATAGACTTAATATGATCTGACATACCGAGTATATTTGGCAAGAGCATCTC 3960  
3901 TATCATTAAGATAGACTTAATATGATCTGACATACCGAGTATATTTGGCAAGAGCATCTC 3960  
3961 AGGAACATCACCTTAAGTGAAGAAACAAATGTTGCTGAGTGTCTTCAAGTGA 4020  
3961 AGGAACATCACCTTAAGTGAAGAAACAAATGTTGCTGAGTGTCTTCAAGTGA 4020  
4021 GTGAATTTGAAAGACTTGAATGCAAAATACAAACACCCAGAGATCTTTCTGATTTGCTT 4080  
4021 GTGAATTTGAAAGACTTGAATGCAAAATACAAACACCCAGAGATCTTTCTGATTTGCTT 4080  
4081 CCAACCAATGAGGATCAAGCTGAAAGCCAGAGAGTGTGCTGAGTGAACAAAGATTTG 4140  
4081 CCAACCAATGAGGATCAAGCTGAAAGCCAGAGAGTGTGCTGAGTGAACAAAGATTTG 4140  
4141 TTTGAGATGATGAAGAAAGAGAAACGGGCTTGAAGAAATTAATCAAGAGAGCA 4200  
4141 TTTGAGATGATGAAGAAAGAGAAACGGGCTTGAAGAAATTAATCAAGAGAGCA 4200  
4201 TGAATTAACCTTGAAGTGAAGAGACATCTGGTGTGAGTGAAGAAACAGGCTCTCTAG 4260  
4201 TGAATTAACCTTGAAGTGAAGAGACATCTGGTGTGAGTGAAGAAACAGGCTCTCTAG 4260  
4261 ACTGCTCAGGCTATCTCTCAGAGTGAACATTTTAACCACTCAGAGAGGATACATGTC 4320  
4261 ACTGCTCAGGCTATCTCTCAGAGTGAACATTTTAACCACTCAGAGAGGATACATGTC 4320  
4321 AACATTAACCTGATTAAGCTCCAGAGAGAAATGCTGAACATAAGAGCTGTGTTAAGAC 4380  
4321 AACATTAACCTGATTAAGCTCCAGAGAGAAATGCTGAACATAAGAGCTGTGTTAAGAC 4380  
4381 ATGGAAGCCAGCTTCTTAACAGCTACCTTCCATCAATAGAGCTCTTCTGCGCTTGAAG 4440  
4381 ATGGAAGCCAGCTTCTTAACAGCTACCTTCCATCAATAGAGCTCTTCTGCGCTTGAAG 4440  
4441 ACTGCGAAATCCAGAACAAAGCACATCAGAAAGAGATTAATCACTTCACAGAAAGTA 4500  
4441 ACTGCGAAATCCAGAACAAAGCACATCAGAAAGAGATTAATCACTTCACAGAAAGTA 4500  
4501 GTGAATACCTTATTAAGCCAGAGATCCAGAGAGCTTCTGCTGACAAAGTGTGCTG 4560  
4501 GTGAATACCTTATTAAGCCAGAGATCCAGAGAGCTTCTGCTGACAAAGTGTGCTG 4560  
4561 CAGATAGTCTTAACAGTAAATTAAGAACAGAGAGTGAAGAGTCACTCCCTCTTAAT 4620  
4561 CAGATAGTCTTAACAGTAAATTAAGAACAGAGAGTGAAGAGTCACTCCCTCTTAAT 4620  
4621 GCCCATATTAAGATGAAGGTTGTAATGCAAGTGTCTGCGGAGCTTCAGAAATGAA 4680  
4621 GCCCATATTAAGATGAAGGTTGTAATGCAAGTGTCTGCGGAGCTTCAGAAATGAA 4680  
4681 ACTACCATCTCAGAGAGCTCAATTAAGGTTGTTGTAATGAGAGCAACAGCTGAG 4740  
4681 ACTACCATCTCAGAGAGCTCAATTAAGGTTGTTGTAATGAGAGCAACAGCTGAG 4740  
4741 AGTCTGAGCAACAGATTTGAAGAGAAATCTTAATCTTGAAGAGCAAGATCTAGAGGAA 4800  
4741 AGTCTGAGCAACAGATTTGAAGAGAAATCTTAATCTTGAAGAGCAAGATCTAGAGGAA 4800  
4801 CCCCTTACCTGGAATCTGGAATACAGCTCTTCTCTGATGACCTGAAATCTGATCTCTG 4860



```

Db 4801 CCCCTTACTGGAATCTGGAATCAGACCTCTCTCTGATGAGACCCGTAATCTGATCTCTG 4860
Qy 4861 AAGACAGAGCCCGAGAGTCACTGCTGTTGGCAATACATCTTCAACCTTGATGGA 4920
Db 4861 AAGACAGAGCCCGAGAGTCACTGCTGTTGGCAATACATCTTCAACCTTGATGGA 4920
Qy 4921 AAGTCCCAATTTGAAAGTTGCAAGATCTGCCCAGAGTCCAGCTGCTGCTACTACTG 4980
Db 4921 AAGTCCCAATTTGAAAGTTGCAAGATCTGCCCAGAGTCCAGCTGCTGCTACTACTG 4980
Qy 4981 ATACTGCTGGGTATATATGCAATGAAAGAAAGTGTGAGCAGGAGAAAGCAGAAATTGACG 5040
Db 4981 ATACTGCTGGGTATATATGCAATGAAAGAAAGTGTGAGCAGGAGAAAGCAGAAATTGACG 5040
Qy 5041 CTTCAACAGAAAGGTTCAACAAAGAAATGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5100
Db 5041 CTTCAACAGAAAGGTTCAACAAAGAAATGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5100
Qy 5101 AATTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5160
Db 5101 AATTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5160
Qy 5161 CTGAAGAGACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5220
Db 5161 CTGAAGAGACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5220
Qy 5221 TGAATATTTTCTGAGATTTGGGGAGGAAATGGGTAGTTAGTTAGTTAGTTAGTTAGTTAGTT 5280
Db 5221 TGAATATTTTCTGAGATTTGGGGAGGAAATGGGTAGTTAGTTAGTTAGTTAGTTAGTTAGTT 5280
Qy 5281 AGTCTATTTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCTGAGAGAGATGAG 5340
Db 5281 AGTCTATTTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCTGAGAGAGATGAG 5340
Qy 5341 TCAATGAGAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCTGAGAGAGATGAG 5400
Db 5341 TCAATGAGAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCTGAGAGAGATGAG 5400
Qy 5401 TCAGGGGGCTGAGAAATCTGTTGCTATGAGGCTCTTCAACCAATGCTGCTGCTGCTGCTG 5460
Db 5401 TCAGGGGGCTGAGAAATCTGTTGCTATGAGGCTCTTCAACCAATGCTGCTGCTGCTGCTG 5460
Qy 5461 AATGATGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5520
Db 5461 AATGATGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5520
Qy 5521 GCACAGGTGTCACCCCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5580
Db 5521 GCACAGGTGTCACCCCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5580
Qy 5581 TCATGCAATTTGGGAGAGTGTGTGAGGCACTGTGTGTGAGCCGAGAGTGTGTGTGAGCA 5640
Db 5581 TCATGCAATTTGGGAGAGTGTGTGAGGCACTGTGTGTGAGCCGAGAGTGTGTGTGAGCA 5640
Qy 5641 GTGAGCACTCTACAGTGCAGAGGCTGAGCACTTACTATATACCCAGATTTCCCAACA 5700
Db 5641 GTGAGCACTCTACAGTGCAGAGGCTGAGCACTTACTATATACCCAGATTTCCCAACA 5700
Qy 5701 GCCACTACTGA 5711
Db 5701 GCCACTACTGA 5711

```

```

RESULT 14
US-08-986-106-1
: Sequence 1, Application US/08986106
: Patent No. 6177410
: GENERAL INFORMATION:
: APPLICANT: HOLT, JEFFREY T.
: APPLICANT: JENSEN, ROY A.
: APPLICANT: KING, MARY-CLAIRE
: APPLICANT: STEINER, MITCHELL S.

```

```

: APPLICANT: ROBINSON-BENION, CHERYL L.
: APPLICANT: THOMPSON, MARILYN E.
: TITLE OF INVENTION: THERAPEUTIC METHODS FOR
: TITLE OF INVENTION: PROSTATE CANCER
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: ARLES A. TAYLOR, JR.
: STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER
: STREET: BOULEVARD
: CITY: DURHAM
: STATE: NORTH CAROLINA
: COUNTRY: USA
: ZIP: 27707
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB storage
: COMPUTER: IBM PC/XT/AT compatible
: OPERATING SYSTEM: Windows 3.1
: SOFTWARE: WORD PERFECT 6.1 and ASCII
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/986,106
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/603,753
: FILING DATE: 20 FEB 1996
: ATTORNEY/AGENT INFORMATION:
: NAME: ARLES A. TAYLOR, JR.
: REGISTRATION NUMBER: 39,395
: REFERENCE/DOCKET NUMBER: 1242/3
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (919) 493-8000
: TELEFAX: (919) 419-0383
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5712
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: BRCA1
: LOCATION: Genbank accession no. U14680
: PUBLICATION INFORMATION:
: AUTHORS: Miki, Y., et. al.
: TITLE: A strong candidate gene for the breast and
: TITLE: ovarian cancer susceptibility gene BRCA1.
: JOURNAL: Science
: VOLUME: 266
: PAGES: 66-71
: DATE: 1994
:
: US-08-986-106-1
:
: Query Match 99.8%; Score 5699.8; DB 3; Length 5712;
: Best Local Similarity 99.9%; Pred. No. 0;
: Matches 5704; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
:
: Qy 1 AGCTGCTGAGAACTTCTGAGACCCCGACAGGCTGTGGGTTTCTGATTAATCTGGGCC 60
: Db 1 AGCTGCTGAGAACTTCTGAGACCCCGACAGGCTGTGGGTTTCTGATTAATCTGGGCC 60
:
: Qy 61 CTTGGGCTCAGAGAGCCCTTCAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
: Db 61 CTTGGGCTCAGAGAGCCCTTCAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
:
: Qy 121 TGAATTTATCTGCTCTTGGCGTTGAGAAAGTAAAGTAAATGCTATTAATGCTAGAGAAA 180
: Db 121 TGAATTTATCTGCTCTTGGCGTTGAGAAAGTAAAGTAAATGCTATTAATGCTAGAGAAA 180
:
: Qy 181 TCTTAGAGTGTCCCATCTGTCTGAGAGTTGAGAGAAAGTCTCTCCCAAGAGTGTGACC 240
: Db 181 TCTTAGAGTGTCCCATCTGTCTGAGAGTTGAGAGAAAGTCTCTCCCAAGAGTGTGACC 240
:
: Qy 241 ACATATTTGCAATTTTGCATGCTGAGAACTTCTCAACAGAGAAAGGAGGCTTCAAGT 300

```

Db 241 ACATATTTTGCAAAATTTTGCAAGCTGAAATCTTCAACCGAAGAAAGGCGCTTCAACGT 300  
Qy 301 GTCTTTATGTAAGAAATATATTAACCAAAAGAGCTTCAAGAAAGTACGATTTTATC 360  
Db 301 GTCTTTATGTAAGAAATATTAACCAAAAGAGCTTCAAGAAAGTACGATTTTATC 360  
Qy 361 AACTGTGGAAGAGCTATTTGAAAATCATTTGTGCTTTTCACTTGCACACAGGTTTGGAGT 420  
Db 361 AACTGTGGAAGAGCTATTTGAAAATCATTTGTGCTTTTCACTTGCACACAGGTTTGGAGT 420  
Qy 421 ATGCAACAGCTATTAATTTTGCAAAAAAGAAAATTAATCTTCTGCAATCTTAAGATG 480  
Db 421 ATGCAACAGCTATTAATTTTGCAAAAAAGAAAATTAATCTTCTGCAATCTTAAGATG 480  
Qy 481 AAGTTTCTATCATCAAAAGTATGAGGCTACAAAACCGGCAAAAGACTTCTACAGAGT 540  
Db 481 AAGTTTCTATCATCAAAAGTATGAGGCTACAAAACCGGCAAAAGACTTCTACAGAGT 540  
Qy 541 AACCAGAAATCTTCTGAGGAAACCACTCTCAAGTCCAACTCTTAACCTTGGAA 600  
Db 541 AACCAGAAATCTTCTGAGGAAACCACTCTCAAGTCCAACTCTTAACCTTGGAA 600  
Qy 601 CTGTGAGAACTCTGAGCAAAAGCAGCGGATCAACTCAAAAAGCTCTGTCTTACATG 660  
Db 601 CTGTGAGAACTCTGAGCAAAAGCAGCGGATCAACTCAAAAAGCTCTGTCTTACATG 660  
Qy 661 AATTGGGATCTGATTTCTGAAAGTACCGTTAATTAAGGCAACTTAATGCGATGGAG 720  
Db 661 AATTGGGATCTGATTTCTGAAAGTACCGTTAATTAAGGCAACTTAATGCGATGGAG 720  
Qy 721 ATCAAGAAATGTTCAAAATCAACCCCTCAAGAACCAAGGATGAATCAGTTTGGATCTG 780  
Db 721 ATCAAGAAATGTTCAAAATCAACCCCTCAAGAACCAAGGATGAATCAGTTTGGATCTG 780  
Qy 781 CAAAAAGGCTCTTGTGAATTTTCTGACGAGATTAACAATTAATCAATCAATCAAC 840  
Db 781 CAAAAAGGCTCTTGTGAATTTTCTGACGAGATTAACAATTAATCAATCAATCAAC 840  
Qy 841 CCAGTAATTAATGATTTGAACCACTGAGAGCGGCTGAGAGGATCAAAAAAGT 900  
Db 841 CCAGTAATTAATGATTTGAACCACTGAGAGCGGCTGAGAGGATCAAAAAAGT 900  
Qy 901 ATCAAGGAGTCTTGTTCAAACTGTCATGTGAGCCATGTGGCAAAATCTCATGCA 960  
Db 901 ATCAAGGAGTCTTGTTCAAACTGTCATGTGAGCCATGTGGCAAAATCTCATGCA 960  
Qy 961 GCTCATTAACAGACGAGAACGAGTTTATTACTCACTAAAGACAGATGATGAGAA 1020  
Db 961 GCTCATTAACAGACGAGAACGAGTTTATTACTCACTAAAGACAGATGATGAGAA 1020  
Qy 1021 AGGCTGAATTTCTGTAATTAAGCAAAACAGCTGGCTTGAAGAGGCAACATAACGAT 1080  
Db 1021 AGGCTGAATTTCTGTAATTAAGCAAAACAGCTGGCTTGAAGAGGCAACATAACGAT 1080  
Qy 1081 GGGGTGGAAGTAAAGAAACATGTAATGATAGCGGACTCCAGACACAAAAAGGATG 1140  
Db 1081 GGGGTGGAAGTAAAGAAACATGTAATGATAGCGGACTCCAGACACAAAAAGGATG 1140  
Qy 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAGATGAGATTAAGCAAACTGCCATGCT 1200  
Db 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAGATGAGATTAAGCAAACTGCCATGCT 1200  
Qy 1201 CAGAGATCTTAAGATCTAAGATGTTCTTGGATTAACATAATAGCAGCTTGA 1260  
Db 1201 CAGAGATCTTAAGATCTAAGATGTTCTTGGATTAACATAATAGCAGCTTGA 1260  
Qy 1261 AAGTTAATGAGTGTTCAGAAAGTATGATGATGATGATGATGATGATGATGATG 1320  
Db 1261 AAGTTAATGAGTGTTCAGAAAGTATGATGATGATGATGATGATGATGATGATG 1320  
Qy 1321 GGGAGTCTGAATCAAAATGCCAAAGTATGATGATGATGATGATGATGATGATG 1380  
Db 1321 GGGAGTCTGAATCAAAATGCCAAAGTATGATGATGATGATGATGATGATGATG 1380

Qy 1381 AATATCTGCTTTCTTCAAGAAATATAGCTTACTGGCAGATGATCTCATAGGCTTAA 1440  
Db 1381 AATATCTGCTTTCTTCAAGAAATATAGCTTACTGGCAGATGATCTCATAGGCTTAA 1440  
Qy 1441 TATGTAAGAGTAAAGGTTCACTCAAAATCAGTAGAGATTAATTAAGACAAATAT 1500  
Db 1441 TATGTAAGAGTAAAGGTTCACTCAAAATCAGTAGAGATTAATTAAGACAAATAT 1500  
Qy 1501 TTGGAAAACCTATCGAAGAGGCAAGCTCCCAACTTAAGCATGTAATGAAAATC 1560  
Db 1501 TTGGAAAACCTATCGAAGAGGCAAGCTCCCAACTTAAGCATGTAATGAAAATC 1560  
Qy 1561 TAAATTAAGAGCAATTTGTTACTGAGCAAGATTAATCAAGAGGCTCCCTCAAAATA 1620  
Db 1561 TAAATTAAGAGCAATTTGTTACTGAGCAAGATTAATCAAGAGGCTCCCTCAAAATA 1620  
Qy 1621 AATTAAAGCGTAAAGAGACCTACATCAGGCTTCACTCTGAGATTTTATCAAGAAAG 1680  
Db 1621 AATTAAAGCGTAAAGAGACCTACATCAGGCTTCACTCTGAGATTTTATCAAGAAAG 1680  
Qy 1681 CAGATTTGGCACTTCAAAAGACTCTGTAATGATTAATCAGGGAATTAACCAACGAGC 1740  
Db 1681 CAGATTTGGCACTTCAAAAGACTCTGTAATGATTAATCAGGGAATTAACCAACGAGC 1740  
Qy 1741 AGAATGGTCAAGTATGATTAATTAATGATGATGATGATGATGATGATGATGATG 1800  
Db 1741 AGAATGGTCAAGTATGATTAATTAATGATGATGATGATGATGATGATGATGATG 1800  
Qy 1801 CTATTCAGAAATGAGAAAAATCTTAACCAATAGAAATCACTGAAAAAGAAATCTGCTTCA 1860  
Db 1801 CTATTCAGAAATGAGAAAAATCTTAACCAATAGAAATCACTGAAAAAGAAATCTGCTTCA 1860  
Qy 1861 AAACGAAAGCTGAACCTTAATAGCAGCGATTAAGCAATATGGAATCTGAATTAATTC 1920  
Db 1861 AAACGAAAGCTGAACCTTAATAGCAGCGATTAAGCAATATGGAATCTGAATTAATTC 1920  
Qy 1921 ACAATTAAGAAAGCACTTAAGAAATGAGGCTGAGAGAGGCTTCAACAGGCAATTC 1980  
Db 1921 ACAATTAAGAAAGCACTTAAGAAATGAGGCTGAGAGAGGCTTCAACAGGCAATTC 1980  
Qy 1981 ATGCGCTTGAACCTTAAGATGATGATGATGATGATGATGATGATGATGATGATG 2040  
Db 1981 ATGCGCTTGAACCTTAAGATGATGATGATGATGATGATGATGATGATGATGATG 2040  
Qy 2041 TTGATAGTGTGTTCTAGCAGTGAAGATTAAGAAAAAGTACCAATATGCACTCA 2100  
Db 2041 TTGATAGTGTGTTCTAGCAGTGAAGATTAAGAAAAAGTACCAATATGCACTCA 2100  
Qy 2101 GGCACAGCAAGAACTTAACCTCATGAGAGTAAAGAACTGCAACTGAGCCAAAGAA 2160  
Db 2101 GGCACAGCAAGAACTTAACCTCATGAGAGTAAAGAACTGCAACTGAGCCAAAGAA 2160  
Qy 2161 GTAACAAAGCAATGAACAGCAAGTAAAGACATGACAGGATCTTCCAGAGCTGA 2220  
Db 2161 GTAACAAAGCAATGAACAGCAAGTAAAGACATGACAGGATCTTCCAGAGCTGA 2220  
Qy 2221 AGTTAACAATGCACTGCTGTTTCTTAAGTCTTAATTAACAGTGAACCTTAAGAT 2280  
Db 2221 AGTTAACAATGCACTGCTGTTTCTTAAGTCTTAATTAACAGTGAACCTTAAGAT 2280  
Qy 2281 TTGTCATCTGAGCTTCCAAAGAGAAAGAAAGAAAGAAAGAAAGAAAGTAAAGT 2340  
Db 2281 TTGTCATCTGAGCTTCCAAAGAGAAAGAAAGAAAGAAAGAAAGAAAGTAAAGT 2340  
Qy 2341 CTATTAATGCTGAAGACCCCAAGATCTCATGTTAATGAGAAAGGTTTTCAGAACTG 2400  
Db 2341 CTATTAATGCTGAAGACCCCAAGATCTCATGTTAATGAGAAAGGTTTTCAGAACTG 2400  
Qy 2401 AAAGATCTGAGAGAGTGAAGATTTCACTGATCTGATGATGATGATGATGATGATG 2460  
Db 2401 AAAGATCTGAGAGAGTGAAGATTTCACTGATCTGATGATGATGATGATGATGATG 2460

QY 2461 AAGTATCTCGTACTGGAAGTAGACACTTAGAGGAGGCAAAAAACAGAACCAATAAT 2520  
| | | | |  
Db 2461 AAGTATCTCGTACTGGAAGTAGACACTTAGAGGAGGCAAAAAACAGAACCAATAAT 2520  
QY 2521 GTGTGAGTCAGTGTGACGACATTGAAAAACCCAGAGGACATAATTCATGAGTGTCCAAAG 2580  
| | | | |  
Db 2521 GTGTGAGTCAGTGTGACGACATTGAAAAACCCAGAGGACATAATTCATGAGTGTCCAAAG 2580  
QY 2581 AATAATGAATGACACAGAAAGCCTTAAGTATCCATTGGGACATGAAGTTAACCAAGTC 2640  
| | | | |  
Db 2581 AATAATGAATGACACAGAAAGCCTTAAGTATCCATTGGGACATGAAGTTAACCAAGTC 2640  
QY 2641 GGGAAACAGAGTGAATGGAAGAAAGTGAACCTGATGCTCAGTATTGGCAGATACAT 2700  
| | | | |  
Db 2641 GGGAAACAGAGTGAATGGAAGAAAGTGAACCTGATGCTCAGTATTGGCAGATACAT 2700  
QY 2701 TCAAGTTTCAAAAGGCGCAGTCAATTTGCTTTTCAAAATCCAGAAATGCAAGAGG 2760  
| | | | |  
Db 2701 TCAAGTTTCAAAAGGCGCAGTCAATTTGCTTTTCAAAATCCAGAAATGCAAGAGG 2760  
QY 2761 AATGTGCAACATCTCTGCCCCACTGGGCTCTTAAAGAACAAAGTCCAAAGTCATT 2820  
| | | | |  
Db 2761 AATGTGCAACATCTCTGCCCCACTGGGCTCTTAAAGAACAAAGTCCAAAGTCATT 2820  
QY 2821 TTGAATGTGAACAAAGAGAAAGAAATCAAGAGAAAGATGAGTCTAATATCAAGCCTGTAC 2880  
| | | | |  
Db 2821 TTGAATGTGAACAAAGAGAAAGAAATCAAGAGAAAGATGAGTCTAATATCAAGCCTGTAC 2880  
QY 2881 AGACATTAATATCACTGCAAGCTTCTGTGTGTGTGTCAGAAAGATGACCAAGTTGATA 2940  
| | | | |  
Db 2881 AGACATTAATATCACTGCAAGCTTCTGTGTGTGTGTCAGAAAGATGACCAAGTTGATA 2940  
QY 2941 ATGCGCAATGTATGATCAAGAGAGCTCTAGGTTTGTCTATCATCTCAGTTCAAGAGCA 3000  
| | | | |  
Db 2941 ATGCGCAATGTATGATCAAGAGAGCTCTAGGTTTGTCTATCATCTCAGTTCAAGAGCA 3000  
QY 3001 AGGAACTGGAATGTATGATCAAGAGAGCTCTAGGTTTGTCTATCATCTCAGTTCAAGAGCA 3060  
| | | | |  
Db 3001 AGGAACTGGAATGTATGATCAAGAGAGCTCTAGGTTTGTCTATCATCTCAGTTCAAGAGCA 3060  
QY 3061 CACCACTTTTCCATCAAGTCAATTTGTTAAACTAAATGTAAAGAAAACTGTCTAGAGG 3120  
| | | | |  
Db 3061 CACCACTTTTCCATCAAGTCAATTTGTTAAACTAAATGTAAAGAAAACTGTCTAGAGG 3120  
QY 3121 AAAACTTTGAGGACATTCATGATGCACTGAAAGAAATGGGAAATGAAACATTTCCA 3180  
| | | | |  
Db 3121 AAAACTTTGAGGACATTCATGATGCACTGAAAGAAATGGGAAATGAAACATTTCCA 3180  
QY 3181 GTACAGTAGGACATTAAGCGGTATTAATATTAGAGAAATGTTTAAAGAGGCACGCT 3240  
| | | | |  
Db 3181 GTACAGTAGGACATTAAGCGGTATTAATATTAGAGAAATGTTTAAAGAGGCACGCT 3240  
QY 3241 CAAGCAATATTAATGAGTAGGTTCCAGTACTAATGAAAGTGGCTCCAGTATTAATGAAA 3300  
| | | | |  
Db 3241 CAAGCAATATTAATGAGTAGGTTCCAGTACTAATGAAAGTGGCTCCAGTATTAATGAAA 3300  
QY 3301 TAGGTTCCAGTAGTAAAAACATTCAAGCAAACTAGTGAAGAAAGAGGCGCAAAATTTGA 3360  
| | | | |  
Db 3301 TAGGTTCCAGTAGTAAAAACATTCAAGCAAACTAGTGAAGAAAGAGGCGCAAAATTTGA 3360  
QY 3361 ATGCTATGCTTAGTAGGAGGTTTGGCAACCTGAGAGTCTATTAACAAAGTCTTCTGGAA 3420  
| | | | |  
Db 3361 ATGCTATGCTTAGTAGGAGGTTTGGCAACCTGAGAGTCTATTAACAAAGTCTTCTGGAA 3420  
QY 3421 GTAATTTGATGATCTGTAATTAATTAATTAATGAGATATGAGATAGTTCAGACTGTGA 3480  
| | | | |  
Db 3421 GTAATTTGATGATCTGTAATTAATTAATTAATGAGATATGAGATAGTTCAGACTGTGA 3480  
QY 3481 ATACGATTTTCTCTCATATCTGATTTTCAAGATTAATTAAGACAGCTTATGGAGAGTATGTC 3540  
| | | | |  
Db 3481 ATACGATTTTCTCTCATATCTGATTTTCAAGATTAATTAAGACAGCTTATGGAGAGTATGTC 3540  
QY 3541 ATGCAATCAGGTTGTTCTGTAGACACCTGATGACCTGTATGATGATGTGAAATTAAGG 3600  
| | | | |

Db 3541 ATGCAATCAGGTTTGTCTGTAGACACCTGATGACCTGTATGATGATGTGAAATTAAGG 3600  
| | | | |  
QY 3601 AAGATCTAGTGTTCGTGAAAAATGACATTAAGAAAGTTCTGTCTTTTATAGCAAAAGC 3660  
| | | | |  
Db 3601 AAGATCTAGTGTTCGTGAAAAATGACATTAAGAAAGTTCTGTCTTTTATAGCAAAAGC 3660  
QY 3661 TCCAGAGGAGAGCTTAGAGAGAGTCTAGCCCTTACACCATACACATTTGGCTCAGG 3720  
| | | | |  
Db 3661 TCCAGAGGAGAGCTTAGAGAGAGTCTAGCCCTTACACCATACACATTTGGCTCAGG 3720  
QY 3721 GTTACCGAAGAGGAGGCAAGAAATTAAGAGTCCCTCAGAAAGAACTTATCTAGTGAAGT 3780  
| | | | |  
Db 3721 GTTACCGAAGAGGAGGCAAGAAATTAAGAGTCCCTCAGAAAGAACTTATCTAGTGAAGT 3780  
QY 3781 AAGAGCTTCCCTGCTTCCACACATTTGTTATTTGTTAAAGTAAACATATACCTTCTCAGT 3840  
| | | | |  
Db 3781 AAGAGCTTCCCTGCTTCCACACATTTGTTATTTGTTAAAGTAAACATATACCTTCTCAGT 3840  
QY 3841 CTACTAGGCATAGACACCGTGTCTACCGAGTGTCTGTAAAGACACAGAGGAAATTAAT 3900  
| | | | |  
Db 3841 CTACTAGGCATAGACACCGTGTCTACCGAGTGTCTGTAAAGACACAGAGGAAATTAAT 3900  
QY 3901 TATCATTTGAAGAAATAGTTAAATGACCTGACAGTAAACAGATATATTTGGCAAAAGCATCTC 3960  
| | | | |  
Db 3901 TATCATTTGAAGAAATAGTTAAATGACCTGACAGTAAACAGATATATTTGGCAAAAGCATCTC 3960  
QY 3961 AGGAAATCACCCTTAGTAGAGAAACAAATATGCTGTAGCTGTTTCTTCAACAGTCA 4020  
| | | | |  
Db 3961 AGGAAATCACCCTTAGTAGAGAAACAAATATGCTGTAGCTGTTTCTTCAACAGTCA 4020  
QY 4021 GTGAATTTGAAGACCTGACCTGCAAAATACAAACACCGAAGATCCCTTCTGATGTGCTT 4080  
| | | | |  
Db 4021 GTGAATTTGAAGACCTGACCTGCAAAATACAAACACCGAAGATCCCTTCTGATGTGCTT 4080  
QY 4081 CCAAAACAATGAGGATCAGTCTGAAAGCCAGAGAGTGTCTGAGTGAACAAGAAATGG 4140  
| | | | |  
Db 4081 CCAAAACAATGAGGATCAGTCTGAAAGCCAGAGAGTGTCTGAGTGAACAAGAAATGG 4140  
QY 4141 TTTGATGATGATGAAGAAAGAGAACGGGCTTGAAGAAATATATCAAGAGAGCAAGCA 4200  
| | | | |  
Db 4141 TTTGATGATGATGAAGAAAGAGAACGGGCTTGAAGAAATATATCAAGAGAGCAAGCA 4200  
QY 4201 TGGATTTCAAATCTTAGGTGAACAGCATCTGGGTGGAAGTGAACAGCGCTCTGAG 4260  
| | | | |  
Db 4201 TGGATTTCAAATCTTAGGTGAACAGCATCTGGGTGGAAGTGAACAGCGCTCTGAG 4260  
QY 4261 ACTGCTCAGGGCTATCCTCTCAGAGTGAACATTTAACCACTCAGCAGAGAGTACCATGC 4320  
| | | | |  
Db 4261 ACTGCTCAGGGCTATCCTCTCAGAGTGAACATTTAACCACTCAGCAGAGAGTACCATGC 4320  
QY 4321 AACATTAACCTGATTAAGCTCCAGCAGAAATGCTGAACCTAGAACCTGTGTTAGAACGC 4380  
| | | | |  
Db 4321 AACATTAACCTGATTAAGCTCCAGCAGAAATGCTGAACCTAGAACCTGTGTTAGAACGC 4380  
QY 4381 ATGGAGGACAGCTTCTTAACAGCTACCTTGCATATATAGTACCTCTGCTGCTTGAAG 4440  
| | | | |  
Db 4381 ATGGAGGACAGCTTCTTAACAGCTACCTTGCATATATAGTACCTCTGCTGCTTGAAG 4440  
QY 4441 ACCTGCAAAATCCAGAACAAAGACATCAGAAAAAGAGTATTAATCTTCAAGAAAAATGA 4500  
| | | | |  
Db 4441 ACCTGCAAAATCCAGAACAAAGACATCAGAAAAAGAGTATTAATCTTCAAGAAAAATGA 4500  
QY 4501 GTGAATTAACCTTAAGACAGAAATCCAGAGGCTTCTGCTGACAGAGTTTGAAGTGTCTG 4560  
| | | | |  
Db 4501 GTGAATTAACCTTAAGACAGAAATCCAGAGGCTTCTGCTGACAGAGTTTGAAGTGTCTG 4560  
QY 4561 CAGATAGTCTTACAGCTAAAAATTAAGAAACAGAGAGTGAAGAGTCAATCCCTCTTAAT 4620  
| | | | |  
Db 4561 CAGATAGTCTTACAGCTAAAAATTAAGAAACAGAGAGTGAAGAGTCAATCCCTCTTAAT 4620  
QY 4621 GCCCATCATTTGATGATGATGAGTGTGATCATGCAACAGTGTCTGGAGAGTCTTCAAGATAGA 4680  
| | | | |

```

Db 4621 GCCCATCTAGATGATAGTGTGTACATGACAGTTCCTGGAGTCTTCAGATAGAA 4680
Qy 4681 ACTACCCATCTCAAGAGAGCTCAATAGTGTGTGAGAGAGAGAGAGAGAGAGAGAG 4740
Db 4681 ACTACCCATCTCAAGAGAGCTCAATAGTGTGTGAGAGAGAGAGAGAGAGAGAGAG 4740
Qy 4741 AGTCTGGGCGACACAGATTTGACGAAACATCTTACCTCCAGAGAGAGAGAGAGAG 4800
Db 4741 AGTCTGGGCGACACAGATTTGACGAAACATCTTACCTCCAGAGAGAGAGAGAGAG 4800
Qy 4801 CCCCTTACCTGGAGATCTGGAATCAGCCCTCTCTGAGAGAGAGAGAGAGAGAGAG 4860
Db 4801 CCCCTTACCTGGAGATCTGGAATCAGCCCTCTCTGAGAGAGAGAGAGAGAGAGAG 4860
Qy 4861 AAGACAGAGCCCGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4920
Db 4861 AAGACAGAGCCCGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4920
Qy 4921 AAGTTCCTCCAAATTTGAGAGATCTGAGAGATCTGAGAGATCTGAGAGATCTGAG 4980
Db 4921 AAGTTCCTCCAAATTTGAGAGATCTGAGAGATCTGAGAGATCTGAGAGATCTGAG 4980
Qy 4981 AATCTGCTGGGTATATGCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5040
Db 4981 AATCTGCTGGGTATATGCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5040
Qy 5041 CTTCAACAGAAAGGCTCAACAAAGATGTCATGTGTGTGTGTGTGTGTGTGTGTGTGT 5100
Db 5041 CTTCAACAGAAAGGCTCAACAAAGATGTCATGTGTGTGTGTGTGTGTGTGTGTGTGT 5100
Qy 5101 AATTTATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5160
Db 5101 AATTTATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5160
Qy 5161 CTGAGAGAGACTATCTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5220
Db 5161 CTGAGAGAGACTATCTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5220
Qy 5221 TGAATATATTTCTAGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5280
Db 5221 TGAATATATTTCTAGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5280
Qy 5281 AGTCTATTTAAAGAAAGAAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5340
Db 5281 AGTCTATTTAAAGAAAGAAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5340
Qy 5341 TCATAGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5400
Db 5341 TCATAGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5400
Qy 5401 TCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5460
Db 5401 TCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5460
Qy 5461 AATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5520
Db 5461 AATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5520
Qy 5521 GCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5580
Db 5521 GCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5580
Qy 5581 TCACATGCAATTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5640
Db 5581 TCACATGCAATTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5640
Qy 5641 GTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5700
Db 5641 GTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5700
Qy 5701 GCCACTACTGA 5711
Db 5701 GCCACTACTGA 5711

```

```

RESULT 15
US-09-007-678B-47
; Sequence 47, Application US/09007678B
; Patent No. 6342483
; GENERAL INFORMATION:
; APPLICANT: HOLZ, JEFFREY T.
; APPLICANT: JENSEN, ROY A.
; APPLICANT: PABE, DAVID L.
; APPLICANT: OBERMILLER, PATRICE S.
; APPLICANT: ROBINSON-BENION, CHERYL L.
; APPLICANT: THOMPSON, MARILYN E.
; TITLE OF INVENTION: METHOD FOR DETECTION AND TREATMENT OF BREAST CANCER
; FILE REFERENCE: Attorney Docket No. 6342483 1242-1-2-2
; CURRENT APPLICATION NUMBER: US/09/007,678B
; PRIOR FILING DATE: 1998-01-15
; PRIOR APPLICATION NUMBER: 08/373,799
; PRIOR FILING DATE: 1995-01-17
; PRIOR APPLICATION NUMBER: 08/182,961
; PRIOR FILING DATE: 1994-01-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Microsoft Wordpad
; SEQ ID NO: 47
; LENGTH: 5712
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (120)..(5708)
; NAME/KEY: misc feature
; LOCATION: (4532)..(4535)
; OTHER INFORMATION: Xaa-any amino acid
US-09-007-678B-47

```

```

Query Match 99.8%; Score 5699.8; DB 4; Length 5712;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5704; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 AGCTGCTGAGACATCTCTGAGACCCCGACAGAGCTGTGGGTTTCTCAGATTAATCTGGGCC 60
Db 1 AGCTGCTGAGACATCTCTGAGACCCCGACAGAGCTGTGGGTTTCTCAGATTAATCTGGGCC 60

Qy 61 CCTGCGCTCAGAGAGCCCTTCAACCTGCTGTGGGTAAGTTCAATGGAACAGAAAGAAA 120
Db 61 CCTGCGCTCAGAGAGCCCTTCAACCTGCTGTGGGTAAGTTCAATGGAACAGAAAGAAA 120

Qy 121 TGAATTTATCTGCTCTTTCGCGGTTGAAGATTAACAAAATGTCATTAATGCTATGAGAAA 180
Db 121 TGAATTTATCTGCTCTTTCGCGGTTGAAGATTAACAAAATGTCATTAATGCTATGAGAAA 180

Qy 181 TCTTAGAGTGTCCATCTGTGTGAGAGTGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Db 181 TCTTAGAGTGTCCATCTGTGTGAGAGTGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 240

Qy 241 ACATATTTTGAAGATTTTGAAGATTTTGAAGATTTTGAAGATTTTGAAGATTTTGAAGAT 300
Db 241 ACATATTTTGAAGATTTTGAAGATTTTGAAGATTTTGAAGATTTTGAAGATTTTGAAGAT 300

Qy 301 GTCTTTATGTAGATGATATTAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db 301 GTCTTTATGTAGATGATATTAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360

Qy 361 AACTTTTGAAGAGAGATTTGAAGATTTTGAAGATTTTGAAGATTTTGAAGATTTTGAAGAGT 420
Db 361 AACTTTTGAAGAGAGATTTGAAGATTTTGAAGATTTTGAAGATTTTGAAGATTTTGAAGAGT 420

Qy 421 ATGCAACAGCTATTAATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Db 421 ATGCAACAGCTATTAATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480

Qy 481 AAGTTTATCATCAAGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 481 AAGTTTATCATCAAGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540

```

Db 481 AAGTTCATCATCCAAAGTATGCGCTACAGAAACCGTCACAAAAGACTTCTACAGATG 540  
Qy 541 AACCCGAAATCTCTTCCCTTGAGAGAAACCACTTCAGTCCCACTCTCTAACCTTGGAA 600  
Db 541 AACCCGAAATCTCTTCCCTTGAGAGAAACCACTTCAGTCCCACTCTCTAACCTTGGAA 600  
Qy 601 CTGTGAGAACTCTGAGACAAAGCAGCGGATCACTCTCAAAAAGAGCTGTCTACATTTG 660  
Db 601 CTGTGAGAACTCTGAGACAAAGCAGCGGATCACTCTCAAAAAGAGCTGTCTACATTTG 660  
Qy 661 AATTGGATCTGATTCCTCTGAAAGTACCGTTAATAGGCACTTATTGCAAGTGTGGAG 720  
Db 661 AATTGGATCTGATTCCTCTGAAAGTACCGTTAATAGGCACTTATTGCAAGTGTGGAG 720  
Qy 721 ATCAAGAACTGTACAAATCAACCCCTCAAGAAACCAAGGATGAATTCAGTTTGGATTTG 780  
Db 721 ATCAAGAACTGTACAAATCAACCCCTCAAGAAACCAAGGATGAATTCAGTTTGGATTTG 780  
Qy 781 CAAAAAGGCTGCTGTGAAATTTTCTGAGACGGATGTAACTAATCTGAACTATCAAC 840  
Db 781 CAAAAAGGCTGCTGTGAAATTTTCTGAGACGGATGTAACTAATCTGAACTATCAAC 840  
Qy 841 CCAGTAATATGATTTGAAACACCACTGAGAGCGTGCAGCTGAGAGGCAATCCAGAAAGT 900  
Db 841 CCAGTAATATGATTTGAAACACCACTGAGAGCGTGCAGCTGAGAGGCAATCCAGAAAGT 900  
Qy 901 ATCAGGGTATGTTCTGTTCAACTTGTCATGTGAGCCATGTGGCACTCAATCTCATGCCA 960  
Db 901 ATCAGGGTATGTTCTGTTCAACTTGTCATGTGAGCCATGTGGCACTCAATCTCATGCCA 960  
Qy 961 GCTCATTCAGCATGAGAACAGCACTTTATTTACTACTAAAGACGAATGTAGAAA 1020  
Db 961 GCTCATTCAGCATGAGAACAGCACTTTATTTACTACTAAAGACGAATGTAGAAA 1020  
Qy 1021 AGGCTGAATTCGTATATAAAGCAACCGCTGCTTACGAGAGGCACTAAACAAT 1080  
Db 1021 AGGCTGAATTCGTATATAAAGCAACCGCTGCTTACGAGAGGCACTAAACAAT 1080  
Qy 1081 GGGCTGGAATGAGAAACATGTATGTAGGCGGACTCCGACACAGAAAAAGGTAG 1140  
Db 1081 GGGCTGGAATGAGAAACATGTATGTAGGCGGACTCCGACACAGAAAAAGGTAG 1140  
Qy 1141 ATCTGAATGCTGATCCCGTGTGAGAGAAAGAAATGAATAGAGAAACCTGATGCT 1200  
Db 1141 ATCTGAATGCTGATCCCGTGTGAGAGAAAGAAATGAATAGAGAAACCTGATGCT 1200  
Qy 1201 CAGAGAACTCTAGAGATCTGAAGATGTTCTTGATTAACCTAAATAGAGCATTTGAGA 1260  
Db 1201 CAGAGAACTCTAGAGATCTGAAGATGTTCTTGATTAACCTAAATAGAGCATTTGAGA 1260  
Qy 1261 AAGTTAATGATGTTTTCCAGAAATGATGAACGTGTAGTTCTGATGACTCACAATGATG 1320  
Db 1261 AAGTTAATGATGTTTTCCAGAAATGATGAACGTGTAGTTCTGATGACTCACAATGATG 1320  
Qy 1321 GGGAGTCTGAATCAATGCCAAAGTATGATGATTTGGAAGCTTCTAAATGAGTATGATG 1380  
Db 1321 GGGAGTCTGAATCAATGCCAAAGTATGATGATTTGGAAGCTTCTAAATGAGTATGATG 1380  
Qy 1381 AATATTTCTGTTCTTCAAGAAAAATAGACTTACTGCGCAGTATCTCTATGAGGCTTTTA 1440  
Db 1381 AATATTTCTGTTCTTCAAGAAAAATAGACTTACTGCGCAGTATCTCTATGAGGCTTTTA 1440  
Qy 1441 TATGTAAAGTGAAGAGTTCTCACTCAATCAGTGAAGTAAATTTGAAAGCAAAATAT 1500  
Db 1441 TATGTAAAGTGAAGAGTTCTCACTCAATCAGTGAAGTAAATTTGAAAGCAAAATAT 1500  
Qy 1501 TTGGGAAAACTATGAGAGAGGCAAGCTCTCCCACTTAAGCCATGTATCTGAAAAATC 1560  
Db 1501 TTGGGAAAACTATGAGAGAGGCAAGCTCTCCCACTTAAGCCATGTATCTGAAAAATC 1560  
Qy 1561 TAAATTATAGAGCATTTGTTACTGAGCCACAGATTAATACAAAGGCTCCCTCACAATA 1620  
Db 1561 TAAATTATAGAGCATTTGTTACTGAGCCACAGATTAATACAAAGGCTCCCTCACAATA 1620

Qy 1621 AATTAAAGCTTAAAGAGAGACTTACATGAGGCTTCACTCTGAGGATTTTATCAAGAAAG 1680  
Db 1621 AATTAAAGCTTAAAGAGAGACTTACATGAGGCTTCACTCTGAGGATTTTATCAAGAAAG 1680  
Qy 1681 CAGATTTGGCAGTTCAAAAGACTCCGTAAATGATTAATCAGGAACTAACCAACGAGAC 1740  
Db 1681 CAGATTTGGCAGTTCAAAAGACTCCGTAAATGATTAATCAGGAACTAACCAACGAGAC 1740  
Qy 1741 AGAATGTCAGATGATGAATTTACTAATAGTGTGATGAGAAATTAACCAAAAGGTGATT 1800  
Db 1741 AGAATGTCAGATGATGAATTTACTAATAGTGTGATGAGAAATTAACCAAAAGGTGATT 1800  
Qy 1801 CTATTCAGATGAGAAAAATCTTAACCCATAGAAATCACTGCAAAAAGATCTGCTTTCA 1860  
Db 1801 CTATTCAGATGAGAAAAATCTTAACCCATAGAAATCACTGCAAAAAGATCTGCTTTCA 1860  
Qy 1861 AAACGAAAGCTGAACCTTAAGCAGCAGTATAGCAATATGGAATTCGAATTAATATCC 1920  
Db 1861 AAACGAAAGCTGAACCTTAAGCAGCAGTATATAGCAATATGGAATTCGAATTAATATCC 1920  
Qy 1921 ACAATTCAAAAGCCTTAAAAAGAAATAGGCTGAGAGAGAGTCTTCTACAGGCAATATTC 1980  
Db 1921 ACAATTCAAAAGCCTTAAAAAGAAATAGGCTGAGAGAGAGTCTTCTACAGGCAATATTC 1980  
Qy 1981 ATGGCCTGAACCTAGTATGATGAATCTTAAGCCCACTTAATTTGACTGAAATTTGCAAA 2040  
Db 1981 ATGGCCTGAACCTAGTATGATGAATCTTAAGCCCACTTAATTTGACTGAAATTTGCAAA 2040  
Qy 2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAAGTAAACCAATGCGCAGTCA 2100  
Db 2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAAGTAAACCAATGCGCAGTCA 2100  
Qy 2101 GGCACAGCAAAACCTACACTCATGAAAGTAAAGAACTGCAACTGAGCCAGAAAGA 2160  
Db 2101 GGCACAGCAAAACCTACACTCATGAAAGTAAAGAACTGCAACTGAGCCAGAAAGA 2160  
Qy 2161 GTTAAACCAATGAACAGCAAGTAAAGACATGACAGATCTTCCAGAGCTGA 2220  
Db 2161 GTTAAACCAATGAACAGCAAGTAAAGACATGACAGATCTTCCAGAGCTGA 2220  
Qy 2221 AGTTAAACAAATGCACTGTTCTTCTTACTTAAGTGTCCAAATACAGTAACCTTAAGAAAT 2280  
Db 2221 AGTTAAACAAATGCACTGTTCTTCTTACTTAAGTGTCCAAATACAGTAACCTTAAGAAAT 2280  
Qy 2281 TTGTCAATCTAGCCCTTCAAGAGAGAAAGAAAGAGAACTAGAAAACGTTAAAGTGT 2340  
Db 2281 TTGTCAATCTAGCCCTTCAAGAGAGAAAGAAAGAGAACTAGAAAACGTTAAAGTGT 2340  
Qy 2341 CTAAATTAATGCTGAGAAACCCCAAAAGTCTCATGTTAAAGTGAAGAGGTTTTGCAACTG 2400  
Db 2341 CTAAATTAATGCTGAGAAACCCCAAAAGTCTCATGTTAAAGTGAAGAGGTTTTGCAACTG 2400  
Qy 2401 AAAAGTCTGTAGAGAGTGAAGATTTTCACTGTAAGTCTGTGTAATGAGCACTGAG 2460  
Db 2401 AAAAGTCTGTAGAGAGTGAAGATTTTCACTGTAAGTCTGTGTAATGAGCACTGAG 2460  
Qy 2461 AAAAGTATCTGTTACTGAAAGTTAGCACTTAAGGAGGCAAAAACAGAACCAATTAAT 2520  
Db 2461 AAAAGTATCTGTTACTGAAAGTTAGCACTTAAGGAGGCAAAAACAGAACCAATTAAT 2520  
Qy 2521 GTGTGATGATGCTGACAGATTTTGAAGAAACCCCAAGGACTAATTAATGTTTCCAAAG 2580  
Db 2521 GTGTGATGATGCTGACAGATTTTGAAGAAACCCCAAGGACTAATTAATGTTTCCAAAG 2580  
Qy 2581 AATAATGAATGAACAGAGGCTTAATAGTATCCATTGGGACATGAAGTTAACCAAGTCC 2640  
Db 2581 AATAATGAATGAACAGAGGCTTAATAGTATCCATTGGGACATGAAGTTAACCAAGTCC 2640  
Qy 2641 GGGAAACAAGCATTAAGAAATGGAAGAGTGAACCTTGAATGCTCATGATTTTGCAGAAATACAT 2700  
Db 2641 GGGAAACAAGCATTAAGAAATGGAAGAGTGAACCTTGAATGCTCATGATTTTGCAGAAATACAT 2700

QY 2701 TCAGGTTTCAAGCGCCAGTCATTTGCTGTGTTTCAATCCAGAAATGCAAGAGG 2760  
Db 2701 TCAGGTTTCAAGCGCCAGTCATTTGCTGTGTTTCAATCCAGAAATGCAAGAGG 2760  
QY 2761 AATGTGCAACATTTCTGTGCCCATCTGTGGTCTTAAAGAAACAAGTCCAAAGTCACTT 2820  
Db 2761 AATGTGCAACATTTCTGTGCCCATCTGTGGTCTTAAAGAAACAAGTCCAAAGTCACTT 2820  
QY 2821 TTGAATGTGAACAAAGAGAAAGAAATCAAGAAAGAAAGATGATATATCAAGCTGTAC 2880  
Db 2821 TTGAATGTGAACAAAGAGAAAGAAATCAAGAAAGAAAGATGATATATCAAGCTGTAC 2880  
QY 2881 AGACAGTAATATATCATCTGACAGGCTTCTGTGTGTGTGACAGAAAGATAGCCAGTTGATA 2940  
Db 2881 AGACAGTAATATATCATCTGACAGGCTTCTGTGTGTGTGACAGAAAGATAGCCAGTTGATA 2940  
QY 2941 ATGCCAAATGTATGATCAAGAGAGGCTCTAGGTTTGTCTATCATCTGACAGGCA 3000  
Db 2941 ATGCCAAATGTATGATCAAGAGAGGCTCTAGGTTTGTCTATCATCTGACAGGCA 3000  
QY 3001 ACGAAACTGCACTCATCTCAATTAACAATGACATTTTACAAACCATATCTGATAC 3060  
Db 3001 ACGAAACTGCACTCATCTCAATTAACAATGACATTTTACAAACCATATCTGATAC 3060  
QY 3061 CACCACTTTTCCCATCAAGTCATTTGTTAAACTTAATGTAAAGAAATCTGTAGAG 3120  
Db 3061 CACCACTTTTCCCATCAAGTCATTTGTTAAACTTAATGTAAAGAAATCTGTAGAG 3120  
QY 3121 AAACTTTGAGAACATTCATGTCACCTGAAAGAAATGGAAATGAAACATTCGA 3180  
Db 3121 AAACTTTGAGAACATTCATGTCACCTGAAAGAAATGGAAATGAAACATTCGA 3180  
QY 3181 GTACAGTAGACATATAGCCGTATTAACATTAAGAAATCTTTTAAAGAGGCACT 3240  
Db 3181 GTACAGTAGACATATAGCCGTATTAACATTAAGAAATCTTTTAAAGAGGCACT 3240  
QY 3241 CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGCTCCAGTATTAAGAA 3300  
Db 3241 CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGCTCCAGTATTAAGAA 3300  
QY 3301 TAGGTTCCAGTGATGAAAAATTCAAGCAAGAACTAGTAAAGCAAGGCGCAAAATTGA 3360  
Db 3301 TAGGTTCCAGTGATGAAAAATTCAAGCAAGAACTAGTAAAGCAAGGCGCAAAATTGA 3360  
QY 3361 ATGCTAGCTTAAGTAAAGGTTTGGCAACCTGAGAGCTCTAATAAAGCTTCTTGAA 3420  
Db 3361 ATGCTAGCTTAAGTAAAGGTTTGGCAACCTGAGAGCTCTAATAAAGCTTCTTGAA 3420  
QY 3421 GTAATTGTAGCATCTGAAATTAAGCAAGATATGAAGATAGTTCAGACTGTTA 3480  
Db 3421 GTAATTGTAGCATCTGAAATTAAGCAAGATATGAAGATAGTTCAGACTGTTA 3480  
QY 3481 ATACAGATTTCTCTCATATCTGATTTCAAGATTAATTGAACAGCTATGGGAATGATC 3540  
Db 3481 ATACAGATTTCTCTCATATCTGATTTCAAGATTAATTGAACAGCTATGGGAATGATC 3540  
QY 3541 ATGCTCTCAGGTTTGTCTGAGACACTGATGACCTGTAGATATGTTGAAATTAAGG 3600  
Db 3541 ATGCTCTCAGGTTTGTCTGAGACACTGATGACCTGTAGATATGTTGAAATTAAGG 3600  
QY 3601 AAGACTAGTTTCTGAAAAATGACATTAAGGAAGTTCGTCTTTTGAAGCAAAAGC 3660  
Db 3601 AAGACTAGTTTCTGAAAAATGACATTAAGGAAGTTCGTCTTTTGAAGCAAAAGC 3660  
QY 3661 TTCAGAGAGAGAGGTTTGAAGAGAGTCTAGCCCTTTCAACCCATACACATTTGGCTCAG 3720  
Db 3661 TTCAGAGAGAGAGGTTTGAAGAGAGTCTAGCCCTTTCAACCCATACACATTTGGCTCAG 3720  
QY 3721 GTTACCGGAAGAGGCGCAAGAAATTAAGATCTGAGAAAGAACTTATCTAGTGAAGT 3780  
Db 3721 GTTACCGGAAGAGGCGCAAGAAATTAAGATCTGAGAAAGAACTTATCTAGTGAAGT 3780  
QY 3781 AAGAGCTTCCCTGTCTCAACACTGTTATTTGTAAAGTAAACAATATACCTTCTCAGT 3840

Db 3781 AAGAGCTTCCCTGTCTCAACACTGTTATTTGTAAAGTAAACAATATACCTTCTCAGT 3840  
QY 3841 CTACTAGGATATAGCACCGTGTCTACAGAGTGTCTGTAAAGAACAGAGAAATTTAT 3900  
Db 3841 CTACTAGGATATAGCACCGTGTCTACAGAGTGTCTGTAAAGAACAGAGAAATTTAT 3900  
QY 3901 TATCATTTGAAGATATGCTTAATGATCTGACAGTAACCAAGTAAATTTGGCAAGGATCTC 3960  
Db 3901 TATCATTTGAAGATATGCTTAATGATCTGACAGTAACCAAGTAAATTTGGCAAGGATCTC 3960  
QY 3961 AGGAACATCACCTTAGTGAAGAAACAAATATGTTCTGTAGCTTGTCTTTCACAGTCA 4020  
Db 3961 AGGAACATCACCTTAGTGAAGAAACAAATATGTTCTGTAGCTTGTCTTTCACAGTCA 4020  
QY 4021 GTGAATTGGAAAGACTTGAAGTCAAAATACAAACACCAGAGATCTTTCTTGAATGTTCTT 4080  
Db 4021 GTGAATTGGAAAGACTTGAAGTCAAAATACAAACACCAGAGATCTTTCTTGAATGTTCTT 4080  
QY 4081 CCAACCAATGAGGATCAGTCTGAAGCCAGGAGTGTGTGATGACAAAGAAATTGG 4140  
Db 4081 CCAACCAATGAGGATCAGTCTGAAGCCAGGAGTGTGTGATGACAAAGAAATTGG 4140  
QY 4141 TTTGATGATGAGAAAGAGAAACGGGCTTGAAGAAATTAATCAAGAGCAAAAGCA 4200  
Db 4141 TTTGATGATGAGAAAGAGAAACGGGCTTGAAGAAATTAATCAAGAGCAAAAGCA 4200  
QY 4201 TGGAATCAAACCTTAGGTGACAGATCTGGGTGTGAAGTGAACAAAGCGCTCTGAA 4260  
Db 4201 TGGAATCAAACCTTAGGTGACAGATCTGGGTGTGAAGTGAACAAAGCGCTCTGAA 4260  
QY 4261 ACTGCTCAGGCTATCCCTCAGAGTGAACATTTTAACACTCAGCAGAGGGATACATGC 4320  
Db 4261 ACTGCTCAGGCTATCCCTCAGAGTGAACATTTTAACACTCAGCAGAGGGATACATGC 4320  
QY 4321 AACATTAACCTGATTAAGCTCCAGCAGAAATGCTGAACCTAGAGCTGTGTAACAGC 4380  
Db 4321 AACATTAACCTGATTAAGCTCCAGCAGAAATGCTGAACCTAGAGCTGTGTAACAGC 4380  
QY 4381 ATGGAGCCAGCTTCTTAACAGCTACCTTCATATATAGTGAATCTCTGCTGCTTGAAG 4440  
Db 4381 ATGGAGCCAGCTTCTTAACAGCTACCTTCATATATAGTGAATCTCTGCTGCTTGAAG 4440  
QY 4441 AACTGCGAAATCCGAACAAAGCAGATCAGAAAGAGCTTAATCTTCAAGAAAGTGA 4500  
Db 4441 AACTGCGAAATCCGAACAAAGCAGATCAGAAAGAGCTTAATCTTCAAGAAAGTGA 4500  
QY 4501 GTGAATACCTTAATTAAGCCAGAAATCCAGAAAGGCTTCTGTGACAAAGTTGAGTGTCTG 4560  
Db 4501 GTGAATACCTTAATTAAGCCAGAAATCCAGAAAGGCTTCTGTGACAAAGTTGAGTGTCTG 4560  
QY 4561 CAGATAGTTCTTAACGATTAATTAAGAAACCAAGAGTGAAGAGTCAATCCCTCTTAAT 4620  
Db 4561 CAGATAGTTCTTAACGATTAATTAAGAAACCAAGAGTGAAGAGTCAATCCCTCTTAAT 4620  
QY 4621 GCCCATCTTAAGATATGAGTGTATCATGCAACAGTGTCTGAGAGCTTCAAGATTAAG 4680  
Db 4621 GCCCATCTTAAGATATGAGTGTATCATGCAACAGTGTCTGAGAGCTTCAAGATTAAG 4680  
QY 4681 ACTACCATCTCAAGAGAGCTCAATTAAGTGTGTGATGTGAGAGCAAGCTGTGAAG 4740  
Db 4681 ACTACCATCTCAAGAGAGCTCAATTAAGTGTGTGATGTGAGAGCAAGCTGTGAAG 4740  
QY 4741 AGTGTGGCCACACAGATTTGAAGGAAACATCTTACTTCCAAAGGCAAGATCTAGAGGAA 4800  
Db 4741 AGTGTGGCCACACAGATTTGAAGGAAACATCTTACTTCCAAAGGCAAGATCTAGAGGAA 4800  
QY 4801 CCCCTTACTGGAATCTGGAATCAGCTCTTCTCTGATGAGCCCTGAATCTTACTTCTG 4860  
Db 4801 CCCCTTACTGGAATCTGGAATCAGCTCTTCTCTGATGAGCCCTGAATCTTACTTCTG 4860  
QY 4861 AAGACAGAGCCCAAGTCAAGCTGTGTGCAACATATCAATCTTCAACTCTGCAATTGA 4920

Db 4861 AAGACAGAGCCCCAGAGCTCAGCTCGTGTGGCAACATACCATCTTCAACTCTGCATTGA 4920  
QY 4921 AAGTCCCCAATTGAAAGTTCSCAAGATCTGCCCAGAGGTCCAGTGCCTCATCTACTG 4980  
Db 4921 AAGTCCCCAATTGAAAGTTCSCAAGATCTGCCCAGAGGTCCAGTGCCTCATCTACTG 4980  
QY 4981 ATACTGCTGGGTATATATGCAATGGAAGAGTGTAGCAGGAGAGAACCCAGAAATTGACAG 5040  
Db 4981 ATACTGCTGGGTATATATGCAATGGAAGAGTGTAGCAGGAGAGAACCCAGAAATTGACAG 5040  
QY 5041 CTTCAACAGAAAGGCTCAACAAAAGATGTCATGTGTGTCTGGCTGAAG 5100  
Db 5041 CTTCAACAGAAAGGCTCAACAAAAGATGTCATGTGTGTCTGGCTGAAG 5100  
QY 5101 AATTATGCTGCTGATACAAAGTTTGCCAGAAAACCATCATCTTAATCTAATTA 5160  
Db 5101 AATTATGCTGCTGATACAAAGTTTGCCAGAAAACCATCATCTTAATCTAATTA 5160  
QY 5161 CTGAAGAGACTACTCATGTGTGTATGAAACAGATGCTGAGTTGTGTGAAGGACAC 5220  
Db 5161 CTGAAGAGACTACTCATGTGTGTATGAAACAGATGCTGAGTTGTGTGAAGGACAC 5220  
QY 5221 TGAATATTTTCTAGAAATTCGGGAGGAAATGGGTAGTTAGCTATTTCTGGGTGACC 5280  
Db 5221 TGAATATTTTCTAGAAATTCGGGAGGAAATGGGTAGTTAGCTATTTCTGGGTGACC 5280  
QY 5281 AGTCTATTAAGAAAGAAATGCTGAATGAGCATGATTTGAAGTCAGAGAGATGG 5340  
Db 5281 AGTCTATTAAGAAAGAAATGCTGAATGAGCATGATTTGAAGTCAGAGAGATGG 5340  
QY 5341 TCAATGGAAGAAACCAACAGAGTCCAAAGCAGCAAGAAATCCAGAGCAGAAAAGATCT 5400  
Db 5341 TCAATGGAAGAAACCAACAGAGTCCAAAGCAGCAAGAAATCCAGAGCAGAAAAGATCT 5400  
QY 5401 TCAGGGGGCTAGAAATCTGTTGCTATGGGCCCTTCACCAACATGCCACAGATCAACTGG 5460  
Db 5401 TCAGGGGGCTAGAAATCTGTTGCTATGGGCCCTTCACCAACATGCCACAGATCAACTGG 5460  
QY 5461 AATGATGCTACAGCTGTGTGTGCTTCTGTGTGAAGAGCTTTCATCATTCACCTTG 5520  
Db 5461 AATGATGCTACAGCTGTGTGTGCTTCTGTGTGAAGAGCTTTCATCATTCACCTTG 5520  
QY 5521 GCACAGGTGTCCACCAATTGTGTGTGACCCAGATGCTTGAACAGAGCAATGAGCT 5580  
Db 5521 GCACAGGTGTCCACCAATTGTGTGTGACCCAGATGCTTGAACAGAGCAATGAGCT 5580  
QY 5581 TCCATGCAATTGGGCAGATGTGTGAGGCACCTGTGTGACCCGAGAGTGGGTGTGACA 5640  
Db 5581 TCCATGCAATTGGGCAGATGTGTGAGGCACCTGTGTGACCCGAGAGTGGGTGTGACA 5640  
QY 5641 GTGTAGCACTTACCAAGTGCAGAGAGCTGGAACCTTACCTGATACCCAGATCCCCACA 5700  
Db 5641 GTGTAGCACTTACCAAGTGCAGAGAGCTGGAACCTTACCTGATACCCAGATCCCCACA 5700  
QY 5701 GCCACTACTGA 5711  
Db 5701 GCCACTACTGA 5711

Search completed: December 14, 2003, 20:34:06  
Job time : 366 secs





GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 14, 2003, 11:42:27 ; Search time 1670 Seconds  
(without alignments)  
11365.913 Million cell updates/sec

Title: US-09-923-327a-263

Perfect score: 5711

Sequence: 1 agctcgtcgtacactctctg.....tcccacacagcactactga 5711

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2201672 seqs, 1661799599 residues

Total number of hits satisfying chosen parameters: 4403344

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:\*

1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*

2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*

3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*

4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*

5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*

6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*

7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*

8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*

9: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*

10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*

11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*

12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*

13: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUBCOMB.seq:\*

14: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*

15: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*

16: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*

17: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUBCOMB.seq:\*

18: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5711	100.0	5711	10	US-09-734-672-1
2	5711	100.0	5711	11	US-09-982-828-1
3	5709.4	100.0	5711	10	US-09-734-672-5
4	5709.4	100.0	5711	11	US-09-982-828-3
5	5709.4	100.0	5711	15	US-10-022-819-1
6	5701.4	99.8	5711	10	US-09-734-672-3
7	5701.4	99.8	5711	11	US-09-982-828-5
8	5649.8	98.9	5709	13	US-10-029-386-268
9	5505.4	10.4	597	13	US-10-029-386-12887
10	500.4	8.8	502	13	US-10-029-386-9876
11	416	7.3	505	13	US-10-029-386-2689
12	364.6	6.4	499	11	US-09-911-904-127
13	277	4.9	277	13	US-10-029-386-16389
14	201	3.5	369	13	US-10-286-628-39
15	173.8	3.0	424	9	US-09-864-761-4552

16	170	3.0	170	13	US-10-029-386-23576	Sequence 23576, A
17	145.1	2.5	147	9	US-09-864-761-21299	Sequence 21299, A
18	121	2.1	121	11	US-09-818-875-653	Sequence 653, App
19	121	2.1	121	11	US-09-818-875-654	Sequence 654, App
20	121	2.1	121	11	US-09-818-875-657	Sequence 657, App
21	121	2.1	121	11	US-09-818-875-658	Sequence 658, App
22	121	2.1	121	11	US-09-818-875-661	Sequence 661, App
23	121	2.1	121	11	US-09-818-875-662	Sequence 662, App
24	121	2.1	121	11	US-09-818-875-665	Sequence 665, App
25	121	2.1	121	11	US-09-818-875-666	Sequence 666, App
26	121	2.1	121	11	US-09-818-875-669	Sequence 669, App
27	121	2.1	121	11	US-09-818-875-670	Sequence 670, App
28	121	2.1	121	11	US-09-818-875-673	Sequence 673, App
29	121	2.1	121	11	US-09-818-875-674	Sequence 674, App
30	121	2.1	121	11	US-09-818-875-677	Sequence 677, App
31	121	2.1	121	11	US-09-818-875-678	Sequence 678, App
32	121	2.1	121	11	US-09-818-875-681	Sequence 681, App
33	121	2.1	121	11	US-09-818-875-682	Sequence 682, App
34	121	2.1	121	11	US-09-818-875-685	Sequence 685, App
35	121	2.1	121	11	US-09-818-875-686	Sequence 686, App
36	121	2.1	121	11	US-09-818-875-689	Sequence 689, App
37	121	2.1	121	11	US-09-818-875-690	Sequence 690, App
38	121	2.1	121	11	US-09-818-875-693	Sequence 693, App
39	121	2.1	121	11	US-09-818-875-694	Sequence 694, App
40	121	2.1	121	11	US-09-818-875-697	Sequence 697, App
41	121	2.1	121	11	US-09-818-875-698	Sequence 698, App
42	121	2.1	121	11	US-09-818-875-701	Sequence 701, App
43	121	2.1	121	11	US-09-818-875-702	Sequence 702, App
44	121	2.1	121	11	US-09-818-875-705	Sequence 705, App
45	121	2.1	121	11	US-09-818-875-706	Sequence 706, App

#### ALIGNMENTS

RESULT 1

US-09-734-672-1

Sequence 1, Application US/09734672

Publication No. US20020183268A1

GENERAL INFORMATION:

APPLICANT: Murphy, Patricia D.

Alvarez, Antonette C.

Critz, Brenda S.

Olson, Sheri U.

Schelter, Denise B.

Zeng, Bin

TITLE OF INVENTION: Coding Sequences of the Human

BRCA1 Gene

NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morgan Lewis & Bockius LLP

STREET: 1111 Pennsylvania Ave., N.W.

CITY: Washington

STATE: District of Columbia

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/734,672

FILING DATE: 03-Dec-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/966,436

FILING DATE: 07-No. US20020183268A1-97

APPLICATION NUMBER: US 08/598,591

FILING DATE: 12-Feb-96

ATTORNEY/AGENT INFORMATION:

NAME: Michael S. Tuscan

REGISTRATION NUMBER: 43,210

REFERENCE/DOCKET NUMBER: 44921-5055-02-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-739-3000  
TELEFAX: 202-739-3001  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5711 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: No. US20020183268A1 Relevant  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
STRAIN: BRCA1  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17  
MAP POSITION: 17q21  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-734-672-1

Query Match 100.0%; Score 5711; DB 10; Length 5711;  
Beet Local Similarity 100.0%; Pred. No. 0;  
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGCTGCTGAGACTTCTGAGACCCCGCACAGGCTGTGGGGTTTCTCAGATTAAGTGGCC 60  
1 AGCTGCTGAGACTTCTGAGACCCCGCACAGGCTGTGGGGTTTCTCAGATTAAGTGGCC 60  
61 CCTGGCTCAGAGAGGCTTCACTCTGCTGTGGGTAAGTTTCAATGGAACAGAAAGAA 120  
61 CCTGGCTCAGAGAGGCTTCACTCTGCTGTGGGTAAGTTTCAATGGAACAGAAAGAA 120  
121 TGGATTTATCTGCTTGTGGCGTTGAAGAGTAAAGTCAATTAAGTCAAGAA 180  
121 TGGATTTATCTGCTTGTGGCGTTGAAGAGTAAAGTCAATTAAGTCAAGAA 180  
181 TCTTAGAGTGTCCACTGTCTGTGAGTGAATCAAGAACTGTCTCAAAAGTGTGACC 240  
181 TCTTAGAGTGTCCACTGTCTGTGAGTGAATCAAGAACTGTCTCAAAAGTGTGACC 240  
241 ACATATTTTGCAGAAATTTTGCATGCTGAACCTTCAACAGAGAAAGGCTTCAAGT 300  
241 ACATATTTTGCAGAAATTTTGCATGCTGAACCTTCAACAGAGAAAGGCTTCAAGT 300  
301 GTCCCTTATGTAAAGATATATTAACCAAGAGGCTCAAGAAAGTACAGATTATTC 360  
301 GTCCCTTATGTAAAGATATATTAACCAAGAGGCTCAAGAAAGTACAGATTATTC 360  
361 AACTTGTGAAGAGCTATTTGAAATCATTTGTGCTTTCAAGTTGACACAGGTTTGAGT 420  
361 AACTTGTGAAGAGCTATTTGAAATCATTTGTGCTTTCAAGTTGACACAGGTTTGAGT 420  
421 ATGCAACAGCTATTAATTTTGCAGAAAGAAATTAATCTCTCGAATCATCAAAAGATG 480  
421 ATGCAACAGCTATTAATTTTGCAGAAAGAAATTAATCTCTCGAATCATCAAAAGATG 480  
481 AAGTTTCTATCATCAAGATTAAGGCTACAGAAACCGGCAAAAGACTTCTACAGATG 540  
481 AAGTTTCTATCATCAAGATTAAGGCTACAGAAACCGGCAAAAGACTTCTACAGATG 540  
541 AACCGGAAATCTTCTCTTGGAGAAACAGCTCAGTGTCCAATCTCTCAACCTTGGAA 600  
541 AACCGGAAATCTTCTCTTGGAGAAACAGCTCAGTGTCCAATCTCTCAACCTTGGAA 600  
601 CTGTGAGAACTCTGAGCAAAAGCAGCGATACAACTCAAAAGAGCTGTCTACATTTG 660  
601 CTGTGAGAACTCTGAGCAAAAGCAGCGATACAACTCAAAAGAGCTGTCTACATTTG 660  
661 AATTTGGATCTGATTTCTTGAAGTACCGTTAATTAAGCAACTTAATGAGTGTGGAG 720  
661 AATTTGGATCTGATTTCTTGAAGTACCGTTAATTAAGCAACTTAATGAGTGTGGAG 720  
721 ATCAAGATTTGTAACAAATCAACCCCTCAAGAACAGGATGAATCAGTTGATTTCTG 780

DB 721 ATCAAGATTTGTAACAAATCAACCCCTCAAGAACAGGATGAATCAGTTGATTTCTG 780  
DB 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGAGGATGTAAACAAATCTGAATCATCTAC 840  
DB 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGAGGATGTAAACAAATCTGAATCATCTAC 840  
DB 841 CCAGTAATTAATGATTTGAACACCTGAGAGCGGAGCTGAGAGGATCCAGAAAGT 900  
DB 841 CCAGTAATTAATGATTTGAACACCTGAGAGCGGAGCTGAGAGGATCCAGAAAGT 900  
DB 901 ATCAAGGATTTCTGTTTCAAACTTGCATGTGAGGCCATGTGGACAAATATCTATGCCA 960  
DB 901 ATCAAGGATTTCTGTTTCAAACTTGCATGTGAGGCCATGTGGACAAATATCTATGCCA 960  
DB 961 GCTCATTTACAGATGAGAAACAGAGTTTATTAATCTAATTAAGACAGAAATGAATGAGAA 1020  
DB 961 GCTCATTTACAGATGAGAAACAGAGTTTATTAATCTAATTAAGACAGAAATGAATGAGAA 1020  
DB 1021 AGGCTGAATTTCTGTAATTAAGCAAAAGCCTGGCTTGAAGGAGCCATATACAGAT 1080  
DB 1021 AGGCTGAATTTCTGTAATTAAGCAAAAGCCTGGCTTGAAGGAGCCATATACAGAT 1080  
DB 1081 GGGCTGGAAGTGAAGAAACATGTATATGATAGCGGACTCCAGACAGAAAAAGGTAG 1140  
DB 1081 GGGCTGGAAGTGAAGAAACATGTATATGATAGCGGACTCCAGACAGAAAAAGGTAG 1140  
DB 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGAATTAAGCAAAATCTGCCATGCT 1200  
DB 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGAATTAAGCAAAATCTGCCATGCT 1200  
DB 1201 CAGAGAAATCTAGAGATCTAGAGATGTTCTTGTGATTAATGAGAGATTGCA 1260  
DB 1201 CAGAGAAATCTAGAGATCTAGAGATGTTCTTGTGATTAATGAGAGATTGCA 1260  
DB 1261 AAGTTAATGAGTGTGTTTCCAGAGTGAATGAATGTTAGTTCTGATGACTCAATGATG 1320  
DB 1261 AAGTTAATGAGTGTGTTTCCAGAGTGAATGAATGTTAGTTCTGATGACTCAATGATG 1320  
DB 1321 GGGAGTCTGAATCAAAATGCCAAGAGTGAATGATTAATGAGAGTTCTAATATGAGTATG 1380  
DB 1321 GGGAGTCTGAATCAAAATGCCAAGAGTGAATGATTAATGAGAGTTCTAATATGAGTATG 1380  
DB 1381 AATATTCGTTCTTCAAGAGAAATAGACTTACTGGCCAGAGATCCCTATGAGGTTTAA 1440  
DB 1381 AATATTCGTTCTTCAAGAGAAATAGACTTACTGGCCAGAGATCCCTATGAGGTTTAA 1440  
DB 1441 TATGTAAAGTGAAGAGTTCACTCAAAATCAGTGAAGATTAATGAGACAAATAT 1500  
DB 1441 TATGTAAAGTGAAGAGTTCACTCAAAATCAGTGAAGATTAATGAGACAAATAT 1500  
DB 1501 TTGGGAAACCTATTCGAGAGAGGAGGAGCTTCCCACTTAAGCCATGTAACTGAAATC 1560  
DB 1501 TTGGGAAACCTATTCGAGAGAGGAGGAGCTTCCCACTTAAGCCATGTAACTGAAATC 1560  
DB 1561 TAAATTAAGAGCAATTTGTTCTGAGCAGAGATTAATCAAGAGGTCCTCAAAATA 1620  
DB 1561 TAAATTAAGAGCAATTTGTTCTGAGCAGAGATTAATCAAGAGGTCCTCAAAATA 1620  
DB 1621 AATTAAGCGTAAAGAGACCTTACATCAGGCTTCAATCTGAGATTTTATCAAGAAAG 1680  
DB 1621 AATTAAGCGTAAAGAGACCTTACATCAGGCTTCAATCTGAGATTTTATCAAGAAAG 1680  
DB 1681 CAGATTGGCAGTTCAAAAGAGCTCTGTAATGAATTAATCAGGGGAATCAACCAAGCGAGC 1740  
DB 1681 CAGATTGGCAGTTCAAAAGAGCTCTGTAATGAATTAATCAGGGGAATCAACCAAGCGAGC 1740  
DB 1741 AGAATGCTCAAGTATGAATTAATTAATTAATGATTAATTAATTAATTAATTAATTAATTAAT 1800  
DB 1741 AGAATGCTCAAGTATGAATTAATTAATTAATGATTAATTAATTAATTAATTAATTAATTAAT 1800  
DB 1801 CTATTCAGATGAGAAAAATCTTAACCAATAGATCACTGAGAAAAAGATCTCTTCA 1860

Db 1801 CTATTCAGAAATGAGAAAAATCTTAACCCAAATAGATCACTCGAAAAAGAACTGCTTCA 1860  
Qy 1861 AAAGAAAGCTGAACCTTAATAGCAGCAGTATATGAAATATGAACTCGAATTAATATCC 1920  
Db 1861 AAAGAAAGCTGAACCTTAATAGCAGCAGTATATGAAATATGAACTCGAATTAATATCC 1920  
Qy 1921 ACAATTCAAAAGCCTTAATAAGAAATAGCTGAGAGAAAGTCTTCTACAGAGCATATTC 1980  
Db 1921 ACAATTCAAAAGCCTTAATAAGAAATAGCTGAGAGAAAGTCTTCTACAGAGCATATTC 1980  
Qy 1981 ATGCGCTTGAACCTATAGTACGTAGAAATCTAAGCCCACTAATGTAATGTAATTCGAA 2040  
Db 1981 ATGCGCTTGAACCTATAGTACGTAGAAATCTAAGCCCACTAATGTAATGTAATTCGAA 2040  
Qy 2041 TTGATAGTGTCTTACGAGTGAAGATTAAGAAAAAAGTACCAACCAATATGCCAGTCA 2100  
Db 2041 TTGATAGTGTCTTACGAGTGAAGATTAAGAAAAAAGTACCAACCAATATGCCAGTCA 2100  
Qy 2101 GGCAACAGCAAAACCTTAACACTGATGAAAGGTAAAGAACTGCAACTGAGCCAGAAAGA 2160  
Db 2101 GGCAACAGCAAAACCTTAACACTGATGAAAGGTAAAGAACTGCAACTGAGCCAGAAAGA 2160  
Qy 2161 GTAACAAAGCCAAATGAACAGACAAAGTAAAGACATGACAGTGAATCTTTCCAGAGCTGA 2220  
Db 2161 GTAACAAAGCCAAATGAACAGACAAAGTAAAGACATGACAGTGAATCTTTCCAGAGCTGA 2220  
Qy 2221 AGTTAAACAAATGCACTCTGTTCTTTTACTAAGTGTCAATACCGTGAATCTTAAGAT 2280  
Db 2221 AGTTAAACAAATGCACTCTGTTCTTTTACTAAGTGTCAATACCGTGAATCTTAAGAT 2280  
Qy 2281 TTGTCATCTTACCTTCCAGAGAAAGAAAAAGAGAAACTAGAAACAGTTAAAGTGT 2340  
Db 2281 TTGTCATCTTACCTTCCAGAGAAAGAAAAAGAGAAACTAGAAACAGTTAAAGTGT 2340  
Qy 2341 CTAAATATGCTGAGAACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTGCAAACTG 2400  
Db 2341 CTAAATATGCTGAGAACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTGCAAACTG 2400  
Qy 2401 AAAATCTGTAAGAGTATGACAGTATTTTCACTGTAACCTGTAATTAATGAGCACTCAG 2460  
Db 2401 AAAATCTGTAAGAGTATGACAGTATTTTCACTGTAACCTGTAATTAATGAGCACTCAG 2460  
Qy 2461 AAAGATCTCGTTACTGGAAGTTAGCACTTACGGAAGGCAAAAACAGAACCAATTAAT 2520  
Db 2461 AAAGATCTCGTTACTGGAAGTTAGCACTTACGGAAGGCAAAAACAGAACCAATTAAT 2520  
Qy 2521 GTGTGAGTCACTGTGACAGCATTTTGAAGAACCCCAAGGAGCTAATTCATGTTTCCAAAG 2580  
Db 2521 GTGTGAGTCACTGTGACAGCATTTTGAAGAACCCCAAGGAGCTAATTCATGTTTCCAAAG 2580  
Qy 2581 ATTAATGAATGACACAGAAAGCTTTAAGTATCCATTGGGACATGAATGTAACCAAGTCC 2640  
Db 2581 ATTAATGAATGACACAGAAAGCTTTAAGTATCCATTGGGACATGAATGTAACCAAGTCC 2640  
Qy 2641 GGGAAACAAAGATGAAATGGAAGAAAGTGAACCTGATGCTCAGTATTTGCGAATATCAT 2700  
Db 2641 GGGAAACAAAGATGAAATGGAAGAAAGTGAACCTGATGCTCAGTATTTGCGAATATCAT 2700  
Qy 2701 TCAAGTTCCTAAAGGCGCAGTCAATTTGCTGTGTTTCAAAATCAGAGAAATGCAAGAGG 2760  
Db 2701 TCAAGTTCCTAAAGGCGCAGTCAATTTGCTGTGTTTCAAAATCAGAGAAATGCAAGAGG 2760  
Qy 2761 AATGTGCAACATTTCTGTCCCACTGTGGGTCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
Db 2761 AATGTGCAACATTTCTGTCCCACTGTGGGTCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
Qy 2821 TTGAATGGAACAAAGAAAGAAATCAAGAAAGAAAGATGATTAATCAAGCCTGTAC 2880  
Db 2821 TTGAATGGAACAAAGAAAGAAATCAAGAAAGAAAGATGATTAATCAAGCCTGTAC 2880  
Qy 2881 AGACAGTTAATATCACTGACAGGCTTCTGTGTGTGTGACAGAAAGATTAAGCAGTTGATA 2940  
Db 2881 AGACAGTTAATATCACTGACAGGCTTCTGTGTGTGTGACAGAAAGATTAAGCAGTTGATA 2940

Qy 2941 ATGCCAAATGATATCAAAAGAGGCTCTAGGTTTTGTCTATCATCTCAGTTACAGAGCA 3000  
Db 2941 ATGCCAAATGATATCAAAAGAGGCTCTAGGTTTTGTCTATCATCTCAGTTACAGAGCA 3000  
Qy 3001 ACGAAACCTGACCTCATTCCTCAAAATGAACATGACCTTTTACAAAACCATATGCTATAC 3060  
Db 3001 ACGAAACCTGACCTCATTCCTCAAAATGAACATGACCTTTTACAAAACCATATGCTATAC 3060  
Qy 3061 CACCACTTTTCCCATCAAGCATTTGTAAATCTAAATGTAAGAAATCTGCTAGAGG 3120  
Db 3061 CACCACTTTTCCCATCAAGCATTTGTAAATCTAAATGTAAGAAATCTGCTAGAGG 3120  
Qy 3121 AAAACCTTGAGAAACATTCATGTCACCTGAAAGAAATGGAATAGAAACATTTCCAA 3180  
Db 3121 AAAACCTTGAGAAACATTCATGTCACCTGAAAGAAATGGAATAGAAACATTTCCAA 3180  
Qy 3181 GTACAGTGAACCAATTAAGCCGTATTAACATTAAGAAATGTTTTTAAAGAGCAGCT 3240  
Db 3181 GTACAGTGAACCAATTAAGCCGTATTAACATTAAGAAATGTTTTTAAAGAGCAGCT 3240  
Qy 3241 CAAGCAATTTAATGAAGTACGTTCCAGTACTAATGAAGTGGCTCCAGTATTAATGA 3300  
Db 3241 CAAGCAATTTAATGAAGTACGTTCCAGTACTAATGAAGTGGCTCCAGTATTAATGA 3300  
Qy 3301 TAGGTTCCAGTATGAAGAAACATTCAGAGCAACTAGTGAAGAAACAGAGGCAAAATGA 3360  
Db 3301 TAGGTTCCAGTATGAAGAAACATTCAGAGCAACTAGTGAAGAAACAGAGGCAAAATGA 3360  
Qy 3361 ATGCTATGCTTATGATTAAGGAGGTTTTGCAACCTGAGGCTATTAACAAAGTCTCTGGA 3420  
Db 3361 ATGCTATGCTTATGATTAAGGAGGTTTTGCAACCTGAGGCTATTAACAAAGTCTCTGGA 3420  
Qy 3421 GTAATTTGAAGCATCTGAATTAAGAAAGCAAGAAATGAAGAGTACTGAGCTGTA 3480  
Db 3421 GTAATTTGAAGCATCTGAATTAAGAAAGCAAGAAATGAAGAGTACTGAGCTGTA 3480  
Qy 3481 ATACAGATTTCTCCCATATCTGATTCAGATTAAGTAAACAGCTATGGAAGTATGTC 3540  
Db 3481 ATACAGATTTCTCCCATATCTGATTCAGATTAAGTAAACAGCTATGGAAGTATGTC 3540  
Qy 3541 ATGCACTCAGGTTTGTCTGAGACACTGATGACCTGTAATGATGATGTTGAAATTAAG 3600  
Db 3541 ATGCACTCAGGTTTGTCTGAGACACTGATGACCTGTAATGATGATGTTGAAATTAAG 3600  
Qy 3601 AAGATTAAGTGTCTGAAATGACATTAAGAAAGTCTGCTGTTTTAGCAAAACCG 3660  
Db 3601 AAGATTAAGTGTCTGAAATGACATTAAGAAAGTCTGCTGTTTTAGCAAAACCG 3660  
Qy 3661 TCCAGAGAGAGCTTATGACAGAGTCTTACCCCTTTTACCCATACATTAATGAGTCCAG 3720  
Db 3661 TCCAGAGAGAGCTTATGACAGAGTCTTACCCCTTTTACCCATACATTAATGAGTCCAG 3720  
Qy 3721 GTTACCGAAGAGGCGCAAGAAATTAAGAGTCTTCCAGAGAGAACTTATCTAGTGAGATG 3780  
Db 3721 GTTACCGAAGAGGCGCAAGAAATTAAGAGTCTTCCAGAGAGAACTTATCTAGTGAGATG 3780  
Qy 3781 AAGAGCTTCCCTGCTTCCAAACATTTTATTTGTTAAAGTAAACATTAATACCTTCCAGT 3840  
Db 3781 AAGAGCTTCCCTGCTTCCAAACATTTTATTTGTTAAAGTAAACATTAATACCTTCCAGT 3840  
Qy 3841 CTACTAGGCAATGACACCGTTCTACCGAGTGTCTGTCTAAGAACACAGAGAAATTAAT 3900  
Db 3841 CTACTAGGCAATGACACCGTTCTACCGAGTGTCTGTCTAAGAACACAGAGAAATTAAT 3900  
Qy 3901 TATCATTAAGAAATGCTTAATGATGCTGACAGTAACAGATATATTTGCAAGGATCTC 3960  
Db 3901 TATCATTAAGAAATGCTTAATGATGCTGACAGTAACAGATATATTTGCAAGGATCTC 3960  
Qy 3961 AGGAAACATCACTTATGAGAGAAACAAATGTTCTGCTAGCTGTTTCTTCAAGTCA 4020  
Db 3961 AGGAAACATCACTTATGAGAGAAACAAATGTTCTGCTAGCTGTTTCTTCAAGTCA 4020

QY	4021	GTGAATTGGAGAAGACTTGACGCAAAATACAAACACCAGAGATCCCTTCTTGATGGTCTCT	4086
Db	4021	GTGAATTGGAGAAGACTTGACGCAAAATACAAACACCAGAGATCCCTTCTTGATGGTCTCT	4086
QY	4081	CCAAACAAATGAGGATCATGCTGAAAGCCAGGAGTTGCTCTGAGTACAAAGAAATTGG	4140
Db	4081	CCAAACAAATGAGGATCATGCTGAAAGCCAGGAGTTGCTCTGAGTACAAAGAAATTGG	4140
QY	4141	TTTCAGATGATGAAAGAAAGGAAACGGGCTTGGAAAGAAATATATCAAGAGCAAGCA	4200
Db	4141	TTTCAGATGATGAAAGAAAGGAAAGGGCTTGGAAAGAAATATATCAAGAGCAAGCA	4200
QY	4201	TGGATTCAACTTGTAGTGAAGAGATCGGGGTGAGAGTGAACAAGCGCTGTGAG	4260
Db	4201	TGGATTCAACTTGTAGTGAAGAGATCGGGGTGAGAGTGAACAAGCGCTGTGAG	4260
QY	4261	ACTGCTCAGGGCTATCCTCTCAGATGTCATTTTAACACTCAGCAGAGGGATACATGC	4320
Db	4261	ACTGCTCAGGGCTATCCTCTCAGATGTCATTTTAACACTCAGCAGAGGGATACATGC	4320
QY	4321	AAACATTAACCTGATTAAGCTCCAGCAGAAATGCTGAACTAGAACCTGTGTAAGACAGC	4380
Db	4321	AAACATTAACCTGATTAAGCTCCAGCAGAAATGCTGAACTAGAACCTGTGTAAGACAGC	4380
QY	4381	ATGGAGGACAGCCTCTTAACAGCTACCCCTTCATATAAGTACCTCCTGCGCTTGAG	4440
Db	4381	ATGGAGGACAGCCTCTCTAACAGCTACCCCTTCATATAAGTACCTCCTGCGCTTGAG	4440
QY	4441	ACCTGCGAAATCCAGAACAAAGCATGAGAAAAAGCAGTATTAACTTCACAGAAAGTA	4500
Db	4441	ACCTGCGAAATCCAGAACAAAGCATGAGAAAAAGCAGTATTAACTTCACAGAAAGTA	4500
QY	4501	GTGAATTAACCTATTAAGCCAGAAATCCAGAAAGCCTTTCTGTGACAAAGTTGAGTGTG	4560
Db	4501	GTGAATTAACCTCTATTAAAGCCAGAAATCCAGAAAGCCTTTCTGTGACAAAGTTGAGTGTG	4560
QY	4561	CAGATAGTTCACGATAAAAATAAGAAACAGAGGTGAAAGATCAATCCCTCTTAAT	4620
Db	4561	CAGATAGTTCACGATAAAAATAAGAAACAGAGGTGAAAGATCAATCCCTCTCTTAAT	4620
QY	4621	GCCCATCTTATGATATATAGTGTGATCATGACAGTGTGCTGGAGTCTTCAGAAATAGA	4680
Db	4621	GCCCATCTTATGATATATAGTGTGATCATGACAGTGTGCTGGAGTCTTCAGAAATAGA	4680
QY	4741	AGTGTGGGCAACACATTTGACAGGAAACATCTTACTTTCGCAAGGCAAAATCTAGAGGAA	4800
Db	4741	AGTGTGGGCAACACATTTGACAGGAAACATCTTACTTTCGCAAGGCAAAATCTAGAGGAA	4800
QY	4801	CCCTTACTGTGAATCTGGAATCAGACCTCTTCTGTGATGACCTCGAATCTGATCCTTCTG	4860
Db	4801	CCCTTACTGTGAATCTGGAATCAGACCTCTTCTGTGATGACCTCGAATCTGATCCTTCTG	4860
QY	4861	AAAGCAGAGCCCCAGAGTACGCTGTGTGGCACAATACATCTTCAACCTCTGCAATGA	4920
Db	4861	AAAGCAGAGCCCCAGAGTACGCTGTGTGGCACAATACATCTTCAACCTCTGCAATGA	4920
QY	4921	AAAGTTCCTCCCAATTGAAAGTTGACAGATCTGCCAGAGTCCAGCTGCTCTCATCTACTG	5040
Db	4921	AAAGTTCCTCCCAATTGAAAGTTGACAGATCTGCCAGAGTCCAGCTGCTCTCATCTACTG	5040
QY	4981	ATACTGCTGGGTATATATGCAATGGAAGAAAGTGTAGACAGGAGGAAGCCAGAAATTGACAG	5100
Db	4981	ATACTGCTGGGTATATATGCAATGGAAGAAAGTGTAGACAGGAGGAAGCCAGAAATTGACAG	5100
QY	5041	CTTCAACAGAAAGGGTCAACAAAGAAATGTCATGATGTGTGTCTTGACCTGACCCCAAG	5160
Db	5041	CTTCAACAGAAAGGGTCAACAAAGAAATGTCATGATGTGTGTCTTGACCTGACCCCAAG	5160
QY	5101	AATTTATGCTGCTGTACAAATTTTGCAGAAAACCAACATCATCTTTAACTAATCTAATTA	5160

Db	5101	AAATTATGCTGTGTACAAAGTTTGCCGAAACACCACTACTTAATTA	5160
QY	5161	CTGAAGAGACTACTCATGTTGTATATGAAAACAGATGCTGAATTTGTGTGAACGAC	5220
Db	5161	CTGAAGAGACTACTCATGTTGTATATGAAAACAGATGCTGAATTTGTGTGAACGAC	5220
QY	5221	TGAAATATTTCTTAGAATTTGCGGAGAGAAATGGATAGTTAGTATTTCTGGGTGACC	5280
Db	5221	TGAAATATTTCTTAGAATTTGCGGAGAGAAATGGATAGTTAGTATTTCTGGGTGACC	5280
QY	5281	AGCTATATTAAGAAAGAAAATGCTGATAGCATGATTTTGAAGTACAGAGATGTGG	5340
Db	5281	AGCTATATTAAGAAAGAAAATGCTGATAGCATGATTTTGAAGTACAGAGATGTGG	5340
QY	5341	TCATATGAAAGAACCAACCAAGGTCCAAGCGAGCAAGAAATCCAGACAGAAAGATCT	5400
Db	5341	TCATATGAAAGAACCAACCAAGGTCCAAGCGAGCAAGAAATCCAGACAGAAAGATCT	5400
QY	5401	TCAGAGGGGCTTGAANAATCTGTGCTATAGGGCCCTTCAACAAATGCCCAAGATCAATCG	5460
Db	5401	TCAGAGGGGCTTGAANAATCTGTGCTATAGGGCCCTTCAACAAATGCCCAAGATCAATCG	5460
QY	5461	AATGATATGATACAGCTGTGTGGTCTTCTGTGTGAAGAGACTTTCATCTTACCCCTTG	5520
Db	5461	AATGATATGATACAGCTGTGTGGTCTTCTGTGTGAAGAGACTTTCATCTTACCCCTTG	5520
QY	5521	GCACAGGTGTCACCCAAATGTGGTTGTGCACAGATGCTCTGACAGAGACAATGGCT	5580
Db	5521	GCACAGGTGTCACCCAAATGTGGTTGTGCACAGATGCTCTGACAGAGACAATGGCT	5580
QY	5581	TCCATGCAATTTGGGCAAGATGTGTAGAGCACTGTGTGTGACCCGAGATGGGTGTGGACA	5640
Db	5581	TCCATGCAATTTGGGCAAGATGTGTAGAGCACTGTGTGTGACCCGAGATGGGTGTGGACA	5640
QY	5641	GTGATAGCACTTACCAAGTGCAGAGAGCTGACACCTTACTATATCCCAATGCCCCACA	5700
Db	5641	GTGATAGCACTTACCAAGTGCAGAGAGCTGACACCTTACTATATCCCAATGCCCCACA	5700
QY	5701	GCCACTACTGA 5711	
Db	5701	GCCACTACTGA 5711	

RESULT 2  
 US-09-982-828-1  
 ; Sequence 1, Application US/09982828  
 ; Publication No. US20030022184A1  
 ;  
 ; GENERAL INFORMATION:  
 ;  
 ; APPLICANT: Murphy, Patricia D.  
 ; Allen, Antoinette C.  
 ; Alvares, Christopher P.  
 ; Critz, Brenda S.  
 ; Olson, Sheri J.  
 ; Thuber, Denise  
 ; Zeng, Bin  
 ;  
 ; TITLE OF INVENTION: Coding Sequences of the Human  
 ; BRCAL Gene  
 ;  
 ; NUMBER OF SEQUENCES: 72  
 ;  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Morgan Lewis & Bockius LLP  
 ; STREET: 1111 Pennsylvania Avenue N. W.  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20004  
 ;  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ;  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/982,828  
 ;

FILED DATE: 22-Oct-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/074,453  
FILING DATE: 1998-05-06  
APPLICATION NUMBER: US 08/798,691  
FILING DATE: 1997-02-12  
APPLICATION NUMBER: US 08/598,591  
FILING DATE: 1996-02-12  
ATTORNEY/AGENT INFORMATION:  
NAME: Michael S. Tuscan  
REGISTRATION NUMBER: 43,210  
REFERENCE/DOCKET NUMBER: 44921-5053-01-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-739-3000  
TELEFAX: 202-739-3001  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5711 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
STRAIN: BRCAL (om11)  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17  
MAP POSITION: 17q21  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-982-828-1

Query Match 100.0%; Score 5711; DB 11; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTCGCTGAGACTTCTGTGAGACCCCGCACAGGCTGTGGGGTTTCTCAGATTAAGTGGCC 60  
DB 1 AGCTCGCTGAGACTTCTGTGAGACCCCGCACAGGCTGTGGGGTTTCTCAGATTAAGTGGCC 60  
QY 61 CTTGCGCTCAGAGGCTTCAACCTCTGCTGTGGTAAAGTTCAATGGAACAGAAAGAA 120  
DB 61 CTTGCGCTCAGAGGCTTCAACCTCTGCTGTGGTAAAGTTCAATGGAACAGAAAGAA 120  
QY 121 TGAATTAATCTGCTCTTGGCGTTGAAGAGTAACAATAATGCTAATATGCAAGAAA 180  
DB 121 TGAATTAATCTGCTCTTGGCGTTGAAGAGTAACAATAATGCTAATATGCAAGAAA 180  
QY 181 TCTTAGAGTGTCCCATCTGTCTGAGTGTGATCAAGAACTGTCTCCCAAAAGTGTGACC 240  
DB 181 TCTTAGAGTGTCCCATCTGTCTGAGTGTGATCAAGAACTGTCTCCCAAAAGTGTGACC 240  
QY 241 ACATATTTTGGCAAAATTTTGCATGCTGAACCTTCTCAACAGAAAGAAAGGCTTCAAGT 300  
DB 241 ACATATTTTGGCAAAATTTTGCATGCTGAACCTTCTCAACAGAAAGAAAGGCTTCAAGT 300  
QY 301 GTCTCTTAATGTAAGATATATAACCAAAAGAGCTTCAAGAAAGTAAGAGATTAGTC 360  
DB 301 GTCTCTTAATGTAAGATATATAACCAAAAGAGCTTCAAGAAAGTAAGAGATTAGTC 360  
QY 361 AACTTTTGAAGAGTATTTGAAGAAATCAATTTGCTTCAAGTGTGACAGGTTTGGAGT 420  
DB 361 AACTTTTGAAGAGTATTTGAAGAAATCAATTTGCTTCAAGTGTGACAGGTTTGGAGT 420  
QY 421 ATGCAAAAGCTATTAATTTTGCAGAAAGAAAGAAATTAATCTCTGCAAGATCTAAAGATG 480  
DB 421 ATGCAAAAGCTATTAATTTTGCAGAAAGAAAGAAATTAATCTCTGCAAGATCTAAAGATG 480  
QY 481 AAGTTTATATCATCAAAAGATGAGGCTACAGAAACCGTGCAGAAAGACTTCTACAGAGTG 540  
DB 481 AAGTTTATATCATCAAAAGATGAGGCTACAGAAACCGTGCAGAAAGACTTCTACAGAGTG 540  
QY 541 AACCCGAAATTCCTTCTTGCAAGAAACCAAGTCTAGTGTCAACTCTCTAAGCTTTGAA 600

DB 541 AACCCGAAATTCCTTCTTGCAAGAAACCAAGTCTAGTGTCAACTCTCTAAGCTTTGAA 600  
QY 601 CTGTGAGAACTCTGAGCAAAAGCAGCGGATACAACTTCAAAAGACGTCTGTATCATTTG 660  
DB 601 CTGTGAGAACTCTGAGCAAAAGCAGCGGATACAACTTCAAAAGACGTCTGTATCATTTG 660  
QY 661 AATTGGATCTGATCTCTCTGAGATACCGTTAATTAAGCAACTTAATGCAAGTGGAG 720  
DB 661 AATTGGATCTGATCTCTCTGAGATACCGTTAATTAAGCAACTTAATGCAAGTGGAG 720  
QY 721 ATCAAGAAATTTGTAACAATCAACCCCTCAAGAACAGGATGAATCAGTTTGGATTCTG 780  
DB 721 ATCAAGAAATTTGTAACAATCAACCCCTCAAGAACAGGATGAATCAGTTTGGATTCTG 780  
QY 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGACGATGTAACTGAACATCATCAAC 840  
DB 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGACGATGTAACTGAACATCATCAAC 840  
QY 841 CCAGTAATTAATGATTGTAACCACTGAGAACCGTGCAGTGAAGGATCCAGAAAGT 900  
DB 841 CCAGTAATTAATGATTGTAACCACTGAGAACCGTGCAGTGAAGGATCCAGAAAGT 900  
QY 901 ATCAGGAGTATCTGTTTCAAACTTGCAATGTGAGCCATGTGGCAAAATCTCATGCCA 960  
DB 901 ATCAGGAGTATCTGTTTCAAACTTGCAATGTGAGCCATGTGGCAAAATCTCATGCCA 960  
QY 961 GCTCATTAACAGCATGAGAACAGAGTTTACTTCACTTAAGACAGAAATGATAGAAA 1020  
DB 961 GCTCATTAACAGCATGAGAACAGAGTTTACTTCACTTAAGACAGAAATGATAGAAA 1020  
QY 1021 AGGCTGAATTTCTGTAATTAAGCAAAACGCTGTGCTTGAAGAGCCCAATATCAAT 1080  
DB 1021 AGGCTGAATTTCTGTAATTAAGCAAAACGCTGTGCTTGAAGAGCCCAATATCAAT 1080  
QY 1081 GGGCTGGAAGTAAAGAAACATGTATGATGAGCGGACTCCAGACAGAAAAAGTAG 1140  
DB 1081 GGGCTGGAAGTAAAGAAACATGTATGATGAGCGGACTCCAGACAGAAAAAGTAG 1140  
QY 1141 ATCTGAATCTGATCCCTGTGTGAGAGAAAAAGATGAATTAAGCAAACTGCCATCT 1200  
DB 1141 ATCTGAATCTGATCCCTGTGTGAGAGAAAAAGATGAATTAAGCAAACTGCCATCT 1200  
QY 1201 CAGAGAACTCTAGAGATCTGAAGATGTTCTTGGATTAACCTAAATGCAAGCATTCGA 1260  
DB 1201 CAGAGAACTCTAGAGATCTGAAGATGTTCTTGGATTAACCTAAATGCAAGCATTCGA 1260  
QY 1261 AAGTTAATGAGTGGTTTCCAGAAAGTGAAGTGAAGTTGAGTTGATGACTCAATGATG 1320  
DB 1261 AAGTTAATGAGTGGTTTCCAGAAAGTGAAGTGAAGTTGAGTTGATGACTCAATGATG 1320  
QY 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGTGTATTTGAGAGTTCTAAATGAGTAGATG 1380  
DB 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGTGTATTTGAGAGTTCTAAATGAGTAGATG 1380  
QY 1381 AATATTTCTGTTCTTCAAGAAAAATGACTTACCTGCGCAGTATCTCATGAGCTTTAA 1440  
DB 1381 AATATTTCTGTTCTTCAAGAAAAATGACTTACCTGCGCAGTATCTCATGAGCTTTAA 1440  
QY 1441 TATGTAAGAGTAAGAGTCACTCCAAATAGTAGAGTAATTTGAAGCAAAATAT 1500  
DB 1441 TATGTAAGAGTAAGAGTCACTCCAAATAGTAGAGTAATTTGAAGCAAAATAT 1500  
QY 1501 TTGGAAAAACCTATCGAAGAAAGCAAGCTTCCCAACTTAAGGCATGAATCTGAATTC 1560  
DB 1501 TTGGAAAAACCTATCGAAGAAAGCAAGCTTCCCAACTTAAGGCATGAATCTGAATTC 1560  
QY 1561 TAAATTAAGAGCAATTTGTTACTGAGCCAGATTAATCAAGAGCTTCCCTCAAAATTA 1620  
DB 1561 TAAATTAAGAGCAATTTGTTACTGAGCCAGATTAATCAAGAGCTTCCCTCAAAATTA 1620  
QY 1621 AATTAAGAGCTTAAGAGGAGCTTCAATCAGGCTTCAATCTGAGAGTTTATCAAGAAAG 1680

Db 1621 AATTAAGGTTAAAGAGACCTACATGAGCCTTCATCTGTGAGGATTTTATCAAGAAAG 1680  
Qy 1661 CAGATTGGCAGTTCAAAAAGACTCTGAAATGATTAATCAAGGAACTAACCAAGGAGC 1740  
Db 1661 CAGATTGGCAGTTCAAAAAGACTCTGAAATGATTAATCAAGGAACTAACCAAGGAGC 1740  
Qy 1741 AGAATGCTCAAGTGAATATTTACTTAATAGTGCATGAGAAATTAACCAAAAGGTGATT 1800  
Db 1741 AGAATGCTCAAGTGAATATTTACTTAATAGTGCATGAGAAATTAACCAAAAGGTGATT 1800  
Qy 1801 CTATTCAGATGAGAAAAATCTTAACCAATGAAATCACTGCAAAAAAGATCTGCTTTCA 1860  
Db 1801 CTATTCAGATGAGAAAAATCTTAACCAATGAAATCACTGCAAAAAAGATCTGCTTTCA 1860  
Qy 1861 AAAGCAAGCTGAACCTTAAGCAGACAGATTAAGAAATTAAGAACTGCAATTAATATACC 1920  
Db 1861 AAAGCAAGCTGAACCTTAAGCAGACAGATTAAGAAATTAAGAACTGCAATTAATATACC 1920  
Qy 1921 ACAATTTCAAAAGCACTTAATAAAGATAGGCTGAGAGAGAGTCTTCAACGAGCATATTC 1980  
Db 1921 ACAATTTCAAAAGCACTTAATAAAGATAGGCTGAGAGAGAGTCTTCAACGAGCATATTC 1980  
Qy 1981 ATGCGCTTGAACCTAGTACGTAGAGAAATCTTAAGCCCACTTAATTTGATCTGAATTCGAAA 2040  
Db 1981 ATGCGCTTGAACCTAGTACGTAGAGAAATCTTAAGCCCACTTAATTTGATCTGAATTCGAAA 2040  
Qy 2041 TTGAATGTTGTTCTGACGTGAAGATTAAGAAAAAGTAAACCAATATGCCAGTCA 2100  
Db 2041 TTGAATGTTGTTCTGACGTGAAGATTAAGAAAAAGTAAACCAATATGCCAGTCA 2100  
Qy 2101 GGCAAGAGCAAAAACCTTAACAATCATGAGAGTAAAGAACTGCAACTGAGGCAAGAGA 2160  
Db 2101 GGCAAGAGCAAAAACCTTAACAATCATGAGAGTAAAGAACTGCAACTGAGGCAAGAGA 2160  
Qy 2161 GTAAACAGCCAAATGAACAGACAAAGTAAAGACATGACATGATATCTTCCAGAGCTGA 2220  
Db 2161 GTAAACAGCCAAATGAACAGACAAAGTAAAGACATGACATGATATCTTCCAGAGCTGA 2220  
Qy 2221 AGTTAACAAATGSCACTGGTCTTTTACTAAGTGTCAAAATACCAATGCTTAAGAAAT 2280  
Db 2221 AGTTAACAAATGSCACTGGTCTTTTACTAAGTGTCAAAATACCAATGCTTAAGAAAT 2280  
Qy 2281 TTGTCAATCTAGCTTCCAGAGAGAAAGAAAGAAAGAACTAAGAAACAGTTAAAGTGT 2340  
Db 2281 TTGTCAATCTAGCTTCCAGAGAGAGAAAGAAAGAAAGAACTAAGAAACAGTTAAAGTGT 2340  
Qy 2341 CTAAATTAATGCTGAGAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTGCACATG 2400  
Db 2341 CTAAATTAATGCTGAGAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTGCACATG 2400  
Qy 2401 AAAGATCTGTAGAGAGTGAAGATTTTCACTGTGTAACCTGTATATGSCACTCAGG 2460  
Db 2401 AAAGATCTGTAGAGAGTGAAGATTTTCACTGTGTAACCTGTATATGSCACTCAGG 2460  
Qy 2461 AAAGATCTGTAGAGAGTGAAGATTTTCACTGTGTAACCTGTATATGSCACTCAGG 2520  
Db 2461 AAAGATCTGTAGAGAGTGAAGATTTTCACTGTGTAACCTGTATATGSCACTCAGG 2520  
Qy 2521 GTGTGATGCTAGTGTGAGACATTTGAAAAACCCCAAGGAGCTAATTCATGTTGTTCCAAAG 2580  
Db 2521 GTGTGATGCTAGTGTGAGACATTTGAAAAACCCCAAGGAGCTAATTCATGTTGTTCCAAAG 2580  
Qy 2581 AATAATAGAAATGACACAGAGGCTTAAGTATCCATTGGGACATGAACTTAACCACTC 2640  
Db 2581 AATAATAGAAATGACACAGAGGCTTAAGTATCCATTGGGACATGAACTTAACCACTC 2640  
Qy 2641 GGGAAACAGAGATGAAATGGAAGAAAGTGAACCTGATGCTCAGATTTGCAAGATATCAT 2700  
Db 2641 GGGAAACAGAGATGAAATGGAAGAAAGTGAACCTGATGCTCAGATTTGCAAGATATCAT 2700  
Qy 2701 TCAAGGTTTCAAGGCGCAGTCAATTTGCTGTGTTTCAAAATCCAGAAATGCAAGAGG 2760  
Db 2701 TCAAGGTTTCAAGGCGCAGTCAATTTGCTGTGTTTCAAAATCCAGAAATGCAAGAGG 2760

Qy 2761 AATGNGCAACAATTCTGCGCCCACTCTGGGTCCTTTAAAGAAACAAAGTCCAAAGCACTT 2820  
Db 2761 AATGNGCAACAATTCTGCGCCCACTCTGGGTCCTTTAAAGAAACAAAGTCCAAAGCACTT 2820  
Qy 2821 TTGAATGTAACAAAGAGAAAGAAATCAAGAGAAAGATGATCTTAATCAAGCCTGTAC 2880  
Db 2821 TTGAATGTAACAAAGAGAAAGAAATCAAGAGAAAGATGATCTTAATCAAGCCTGTAC 2880  
Qy 2881 AGACATTAATATCACTGACAGCTTTCTGTGTTGGTCAAGAAAGATTAAGCAAGTTGATA 2940  
Db 2881 AGACATTAATATCACTGACAGCTTTCTGTGTTGGTCAAGAAAGATTAAGCAAGTTGATA 2940  
Qy 2941 ATGCGCAATGATATCAAGAGAGCTCTAGTTTGTCTATCATCTCAGTTCAAGAGCA 3000  
Db 2941 ATGCGCAATGATATCAAGAGAGCTCTAGTTTGTCTATCATCTCAGTTCAAGAGCA 3000  
Qy 3001 ACAGAACTGACCTCATTACTCCAAATTAACATGACCTTTTCAAAAACCATATGCTATAC 3060  
Db 3001 ACAGAACTGACCTCATTACTCCAAATTAACATGACCTTTTCAAAAACCATATGCTATAC 3060  
Qy 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAACTAAATGTAAGAAAAATCTGCTAGAG 3120  
Db 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAACTAAATGTAAGAAAAATCTGCTAGAG 3120  
Qy 3121 AAAACCTTGAGGAACATTCAATGTCACTGAAAGAGAAATGGGAAATGAGAACTTCCAA 3180  
Db 3121 AAAACCTTGAGGAACATTCAATGTCACTGAAAGAGAAATGGGAAATGAGAACTTCCAA 3180  
Qy 3181 GTACAGTGAAGCAATTAAGCCGTAAATTAATTAAGAAATGTTTTTAAAGAGCAGCT 3240  
Db 3181 GTACAGTGAAGCAATTAAGCCGTAAATTAATTAAGAAATGTTTTTAAAGAGCAGCT 3240  
Qy 3241 CAAGCAATTAATTAAGAGTACGTTCCAGTACTTAATGAAGTGGGCTCCAGTATTAATGAAA 3300  
Db 3241 CAAGCAATTAATTAAGAGTACGTTCCAGTACTTAATGAAGTGGGCTCCAGTATTAATGAAA 3300  
Qy 3301 TAGGTTCCAGTATGAAAGAAACCTCAAGAGAGAACTAAGTGAAGAAAGAGGCGCAAAATGGA 3360  
Db 3301 TAGGTTCCAGTATGAAAGAAACCTCAAGAGAGAACTAAGTGAAGAAAGAGGCGCAAAATGGA 3360  
Qy 3361 ATGCTATGCTTAAGATTAAGGGGTTTTTGGCAACCTGAGGTCATTAACAAAGCTTCTGGAA 3420  
Db 3361 ATGCTATGCTTAAGATTAAGGGGTTTTTGGCAACCTGAGGTCATTAACAAAGCTTCTGGAA 3420  
Qy 3421 GTAAATGTAAGCATCTGAAATTAAGAAAGCAAGAAATGAAGAAAGTGTCAAGCTGTTA 3480  
Db 3421 GTAAATGTAAGCATCTGAAATTAAGAAAGCAAGAAATGAAGAAAGTGTCAAGCTGTTA 3480  
Qy 3481 ATACAGATTTCTCCATATCTGATTCAGATTAAGAAACAGCTATGGAAGTATGTC 3540  
Db 3481 ATACAGATTTCTCCATATCTGATTCAGATTAAGAAACAGCTATGGAAGTATGTC 3540  
Qy 3541 ATGCACTCAGAGTTGTTCTGAGACACCTGATGACCTGTTAGATGATGAGTGAATTAAGG 3600  
Db 3541 ATGCACTCAGAGTTGTTCTGAGACACCTGATGACCTGTTAGATGATGAGTGAATTAAGG 3600  
Qy 3601 AAGATPACTAGTTTGTGCGAAATGACATTAAGAAAGTTCGTCTGTTTATGCAAAAGCG 3660  
Db 3601 AAGATPACTAGTTTGTGCGAAATGACATTAAGAAAGTTCGTCTGTTTATGCAAAAGCG 3660  
Qy 3661 TCCAGAGAGGAGCTTAAGCAGAGAGTCCCTAGCCCTTCAACCATACATTTGGCTCAGG 3720  
Db 3661 TCCAGAGAGGAGCTTAAGCAGAGAGTCCCTAGCCCTTCAACCATACATTTGGCTCAGG 3720  
Qy 3721 GTTACCGAAGAGGGGCAAGAAATTAAGAGTCTCAGAGAGAACTTATCTAGTGAAGATG 3780  
Db 3721 GTTACCGAAGAGGGGCAAGAAATTAAGAGTCTCAGAGAGAACTTATCTAGTGAAGATG 3780  
Qy 3781 AAGAGCTTCCCTGCTTCCAAACATTTGTTATTTGTTAAAGTAAACATATATACCTTCTCAGT 3840  
Db 3781 AAGAGCTTCCCTGCTTCCAAACATTTGTTATTTGTTAAAGTAAACATATATACCTTCTCAGT 3840



3841 CTACAGCATAGACACCGTCTGACCGAGTGTCTGTAAAGACACAGAGGAATTTAT 3900  
3841 CTACAGCATAGACACCGTCTGACCGAGTGTCTGTAAAGACACAGAGGAATTTAT 3900  
3901 TATCATTTAGAGATAGCTTAAATGACCTGACGATACCAAGTAAATTTGGCAAGGATCTC 3960  
3901 TATCATTTAGAGATAGCTTAAATGACCTGACGATACCAAGTAAATTTGGCAAGGATCTC 3960  
3961 AGGAACATCACCCTTAGTAGAGAAACAAATGTTCTGCTAGCTTTCTTCAAGTGA 4020  
3961 AGGAACATCACCCTTAGTAGAGAAACAAATGTTCTGCTAGCTTTCTTCAAGTGA 4020  
4021 GTGAATTTGAGAACTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4080  
4021 GTGAATTTGAGAACTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4080  
4081 CCAACCAATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4140  
4081 CCAACCAATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4140  
4141 TTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4200  
4141 TTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4200  
4201 TGGATTTCAAACTTAGTGAAGGATGATGATGATGATGATGATGATGATGATGATG 4260  
4201 TGGATTTCAAACTTAGTGAAGGATGATGATGATGATGATGATGATGATGATGATG 4260  
4261 ACTGCTCAGAGGCTATCTCTCAGAGTGAATTTTAACTGACGAGAGGATGATGATG 4320  
4261 ACTGCTCAGAGGCTATCTCTCAGAGTGAATTTTAACTGACGAGAGGATGATGATG 4320  
4281 ACTGCTCAGAGGCTATCTCTCAGAGTGAATTTTAACTGACGAGAGGATGATGATG 4320  
4281 ACTGCTCAGAGGCTATCTCTCAGAGTGAATTTTAACTGACGAGAGGATGATGATG 4320  
4321 AACATTAACCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 4380  
4321 AACATTAACCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 4380  
4381 ATGGAGGAGGCTTCTAAGGATGATGATGATGATGATGATGATGATGATGATGATG 4440  
4381 ATGGAGGAGGCTTCTAAGGATGATGATGATGATGATGATGATGATGATGATGATG 4440  
4441 ACCCTGCAAGATCAGAAACCAAGCAGATCAGAAACCAAGCAGATCAGAAACCAAG 4500  
4441 ACCCTGCAAGATCAGAAACCAAGCAGATCAGAAACCAAGCAGATCAGAAACCAAG 4500  
4501 GTGAATTAACCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 4560  
4501 GTGAATTAACCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 4560  
4561 CAGATAGTCTTCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 4620  
4561 CAGATAGTCTTCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 4620  
4621 GCCCATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4680  
4621 GCCCATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4680  
4681 ACTACCATCTTCAAGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 4740  
4681 ACTACCATCTTCAAGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 4740  
4741 AGTCTGGGCGACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4800  
4741 AGTCTGGGCGACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4800  
4801 CCCCTTACCTGGAATCTGGAATCAGGCTCTTCTGATGATGATGATGATGATGATG 4860  
4801 CCCCTTACCTGGAATCTGGAATCAGGCTCTTCTGATGATGATGATGATGATGATG 4860  
4861 AAGACAGAGGCGCAGAGTCAAGTCTGTTGGCAACATCAATCTTCAATCTTCAATG 4920  
4861 AAGACAGAGGCGCAGAGTCAAGTCTGTTGGCAACATCAATCTTCAATCTTCAATG 4920  
4881 AAGACAGAGGCGCAGAGTCAAGTCTGTTGGCAACATCAATCTTCAATCTTCAATG 4920  
4881 AAGACAGAGGCGCAGAGTCAAGTCTGTTGGCAACATCAATCTTCAATCTTCAATG 4920  
4921 AAGTCCCAATTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 4980  
4921 AAGTCCCAATTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 4980

4921 AAGTCCCAATTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 4980  
4981 AATCTGCTGGGTATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 5040  
4981 AATCTGCTGGGTATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 5040  
4981 AATCTGCTGGGTATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 5040  
5041 CTTCAACGAGAGGCTCAACAAAGATGATGATGATGATGATGATGATGATGATGATG 5100  
5041 CTTCAACGAGAGGCTCAACAAAGATGATGATGATGATGATGATGATGATGATGATG 5100  
5101 AATTTATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5160  
5101 AATTTATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5160  
5161 CTGAAGAGATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5220  
5161 CTGAAGAGATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5220  
5221 TGAATATTTTCTAGAAATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5280  
5221 TGAATATTTTCTAGAAATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5280  
5281 AGTCTATTTAAAGAAAGAAATGCTGAATGATGATGATGATGATGATGATGATGATG 5340  
5281 AGTCTATTTAAAGAAAGAAATGCTGAATGATGATGATGATGATGATGATGATGATG 5340  
5341 TCAATGAAGAAACCAACAGGATGATGATGATGATGATGATGATGATGATGATGATG 5400  
5341 TCAATGAAGAAACCAACAGGATGATGATGATGATGATGATGATGATGATGATGATG 5400  
5401 TCAAGGAGGCTGAATCTGATGATGATGATGATGATGATGATGATGATGATGATG 5460  
5401 TCAAGGAGGCTGAATCTGATGATGATGATGATGATGATGATGATGATGATGATG 5460  
5461 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5520  
5461 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5520  
5521 GCACAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5580  
5521 GCACAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5580  
5581 TCCATGCAATTTGGGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 5640  
5581 TCCATGCAATTTGGGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 5640  
5641 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5700  
5641 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5700  
5701 GCCACTACTGA 5711  
5701 GCCACTACTGA 5711

RESULT 3  
US-09-734-672-5  
Sequence 5, Application US/09734672  
Publication No. US20020183268A1  
GENERAL INFORMATION:  
APPLICANT: Murphy, Patricia D.  
Allen, Antoinette C.  
Alvares, Christopher P.  
Critz, Brenda S.  
Olson, Sheri J.  
Schelter, Denise B.  
Zeng, Bin  
TITLE OF INVENTION: Coding Sequences of the Human  
BRCA1 Gene  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morgan Lewis & Bockius LLP

STREET: 1111 Pennsylvania Ave., N.W.  
CITY: Washington  
STATE: District of Columbia  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/734,672  
FILING DATE: 03-Dec-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/966,436  
FILING DATE: 07-No. US20020183268A1-97  
APPLICATION NUMBER: US 08/598,591  
FILING DATE: 12-Feb-96  
ATTORNEY/AGENT INFORMATION:  
NAME: Michael S. Tuscan  
REGISTRATION NUMBER: 43,210  
REFERENCE/DOCKET NUMBER: 44921-5055-02-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-739-3000  
TELEFAX: 202-739-3001  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5711 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: No. US20020183268A1 Relevant  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
STRAIN: BRCA1  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17  
MAP POSITION: 17q21  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-734-672-5  
Query Match 100.0%; Score 5709.4; DB 10; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 AGCTGCTGAGACTCTCTGGAGCCCGGACACGAGCTGTGGGGTTTCTCAGATATCTAGGCGC 60  
DB 1 AGCTGCTGAGACTCTCTGGAGCCCGGACACGAGCTGTGGGGTTTCTCAGATATCTAGGCGC 60  
QY 61 CTTGGCTCAGAGGCTTCACTCTGCTCTGGTAAAGTTCATTGGAAACAGAAAGAA 120  
DB 61 CTTGGCTCAGAGGCTTCACTCTGCTCTGGTAAAGTTCATTGGAAACAGAAAGAA 120  
QY 121 TGGATTATCTGCTCTTGGCGTTGAAGAGTCAAAATGTCTATATGCTATGCAAAA 180  
DB 121 TGGATTATCTGCTCTTGGCGTTGAAGAGTCAAAATGTCTATATGCTATGCAAAA 180  
QY 121 TGGATTATCTGCTCTTGGCGTTGAAGAGTCAAAATGTCTATATGCTATGCAAAA 180  
DB 121 TGGATTATCTGCTCTTGGCGTTGAAGAGTCAAAATGTCTATATGCTATGCAAAA 180  
QY 181 TCTTAGAGTGTCCATCTGTCTGAGTTGATCAAGAACTGTCTCCCAAAAGTGTGACC 240  
DB 181 TCTTAGAGTGTCCATCTGTCTGAGTTGATCAAGAACTGTCTCCCAAAAGTGTGACC 240  
QY 181 TCTTAGAGTGTCCATCTGTCTGAGTTGATCAAGAACTGTCTCCCAAAAGTGTGACC 240  
DB 181 TCTTAGAGTGTCCATCTGTCTGAGTTGATCAAGAACTGTCTCCCAAAAGTGTGACC 240  
QY 241 ACATATTTTGGCAATTTTGGCATGTGAAACTTCTCAACAGAAAGAGGCTTCAACAGT 300  
DB 241 ACATATTTTGGCAATTTTGGCATGTGAAACTTCTCAACAGAAAGAGGCTTCAACAGT 300  
QY 241 ACATATTTTGGCAATTTTGGCATGTGAAACTTCTCAACAGAAAGAGGCTTCAACAGT 300  
DB 241 ACATATTTTGGCAATTTTGGCATGTGAAACTTCTCAACAGAAAGAGGCTTCAACAGT 300  
QY 301 GTCTTTATGTAGAATGATATTAACCAAAAGAGGCTTCAAGAAAGTACGAGATTAGTC 360  
DB 301 GTCTTTATGTAGAATGATATTAACCAAAAGAGGCTTCAAGAAAGTACGAGATTAGTC 360  
QY 301 GTCTTTATGTAGAATGATATTAACCAAAAGAGGCTTCAAGAAAGTACGAGATTAGTC 360  
DB 301 GTCTTTATGTAGAATGATATTAACCAAAAGAGGCTTCAAGAAAGTACGAGATTAGTC 360  
QY 361 AACTGTTGAAGAGCTATTTGAAATCATTTTGTGCTTTTCAAGTTGACAGAGTTGGAGT 420  
DB 361 AACTGTTGAAGAGCTATTTGAAATCATTTTGTGCTTTTCAAGTTGACAGAGTTGGAGT 420

QY 421 ATGCAGAGCTATATTTTGCAGAAAAAGAAATTAATCTCTCTGACATCTAAAGATG 480  
DB 421 ATGCAGAGCTATATTTTGCAGAAAAAGAAATTAATCTCTCTGACATCTAAAGATG 480  
QY 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTCCAAAGACTTCTACAGAGT 540  
DB 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTCCAAAGACTTCTACAGAGT 540  
QY 541 AACCCGAAATCTCTCTTGGAGGAAACCAAGTCTCAGTGTCCAACTCTTAACCTTGA 600  
DB 541 AACCCGAAATCTCTCTTGGAGGAAACCAAGTCTCAGTGTCCAACTCTTAACCTTGA 600  
QY 541 AACCCGAAATCTCTCTTGGAGGAAACCAAGTCTCAGTGTCCAACTCTTAACCTTGA 600  
DB 541 AACCCGAAATCTCTCTTGGAGGAAACCAAGTCTCAGTGTCCAACTCTTAACCTTGA 600  
QY 601 CTGTGAGAACTCTGAGACCAAGACCGGATACAACTCAAAAGACGTCTGTCTACATG 660  
DB 601 CTGTGAGAACTCTGAGACCAAGACCGGATACAACTCAAAAGACGTCTGTCTACATG 660  
QY 601 CTGTGAGAACTCTGAGACCAAGACCGGATACAACTCAAAAGACGTCTGTCTACATG 660  
DB 601 CTGTGAGAACTCTGAGACCAAGACCGGATACAACTCAAAAGACGTCTGTCTACATG 660  
QY 661 AATTGGATCTGATTTCTTCTGAAGTATACCGTTTATTAAGCACTTATTTGCGATGG 720  
DB 661 AATTGGATCTGATTTCTTCTGAAGTATACCGTTTATTAAGCACTTATTTGCGATGG 720  
QY 661 AATTGGATCTGATTTCTTCTGAAGTATACCGTTTATTAAGCACTTATTTGCGATGG 720  
DB 661 AATTGGATCTGATTTCTTCTGAAGTATACCGTTTATTAAGCACTTATTTGCGATGG 720  
QY 721 ATCAAGATTTGTCAATCAACCCCTCAAGGACCAAGGATGAATCAGTTTGAATCTG 780  
DB 721 ATCAAGATTTGTCAATCAACCCCTCAAGGACCAAGGATGAATCAGTTTGAATCTG 780  
QY 721 ATCAAGATTTGTCAATCAACCCCTCAAGGACCAAGGATGAATCAGTTTGAATCTG 780  
DB 721 ATCAAGATTTGTCAATCAACCCCTCAAGGACCAAGGATGAATCAGTTTGAATCTG 780  
QY 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGACGATGTAACTCAATCAATCATCAAC 840  
DB 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGACGATGTAACTCAATCAATCATCAAC 840  
QY 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGACGATGTAACTCAATCAATCATCAAC 840  
DB 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGACGATGTAACTCAATCAATCATCAAC 840  
QY 841 CCAATTAATGATTTTGAACACCACTGAGAAAGCGTGCAGCTGAGAGGATCCAGAAAAGT 900  
DB 841 CCAATTAATGATTTTGAACACCACTGAGAAAGCGTGCAGCTGAGAGGATCCAGAAAAGT 900  
QY 841 CCAATTAATGATTTTGAACACCACTGAGAAAGCGTGCAGCTGAGAGGATCCAGAAAAGT 900  
DB 841 CCAATTAATGATTTTGAACACCACTGAGAAAGCGTGCAGCTGAGAGGATCCAGAAAAGT 900  
QY 901 ATCAAGATTTGTCAATCAACCCCTCAAGGACCAAGGATGAATCAGTTTGAATCTG 960  
DB 901 ATCAAGATTTGTCAATCAACCCCTCAAGGACCAAGGATGAATCAGTTTGAATCTG 960  
QY 901 ATCAAGATTTGTCAATCAACCCCTCAAGGACCAAGGATGAATCAGTTTGAATCTG 960  
DB 901 ATCAAGATTTGTCAATCAACCCCTCAAGGACCAAGGATGAATCAGTTTGAATCTG 960  
QY 961 GCTCATTAACAGATGAGAACGAGTTTATTAATCACTAAAGACAGAAATGATAGAAA 1020  
DB 961 GCTCATTAACAGATGAGAACGAGTTTATTAATCACTAAAGACAGAAATGATAGAAA 1020  
QY 1021 AAGCTGAATTTCTGATATTAAGCAACAGCTGCTTGAAGAGGATCAATCAAGAT 1080  
DB 1021 AAGCTGAATTTCTGATATTAAGCAACAGCTGCTTGAAGAGGATCAATCAAGAT 1080  
QY 1021 AAGCTGAATTTCTGATATTAAGCAACAGCTGCTTGAAGAGGATCAATCAAGAT 1080  
DB 1021 AAGCTGAATTTCTGATATTAAGCAACAGCTGCTTGAAGAGGATCAATCAAGAT 1080  
QY 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGGCGGACTCCAGACAGAAAAAAGTAG 1140  
DB 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGGCGGACTCCAGACAGAAAAAAGTAG 1140  
QY 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGGCGGACTCCAGACAGAAAAAAGTAG 1140  
DB 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGGCGGACTCCAGACAGAAAAAAGTAG 1140  
QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGAAATAGAGAAATGCGCATGCT 1200  
DB 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGAAATAGAGAAATGCGCATGCT 1200  
QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGAAATAGAGAAATGCGCATGCT 1200  
DB 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGAAATAGAGAAATGCGCATGCT 1200  
QY 1201 CAGAGAACTCTAGAGATTAAGTAAGTATGTTCTTGGATTAACCTAAATGCGAGATTGCA 1260  
DB 1201 CAGAGAACTCTAGAGATTAAGTAAGTATGTTCTTGGATTAACCTAAATGCGAGATTGCA 1260  
QY 1201 CAGAGAACTCTAGAGATTAAGTAAGTATGTTCTTGGATTAACCTAAATGCGAGATTGCA 1260  
DB 1201 CAGAGAACTCTAGAGATTAAGTAAGTATGTTCTTGGATTAACCTAAATGCGAGATTGCA 1260  
QY 1261 AAGTTAATGAGTGGTTTCCAGAAAGTGAATGTAAGTGTGATGATGATCAATGATG 1320  
DB 1261 AAGTTAATGAGTGGTTTCCAGAAAGTGAATGTAAGTGTGATGATGATCAATGATG 1320  
QY 1261 AAGTTAATGAGTGGTTTCCAGAAAGTGAATGTAAGTGTGATGATGATCAATGATG 1320  
DB 1261 AAGTTAATGAGTGGTTTCCAGAAAGTGAATGTAAGTGTGATGATGATCAATGATG 1320  
QY 1321 GGGAGTCTGAATCAAAATGCCAAAGTGAATGTAATGGAAGTTCTAAATAGGATAGT 1380  
DB 1321 GGGAGTCTGAATCAAAATGCCAAAGTGAATGTAATGGAAGTTCTAAATAGGATAGT 1380  
QY 1321 GGGAGTCTGAATCAAAATGCCAAAGTGAATGTAATGGAAGTTCTAAATAGGATAGT 1380  
DB 1321 GGGAGTCTGAATCAAAATGCCAAAGTGAATGTAATGGAAGTTCTAAATAGGATAGT 1380  
QY 1381 AATATTTCTGTTCTTCAAGAGAAATAGACTTAATGAGTATGATGATGATGATGAT 1440  
DB 1381 AATATTTCTGTTCTTCAAGAGAAATAGACTTAATGAGTATGATGATGATGATGATGAT 1440  
QY 1381 AATATTTCTGTTCTTCAAGAGAAATAGACTTAATGAGTATGATGATGATGATGATGAT 1440  
DB 1381 AATATTTCTGTTCTTCAAGAGAAATAGACTTAATGAGTATGATGATGATGATGATGAT 1440  
QY 1441 TATGTAAGAGTGAAGGATGATCACTCAATATGATGAGAGTAAATATGAAACAAATAT 1500  
DB 1441 TATGTAAGAGTGAAGGATGATCACTCAATATGATGAGAGTAAATATGAAACAAATAT 1500  
QY 1441 TATGTAAGAGTGAAGGATGATCACTCAATATGATGAGAGTAAATATGAAACAAATAT 1500  
DB 1441 TATGTAAGAGTGAAGGATGATCACTCAATATGATGAGAGTAAATATGAAACAAATAT 1500  
QY 1501 TTGGAAAACTATTCGAAAGGCAAGCTCCCAACTTAAGCATGTAATGTAATG 1560

Db 1501 TTGGAAAACTTATCGAAGAGGAGCCTCCCACTTAAGCATTTAATGTAATC 1560  
Qy 1561 TAATTATATGAGCAATTTGTTACTGAGCCAAGATATATCAAGAGGTCCTCCACAAATA 1620  
Db 1561 TAATTATATGAGCAATTTGTTACTGAGCCAAGATATATCAAGAGGTCCTCCACAAATA 1620  
Qy 1621 AATTAAAGCGTAAAGAGAGCCTCATGAGGCTTCATCTGAGGATTTTATCAAGAAAG 1680  
Db 1621 AATTAAAGCGTAAAGAGAGCCTCATGAGGCTTCATCTGAGGATTTTATCAAGAAAG 1680  
Qy 1681 CAGATTTGGCAGTTCAAAAGACTCCTGAAATGATTAATCAAGGAACTAACCAGAGAGC 1740  
Db 1681 CAGATTTGGCAGTTCAAAAGACTCCTGAAATGATTAATCAAGGAACTAACCAGAGAGC 1740  
Qy 1741 AGAATGGTCAGATGATGATTAATTAATTAAGTGTATGAGATTAACAAAGGTGATT 1800  
Db 1741 AGAATGGTCAGATGATGATTAATTAATTAAGTGTATGAGATTAACAAAGGTGATT 1800  
Qy 1801 CTATTCAGATGAGAAAAATCTTAACCAATGAAATCTCGAAAAAGAAATCTGTTTCA 1860  
Db 1801 CTATTCAGATGAGAAAAATCTTAACCAATGAAATCTCGAAAAAGAAATCTGTTTCA 1860  
Qy 1861 AAACGAAAGCTGAACCTTAAGCAGCAGTATATGCAATATGGAATCTCGAATTAATATCC 1920  
Db 1861 AAACGAAAGCTGAACCTTAAGCAGCAGTATATGCAATATGGAATCTCGAATTAATATCC 1920  
Qy 1921 ACAATTCAAAAGCACTTAAGAAATAGGCTGAGAGAGAGTCTTCTACAGAGCATATTC 1980  
Db 1921 ACAATTCAAAAGCACTTAAGAAATAGGCTGAGAGAGAGTCTTCTACAGAGCATATTC 1980  
Qy 1981 ATGGCTTGAATCTAGTACTGATGAGAAATCTTAAGCCCACTTAATGTAATGTAATTCGAAA 2040  
Db 1981 ATGGCTTGAATCTAGTACTGATGAGAAATCTTAAGCCCACTTAATGTAATGTAATTCGAAA 2040  
Qy 2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAAAGTACCAACCAATATGCGAGTCA 2100  
Db 2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAAAGTACCAACCAATATGCGAGTCA 2100  
Qy 2101 GGCAACAGAGAAAACCTACAACTCATGGAAGGTAAAGAACTGCAACTGAGGCAAGAAAG 2160  
Db 2101 GGCAACAGAGAAAACCTACAACTCATGGAAGGTAAAGAACTGCAACTGAGGCAAGAAAG 2160  
Qy 2161 GTAAACAGCCAAATGTAACAGACAGTAAAGACATGACAGTATCTTTCCAGAGCTGA 2220  
Db 2161 GTAAACAGCCAAATGTAACAGACAGTAAAGACATGACAGTATCTTTCCAGAGCTGA 2220  
Qy 2221 AGTTAAACAATGCACTGGTCTTTTACTTAAGTGTCAAAATCAAGTGAATCTTAAGAAAT 2280  
Db 2221 AGTTAAACAATGCACTGGTCTTTTACTTAAGTGTCAAAATCAAGTGAATCTTAAGAAAT 2280  
Qy 2281 TTGTCAATCTTAGCTTCAAGAGAGAAAGAAAGAAAGAACTAGAAAAGTTAAAGTGT 2340  
Db 2281 TTGTCAATCTTAGCTTCAAGAGAGAAAGAAAGAAAGAAAGAAAGTTAAAGTGT 2340  
Qy 2341 CTAATTAATGCTGAGAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTCGAACTG 2400  
Db 2341 CTAATTAATGCTGAGAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTCGAACTG 2400  
Qy 2401 AAAAGTCTGAGAGAGTGAAGTGAATTTGCACTGGTACTGGTACTGATTAAGGCACTCAGG 2460  
Db 2401 AAAAGTCTGAGAGAGTGAAGTGAATTTGCACTGGTACTGGTACTGATTAAGGCACTCAGG 2460  
Qy 2461 AAAGATCTCGTTACTGGAAGTTAGCACTTAAGGAGGCAAAAACAGAACCAAAATAAT 2520  
Db 2461 AAAGATCTCGTTACTGGAAGTTAGCACTTAAGGAGGCAAAAACAGAACCAAAATAAT 2520  
Qy 2521 GTGTAGTCAAGTGTGCAAGCATTTGAAAACCCCAAGGACTAATTCATGGTGTCCAAAG 2580  
Db 2521 GTGTAGTCAAGTGTGCAAGCATTTGAAAACCCCAAGGACTAATTCATGGTGTCCAAAG 2580  
Qy 2581 ATTAATGAAATGACACAGAGGCTTTAAGTATCCATTGGGACATGAAAGTTAACACAGATC 2640  
Db 2581 ATTAATGAAATGACACAGAGGCTTTAAGTATCCATTGGGACATGAAAGTTAACACAGATC 2640

Db 2581 ATTAATGAAATGACACAGAGGCTTTAAGTATCCATTGGGACATGAAAGTTAACACAGATC 2640  
Qy 2641 GGGAAACAGAGATGAATGGAAGAGTGAATGATGTCAGATTTGAGATATCAT 2700  
Db 2641 GGGAAACAGAGATGAATGGAAGAGTGAATGATGTCAGATTTGAGATATCAT 2700  
Qy 2701 TCAAGTTTCAAAAGCGCAGTCAATTTGCTCTGTTTCAATTCAGAAATCAGAAAGG 2760  
Db 2701 TCAAGTTTCAAAAGCGCAGTCAATTTGCTCTGTTTCAATTCAGAAATCAGAAAGG 2760  
Qy 2761 AATGTGCAACATCTCTGCCCATCTGAGCTCTTAAGAAACAAAGTCCAAAGTCACTT 2820  
Db 2761 AATGTGCAACATCTCTGCCCATCTGAGCTCTTAAGAAACAAAGTCCAAAGTCACTT 2820  
Qy 2821 TTGAATGTGAACAAAGGAAAGAAATCAAGAAAGAAAGTCAATTAATCAAGCTGTAC 2880  
Db 2821 TTGAATGTGAACAAAGGAAAGAAATCAAGAAAGAAAGTCAATTAATCAAGCTGTAC 2880  
Qy 2881 AGACAGTTAATATCACTGCAAGCTTTCTGAGTGTGTCAGAAAGATTAAGCAGTTGATA 2940  
Db 2881 AGACAGTTAATATCACTGCAAGCTTTCTGAGTGTGTCAGAAAGATTAAGCAGTTGATA 2940  
Qy 2941 ATGCCAAATGTATATCAAGAGAGCTTAGGTTTGTCTATCATCTCAGTTCAAGAGCA 3000  
Db 2941 ATGCCAAATGTATATCAAGAGAGCTTAGGTTTGTCTATCATCTCAGTTCAAGAGCA 3000  
Qy 3001 ACGAACTGACCTATTAATCTCAAAATTAACATGCACTTTTCAAAAACCAATATCTATAC 3060  
Db 3001 ACGAACTGACCTATTAATCTCAAAATTAACATGCACTTTTCAAAAACCAATATCTATAC 3060  
Qy 3061 CACCACTTTTCCATCAAGTCAATTTGTTAAACAAATGTAAGAAATCTGCTAGAGG 3120  
Db 3061 CACCACTTTTCCATCAAGTCAATTTGTTAAACAAATGTAAGAAATCTGCTAGAGG 3120  
Qy 3121 AAAACTTTGAGAAACATTCATTAATGTCACCTGAAGAGAAATGGAATAGAAATCTTCAA 3180  
Db 3121 AAAACTTTGAGAAACATTCATTAATGTCACCTGAAGAGAAATGGAATAGAAATCTTCAA 3180  
Qy 3181 GTACAGTGAACAAATTAAGCCGTATTAACATTAAGAAATGTTTAAAGAGCAGCT 3240  
Db 3181 GTACAGTGAACAAATTAAGCCGTATTAACATTAAGAAATGTTTAAAGAGCAGCT 3240  
Qy 3241 CAAGCAATTAATTAAGTAAGTTCACAGTACTAATGAAGTGGGCTCCAGTTTAATGAAA 3300  
Db 3241 CAAGCAATTAATTAAGTAAGTTCACAGTACTAATGAAGTGGGCTCCAGTTTAATGAAA 3300  
Qy 3301 TAGGTTCCAGTGAAGAAACATTCAGAGCAACTAGTGAAGAAACAGAGGCAAAATTTGA 3360  
Db 3301 TAGGTTCCAGTGAAGAAACATTCAGAGCAACTAGTGAAGAAACAGAGGCAAAATTTGA 3360  
Qy 3361 ATGCTATGCTTAGATTAGGGGTTTGGAACTGAGGCTTATTAACAAAGTCTTCTGAAA 3420  
Db 3361 ATGCTATGCTTAGATTAGGGGTTTGGAACTGAGGCTTATTAACAAAGTCTTCTGAAA 3420  
Qy 3421 GTAATTTGAACATCTTAATTAAGAAAGCAAGAAATGAAGAAAGTACTGAGATGTA 3480  
Db 3421 GTAATTTGAACATCTTAATTAAGAAAGCAAGAAATGAAGAAAGTACTGAGATGTA 3480  
Qy 3481 ATACAGATTTCTCTCCATATCTGATTTAGATTAAGTGAAGAGGCTTATGGAATAGTTC 3540  
Db 3481 ATACAGATTTCTCTCCATATCTGATTTAGATTAAGTGAAGAGGCTTATGGAATAGTTC 3540  
Qy 3541 AATGCATCTCAGGTTGTTCTGAGACACTGTATGACCTGTATGATGATGAGTGAATAAAG 3600  
Db 3541 AATGCATCTCAGGTTGTTCTGAGACACTGTATGACCTGTATGATGATGAGTGAATAAAG 3600  
Qy 3601 AAAGATCTAGTTTGTCTGAAATGAACATTAAGGAAAGTTCGCTGTTTTCGAAAGAGC 3660  
Db 3601 AAAGATCTAGTTTGTCTGAAATGAACATTAAGGAAAGTTCGCTGTTTTCGAAAGAGC 3660  
Qy 3661 TCCAGAGAGAGAGCTTAGCAGAGAGTCTAGCCCTTTACACCATACATTTGGCTCAGG 3720  
Db 3661 TCCAGAGAGAGAGCTTAGCAGAGAGTCTAGCCCTTTACACCATACATTTGGCTCAGG 3720

QY 3721 GTTACGAAGAGGGGCAAGAAATTAGAGTCTCAGAGAGAACTTATCTAGTGAAGT 3780  
DB 3721 GTTACGAAGAGGGGCAAGAAATTAGAGTCTCAGAGAGAACTTATCTAGTGAAGT 3780  
QY 3781 AAGAGCTTCCCTGCTTCCAACTGTTATTTGGTAAAGTAAACAAATATACCTTCTCAGT 3840  
DB 3781 AAGAGCTTCCCTGCTTCCAACTGTTATTTGGTAAAGTAAACAAATATACCTTCTCAGT 3840  
QY 3841 CTACTAGGCATAGCAACCGTGTCTACGAGTGTCTGTCTAAGAACACAGAGAAATTTAT 3900  
DB 3841 CTACTAGGCATAGCAACCGTGTCTACGAGTGTCTGTCTAAGAACACAGAGAAATTTAT 3900  
QY 3901 TATCATTTGAGAAATAGTTAAATGACTGCACTGCAATACAGGTAAATTTGGCAAGCATCTC 3960  
DB 3901 TATCATTTGAGAAATAGTTAAATGACTGCACTGCAATACAGGTAAATTTGGCAAGCATCTC 3960  
QY 3961 AGGAACTACCTTATGTAAGAGAAACAAATGTTCTGTAGCTGTTTTCTTCAAGTCA 4020  
DB 3961 AGGAACTACCTTATGTAAGAGAAACAAATGTTCTGTAGCTGTTTTCTTCAAGTCA 4020  
QY 4021 GTGAATTGGAAGACTTGACTGCAATACAAACCCAGAGATCCCTTTCTTGATTTGTTCTT 4080  
DB 4021 GTGAATTGGAAGACTTGACTGCAATACAAACCCAGAGATCCCTTTCTTGATTTGTTCTT 4080  
QY 4081 CCAAAACAATGAGGATCATGCTGAAAGCCAGGAGTTGCTGTAGTGAACAAGAAATTGG 4140  
DB 4081 CCAAAACAATGAGGATCATGCTGAAAGCCAGGAGTTGCTGTAGTGAACAAGAAATTGG 4140  
QY 4141 TTTGATGATGTAAGAAAGAGAGCGGCTTGAAGAAATATATCAAGAAAGCAACCA 4200  
DB 4141 TTTGATGATGTAAGAAAGAGAGCGGCTTGAAGAAATATATCAAGAAAGCAACCA 4200  
QY 4201 TGGATTCAACTTGAAGTGAAGAGATCTGGGTGTAAGTGAAGCAAGCGCTCTGAG 4260  
DB 4201 TGGATTCAACTTGAAGTGAAGAGATCTGGGTGTAAGTGAAGCAAGCGCTCTGAG 4260  
QY 4261 ACTGCTCAGGCTATCTCTCAGAGTGAATTTTAACTCAGCAGAGAGATACATATC 4320  
DB 4261 ACTGCTCAGGCTATCTCTCAGAGTGAATTTTAACTCAGCAGAGAGATACATATC 4320  
QY 4321 AACATTAACCTTAATAAGCTCCAGCAGAAATGGCTGAATAGAGCTGTGTTAGAACGC 4380  
DB 4321 AACATTAACCTTAATAAGCTCCAGCAGAAATGGCTGAATAGAGCTGTGTTAGAACGC 4380  
QY 4381 ATGGAGGACGCTTCTTAACAGCTACCTTCCATATTAAGTGAATCTCTGCTTGAAG 4440  
DB 4381 ATGGAGGACGCTTCTTAACAGCTACCTTCCATATTAAGTGAATCTCTGCTTGAAG 4440  
QY 4441 ACTGCGAAATTCAGAAACAAAGCATCAGAAAGAGAGTATTAATCTTCAAGAAAGTA 4500  
DB 4441 ACTGCGAAATTCAGAAACAAAGCATCAGAAAGAGAGTATTAATCTTCAAGAAAGTA 4500  
QY 4501 GTGAATACCTTAATAAGCCAGAAATCCAGAGGCTTTCTGTGCAAGATTTGAGTGTCTG 4560  
DB 4501 GTGAATACCTTAATAAGCCAGAAATCCAGAGGCTTTCTGTGCAAGATTTGAGTGTCTG 4560  
QY 4561 CAGATAGTTCTTAACAGTAAATTAAGAACCAAGAGTGAAGAGTCAATCCCTCTTAAT 4620  
DB 4561 CAGATAGTTCTTAACAGTAAATTAAGAACCAAGAGTGAAGAGTCAATCCCTCTTAAT 4620  
QY 4621 GCCCATCATTAAGATAGTGTGATCATGCAAGTTGCTTGGAGTCTTCAAGATTAAGA 4680  
DB 4621 GCCCATCATTAAGATAGTGTGATCATGCAAGTTGCTTGGAGTCTTCAAGATTAAGA 4680  
QY 4681 ACTACCATCTCAAGAGAGCTCATTAAGTGTGATGATGTAAGAGCAAGCTGGAAG 4740  
DB 4681 ACTACCATCTCAAGAGAGCTCATTAAGTGTGATGATGTAAGAGCAAGCTGGAAG 4740  
QY 4741 AGTCTGGGCAACGATTTGAAGGAAACATCTTAATTTCCCAAGGCAAGATCTAGAGGGA 4800  
DB 4741 AGTCTGGGCAACGATTTGAAGGAAACATCTTAATTTCCCAAGGCAAGATCTAGAGGGA 4800

QY 4801 CCCCTTACTGGAATCTGAATCATGACCTCTTCTGTGATGACCTTGAATCTGATCTTCTG 4860  
DB 4801 CCCCTTACTGGAATCTGAATCATGACCTCTTCTGTGATGACCTTGAATCTGATCTTCTG 4860  
QY 4861 AAGACAGAGCCCAAGAGTCACTGCTGTGTGGCAATATCCATCTTCAACCTCTGCAATGA 4920  
DB 4861 AAGACAGAGCCCAAGAGTCACTGCTGTGTGGCAATATCCATCTTCAACCTCTGCAATGA 4920  
QY 4921 AAGTTCCTCCATTAAGAGTTGCAAAATCTGCCCAGGGGTCGAGCTGCTGATCTACTG 4980  
DB 4921 AAGTTCCTCCATTAAGAGTTGCAAAATCTGCCCAGGGGTCGAGCTGCTGATCTACTG 4980  
QY 4981 ATACTGCTGGTATTAATGCAATGGAAGAAAGTGTGAGCAGGAGAGCAAGCAATTTGACAG 5040  
DB 4981 ATACTGCTGGTATTAATGCAATGGAAGAAAGTGTGAGCAGGAGAGCAAGCAATTTGACAG 5040  
QY 5041 CTTCAACAGAAAGGTCACAAAGAAATGTCATGCTGTGTGTCTGCTGACCCAGAG 5100  
DB 5041 CTTCAACAGAAAGGTCACAAAGAAATGTCATGCTGTGTGTCTGCTGACCCAGAG 5100  
QY 5101 AATTATGCTGTGTGTAAGTTGCGCAAGAAACCAATCACTTAACTTAATCTAATTA 5160  
DB 5101 AATTATGCTGTGTGTAAGTTGCGCAAGAAACCAATCACTTAACTTAATCTAATTA 5160  
QY 5161 CTGAAGAGACTCACTCATGTTGTTATGAAACAGATGCTGAGTTGTGTGTAACGACAC 5220  
DB 5161 CTGAAGAGACTCACTCATGTTGTTATGAAACAGATGCTGAGTTGTGTGTAACGACAC 5220  
QY 5221 TGAATATTTTCTAGAAATTTGCGGAGAGAAATGGGTATGCTATTTCTGGGTGACCC 5280  
DB 5221 TGAATATTTTCTAGAAATTTGCGGAGAGAAATGGGTATGCTATTTCTGGGTGACCC 5280  
QY 5281 AGTCTATTAAGAAAGAAATATGCTGAATGAGCATGATTTGAAGTCAAGAGAAATGGG 5340  
DB 5281 AGTCTATTAAGAAAGAAATATGCTGAATGAGCATGATTTGAAGTCAAGAGAAATGGG 5340  
QY 5341 TCAATGGAAGAAACCAACCAAGTCCAAAGCGAGCAAGAGATCCAGAGCAAGAAATCT 5400  
DB 5341 TCAATGGAAGAAACCAACCAAGTCCAAAGCGAGCAAGAGATCCAGAGCAAGAAATCT 5400  
QY 5401 TCAGGGGCTTAAGAAATCTGTTGCTATGAGGCTTTCACCAATGCTCCACAGATCAACTGG 5460  
DB 5401 TCAGGGGCTTAAGAAATCTGTTGCTATGAGGCTTTCACCAATGCTCCACAGATCAACTGG 5460  
QY 5461 AATGATGATGACACTGTGTGTGCTTCTGTGTGAAGAGAGCTTTCATCATCTCACCTTG 5520  
DB 5461 AATGATGATGACACTGTGTGTGCTTCTGTGTGAAGAGAGCTTTCATCATCTCACCTTG 5520  
QY 5521 GCACAGGTGTCACCAATTTGTGTGTGACAGCAGATGCTTGACAGAGCAATGGCT 5580  
DB 5521 GCACAGGTGTCACCAATTTGTGTGTGACAGCAGATGCTTGACAGAGCAATGGCT 5580  
QY 5581 TCATGCAATTTGGCAGATGTGTGAGGACACTGTGTGACCCGAGAGTGGGTGTTGACA 5640  
DB 5581 TCATGCAATTTGGCAGATGTGTGAGGACACTGTGTGACCCGAGAGTGGGTGTTGACA 5640  
QY 5641 GTGTAGCACTCTACAGTGCAGAGAGCTGGAACACTTACCTGATCCCAAGATCCCAACA 5700  
DB 5641 GTGTAGCACTCTACAGTGCAGAGAGCTGGAACACTTACCTGATCCCAAGATCCCAACA 5700  
QY 5701 GCCACTACTGA 5711  
DB 5701 GCCACTACTGA 5711

RESULT 4  
US-09-982-828-3  
; Sequence 3, Application US/09982828  
; Publication No. US20030022184A1  
; GENERAL INFORMATION:  
; APPLICANT: Murphy, Patricia D.  
; Allen, Antoinette C.  
; Alvares, Christopher P.

Critz, Brenda S.  
Olson, Sheri J.  
Thurber, Denise  
Zeng, Bin

TITLE OF INVENTION: Coding Sequences of the Human  
BRCA1 Gene

NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morgan Lewis & Bockius LLP  
STREET: 1111 Pennsylvania Avenue N. W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20004

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/982,828  
FILING DATE: 22-Oct-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/074,453  
FILING DATE: 1998-05-06  
APPLICATION NUMBER: US 08/798,691  
FILING DATE: 1997-02-12  
APPLICATION NUMBER: US 08/598,591  
FILING DATE: 1996-02-12  
ATTORNEY/AGENT INFORMATION:  
NAME: Michael S. Tuscan  
REGISTRATION NUMBER: 43,210  
REFERENCE/DOCKET NUMBER: 44921-5053-01-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-739-3000  
TELEFAX: 202-739-3001

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5711 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear

MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
STRAIN: BRCA1 (om12)  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17  
MAP POSITION: 17q21

SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-982-828-3

Query Match 100.0%; Score 5709.4; DB 11; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCTGCTGAGACTTCTGGAACCCGCAACAGGCTGTGGGTTTCTCAGATTAATGAGCC 60  
DB 1 AGCTGCTGAGACTTCTGGAACCCGCAACAGGCTGTGGGTTTCTCAGATTAATGAGCC 60

QY 61 CCTGGCTCAGAGAGCCTTCAACCTCTGCTCTGGTAAAGTTCAATTGGAACGAAAGAAA 120  
DB 61 CCTGGCTCAGAGAGCCTTCAACCTCTGCTCTGGTAAAGTTCAATTGGAACGAAAGAAA 120

QY 121 TGGATTATCTGCTCTTGGCGTTGAAGAAGTCAAAATGTCATTAATGCTATGACGAGAAA 180  
DB 121 TGGATTATCTGCTCTTGGCGTTGAAGAAGTCAAAATGTCATTAATGCTATGACGAGAAA 180

QY 181 TCTTAGAGTGTCCATCTGTCTGAGATTGATCAAGAACTGTCTTCCAAGAGTGTGACC 240  
DB 181 TCTTAGAGTGTCCATCTGTGTGAGATTGATCAAGAACTGTCTTCCAAGAGTGTGACC 240

QY 241 ACATATTTTGCAGAAATTTTGCATGCTGAAACTTCTCAACCAAGAGAAAGGCGCTTACAGT 300  
DB 241 ACATATTTTGCAGAAATTTTGCATGCTGAAACTTCTCAACCAAGAGAAAGGCGCTTACAGT 300

QY 301 GTCCCTTATGTAAAGATGATTAACCAAGAGCGCTTCAAGAAAGTACGAGATTAGTC 360  
DB 301 GTCCCTTATGTAAAGATGATTAACCAAGAGCGCTTCAAGAAAGTACGAGATTAGTC 360

QY 361 AACTTGTGAAGACTATGTAAGAAATTTGCTGCTTTCAGCTTGACACAGGTTTGAGT 420  
DB 361 AACTTGTGAAGACTATGTAAGAAATTTGCTGCTTTCAGCTTGACACAGGTTTGAGT 420

QY 421 ATGCAAAAGCTATATTTTGCAGAAAGAAATTAATCTCTCTGAAATCTAAAGATG 480  
DB 421 ATGCAAAAGCTATATTTTGCAGAAAGAAATTAATCTCTCTGAAATCTAAAGATG 480

QY 481 AAGTTTCTATCATCCAAAGTATGAGGCTACAGAAACCGTGCCAAAGACTTCTACAGATG 540  
DB 481 AAGTTTCTATCATCCAAAGTATGAGGCTACAGAAACCGTGCCAAAGACTTCTACAGATG 540

QY 541 AACCAGAAATCCCTTCTGAGAGAAACCACTCTCAGTCCCACTCTTAACCTTGGAA 600  
DB 541 AACCAGAAATCCCTTCTGAGAGAAACCACTCTCAGTCCCACTCTTAACCTTGGAA 600

QY 601 CTGTGAGAACTCTGAGAGCAAGCAGCGGATACAACTCAAAAGACGTCTGTCTACATTG 660  
DB 601 CTGTGAGAACTCTGAGAGCAAGCAGCGGATACAACTCAAAAGACGTCTGTCTACATTG 660

QY 661 AATTGGATCTGATTCCTCTGAGAGTACCGTTAAATAGGCAACTTATTCAGTGTGGAG 720  
DB 661 AATTGGATCTGATTCCTCTGAGAGTACCGTTAAATAGGCAACTTATTCAGTGTGGAG 720

QY 721 ATCAAGAAATTTGTACAAATCACCCCTCAAGAACCAAGGATGAAATCATGTTGATCTG 780  
DB 721 ATCAAGAAATTTGTACAAATCACCCCTCAAGAACCAAGGATGAAATCATGTTGATCTG 780

QY 781 CAAAAAGGCTGCTGTGAAATTTTCTGAGAGGATGTAACTAATCTAATCATCAAC 840  
DB 781 CAAAAAGGCTGCTGTGAAATTTTCTGAGAGGATGTAACTAATCTAATCATCAAC 840

QY 841 CCAGTAATATGATTTTGAACCACTGAGAGCGTGACGTGAGAGGATCCAGAAAAGT 900  
DB 841 CCAGTAATATGATTTTGAACCACTGAGAGCGTGAGAGGATCCAGAAAAGT 900

QY 901 ATCAAGGATGTTCTGTTTCAAACTTGCATGTGAGCCATGTGGCAAAATCTCATGCCA 960  
DB 901 ATCAAGGATGTTCTGTTTCAAACTTGCATGTGAGCCATGTGGCAAAATCTCATGCCA 960

QY 961 GCTCATTTACAGCATGAGAACAGAGTTTATTAATCTCACTAAAGACGAATGATGAGAA 1020  
DB 961 GCTCATTTACAGCATGAGAACAGAGTTTATTAATCTCACTAAAGACGAATGATGAGAA 1020

QY 1021 AGGCTGAATTTCTGTATATTAAGCAAAACAGCTGTGCTTGAAGAGCCAACTAACAGAT 1080  
DB 1021 AGGCTGAATTTCTGTATATTAAGCAAAACAGCTGTGCTTGAAGAGCCAACTAACAGAT 1080

QY 1081 GGGCTGAGAGTAAAGAAACATGTATGATGATGAGCGGACTCCAGACACAAAAAAGGTAG 1140  
DB 1081 GGGCTGAGAGTAAAGAAACATGTATGATGATGATGAGCGGACTCCAGACACAAAAAAGGTAG 1140

QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGGAATGAGCAAACTGCCATGCT 1200  
DB 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGGAATGAGCAAACTGCCATGCT 1200

QY 1201 CAGAGAAATCTTGAAGATCTGAAGATGTTCTCTGGAATTAACCTAAATGACAGCATTCAGA 1260  
DB 1201 CAGAGAAATCTTGAAGATCTGAAGATGTTCTCTGGAATTAACCTAAATGACAGCATTCAGA 1260

QY 1261 AAGTTAATGAGTGTGTTTCCAGAGATGATGAACCTTTAGTTCTGATGATCACTGATG 1320  
DB 1261 AAGTTAATGAGTGTGTTTCCAGAGATGATGAACCTTTAGTTCTGATGATCACTGATG 1320

QY 1321 GGGAGTCTGAATCAAATCCCAAGATGATGATGATGAGAGTCTTAATAGATGATG 1380

1321 GGGAGTCTGAATCAATGCAGAAAGTAGCTGATGATTTGGAAGCTTCTAATATGAGTAGATG 1380  
1381 AATATTCGTGTTCTTCAGAGAAATATGACTTATCGCCAGATATCTCTATGAGGCTTTAA 1440  
1381 AATATTCGTGTTCTTCAGAGAAATATGACTTATCGCCAGATATCTCTATGAGGCTTTAA 1440  
1441 TATGTAAAGTGAAGAGTTCACCTCAATCAGTAGAGTAAATTTTGAAGCAAAATAT 1500  
1441 TATGTAAAGTGAAGAGTTCACCTCAATCAGTAGAGTAAATTTTGAAGCAAAATAT 1500  
1501 TTGGAAAACTATCGAAGAAAGGCAAGCTTCCCACTTAAAGCATGTAACTGAAAAATC 1560  
1501 TTGGAAAACTATCGAAGAAAGGCAAGCTTCCCACTTAAAGCATGTAACTGAAAAATC 1560  
1561 TAAATATGAGGACATTTGTTACTGAGCCAGATATTAACAAGAGTCCCTCAAAATA 1620  
1561 TAAATATGAGGACATTTGTTACTGAGCCAGATATTAACAAGAGTCCCTCAAAATA 1620  
1621 AATTAAGCGTAAAGAGACCTATCATCAGGCTTCATCTGAGGATTTTATCAAGAAG 1680  
1621 AATTAAGCGTAAAGAGACCTATCATCAGGCTTCATCTGAGGATTTTATCAAGAAG 1680  
1661 CAGATTTGGCAGTTCAAAAAGACTCCTGAATGATTAATCAAGGAACTAACCAAGAGC 1740  
1661 CAGATTTGGCAGTTCAAAAAGACTCCTGAATGATTAATCAAGGAACTAACCAAGAGC 1740  
1741 AGAATGGTCAAGTGTGAATTAATTAATATGATGATCAAGAAATTAACCAAGGATTT 1800  
1741 AGAATGGTCAAGTGTGAATTAATTAATATGATGATCAAGAAATTAACCAAGGATTT 1800  
1801 CTATTCAGATGAGAAAAATCCTAACCAATGATCACTCGAAAAAAGATCTGTTTCA 1860  
1801 CTATTCAGATGAGAAAAATCCTAACCAATGATCACTCGAAAAAAGATCTGTTTCA 1860  
1861 AAACGAAGCTGAACTTAAAGCAGAGATTAAGCAATATGGAATCTGAATTAATATTC 1920  
1861 AAACGAAGCTGAACTTAAAGCAGAGATTAAGCAATATGGAATCTGAATTAATATTC 1920  
1921 ACAATTCAAAAGCACTTAAAGCAAGATTAAGCAAGATTAAGCAAGATTAAGCAAGATTC 1980  
1921 ACAATTCAAAAGCACTTAAAGCAAGATTAAGCAAGATTAAGCAAGATTAAGCAAGATTC 1980  
1921 ACAATTCAAAAGCACTTAAAGCAAGATTAAGCAAGATTAAGCAAGATTAAGCAAGATTC 1980  
1981 ATGCGCTTGAACCTAGTAGTCAAGTAAATCTAAGCCCACTAATTTGACTGATTTGCAAA 2040  
1981 ATGCGCTTGAACCTAGTAGTCAAGTAAATCTAAGCCCACTAATTTGACTGATTTGCAAA 2040  
2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAAAAGTCAACCAAAATGCCAGTCA 2100  
2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAAAAGTCAACCAAAATGCCAGTCA 2100  
2101 GGCACAGAGAAACCTAACAATCATGGAAGATTAAGAACTCTGCACTGAGCCCAAGAA 2160  
2101 GGCACAGAGAAACCTAACAATCATGGAAGATTAAGAACTCTGCACTGAGCCCAAGAA 2160  
2101 GGCACAGAGAAACCTAACAATCATGGAAGATTAAGAACTCTGCACTGAGCCCAAGAA 2160  
2161 GTAAACAAGCCAAATGAACAGACAAAGTAAAGACATGACAGTATCTTTCCAGAGCTGA 2220  
2161 GTAAACAAGCCAAATGAACAGACAAAGTAAAGACATGACAGTATCTTTCCAGAGCTGA 2220  
2161 GTAAACAAGCCAAATGAACAGACAAAGTAAAGACATGACAGTATCTTTCCAGAGCTGA 2220  
2221 AGTTAAACAATGACCTGTTCTTTTACTAAGTTCAAATACAGTGAACCTTAAAGAT 2280  
2221 AGTTAAACAATGACCTGTTCTTTTACTAAGTTCAAATACAGTGAACCTTAAAGAT 2280  
2281 TTGTCAATCTTACCTTCCAGAGAAAGAAAGAAAGAACTAAGAACTTAAAGAT 2340  
2281 TTGTCAATCTTACCTTCCAGAGAAAGAAAGAAAGAACTAAGAACTTAAAGAT 2340  
2341 CTAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTCAGAACTG 2400  
2341 CTAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTCAGAACTG 2400  
2401 AAAGATCTGTAAGAGTAGAGATTTTCACTGTAAGCTGTAAGTATTTGCACTCAG 2460  
2401 AAAGATCTGTAAGAGTAGAGATTTTCACTGTAAGCTGTAAGTATTTGCACTCAG 2460

2401 AAAGATCTGTAAGAGTAGAGATTTTCACTGTAAGCTGTAAGTATTTGCACTCAG 2460  
2461 AAAGATCTGTTATCGGAAGTATGACCTTAAGGAAGGCAAAACGAACCAATTAAT 2520  
2461 AAAGATCTGTTATCGGAAGTATGACCTTAAGGAAGGCAAAACGAACCAATTAAT 2520  
2521 GTGTGAGTCACTGTGCAAGATTTTGAAGAAACCCCAAGGAGCTAATTCATGTTTCAAG 2580  
2521 GTGTGAGTCACTGTGCAAGATTTTGAAGAAACCCCAAGGAGCTAATTCATGTTTCAAG 2580  
2521 GTGTGAGTCACTGTGCAAGATTTTGAAGAAACCCCAAGGAGCTAATTCATGTTTCAAG 2580  
2581 AATAATGAATGAACAGAGAGCTTTAATGATTCATGTTGGAAGTAAACCAAGTCA 2640  
2581 AATAATGAATGAACAGAGAGCTTTAATGATTCATGTTGGAAGTAAACCAAGTCA 2640  
2641 GGGAAACAAGATGAAGAAATGGAAGAAAGTGAATTTGATGCTCAGATTTTGAAGATAT 2700  
2641 GGGAAACAAGATGAAGAAATGGAAGAAAGTGAATTTGATGCTCAGATTTTGAAGATAT 2700  
2701 TCAAGTTTCAAGCGCCAGTCAATTTGCTCTGTTTCAATCCAGAAATGCAAGAGAG 2760  
2701 TCAAGTTTCAAGCGCCAGTCAATTTGCTCTGTTTCAATCCAGAAATGCAAGAGAG 2760  
2761 AATGTCAACATTTCTCTGCCACTCTGAGTCTTTAAGAAACAAAGTCAAAAGTCACTT 2820  
2761 AATGTCAACATTTCTCTGCCACTCTGAGTCTTTAAGAAACAAAGTCAAAAGTCACTT 2820  
2821 TTGAATGTGAACAAAGAGAAATTAAGAAAGAAATGATGATTAATCAAGCTGTAC 2880  
2821 TTGAATGTGAACAAAGAGAAATTAAGAAAGAAATGATGATTAATCAAGCTGTAC 2880  
2881 AGACATTAATATCATGTCAGAGCTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2940  
2881 AGACATTAATATCATGTCAGAGCTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2940  
2941 ATGCCAAATGTATGATCAAGAGAGCTTCTGAGTCTTTGTTGTTGTTGTTGTTGTTGTTGTT 3000  
2941 ATGCCAAATGTATGATCAAGAGAGCTTCTGAGTCTTTGTTGTTGTTGTTGTTGTTGTTGTT 3000  
3001 ACAGAACTGAGCTATTAATCAAGAGAGCTTCTGAGTCTTTGTTGTTGTTGTTGTTGTTGTTGTT 3060  
3001 ACAGAACTGAGCTATTAATCAAGAGAGCTTCTGAGTCTTTGTTGTTGTTGTTGTTGTTGTTGTT 3060  
3061 CACCACTTTTCCCATCAAGTCAATTTGTTTAAATCTAATGTAAGAAATTCGTTAGAG 3120  
3061 CACCACTTTTCCCATCAAGTCAATTTGTTTAAATCTAATGTAAGAAATTCGTTAGAG 3120  
3121 AAAAATTGAGGAACTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3180  
3121 AAAAATTGAGGAACTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3180  
3181 GTACAGTGAAGCAATTAAGCCGTAAATTAAGTAAAGAAATGTTTAAAGAGCCAGCT 3240  
3181 GTACAGTGAAGCAATTAAGCCGTAAATTAAGTAAAGAAATGTTTAAAGAGCCAGCT 3240  
3241 CAACCAATTAATTAAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3300  
3241 CAACCAATTAATTAAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3300  
3241 CAACCAATTAATTAAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3300  
3301 TAGGTTCCAGTATGAAGAAACCTTCAAGCAGAACTAGGTAGAAACAGAGGCAAAATTTGA 3360  
3301 TAGGTTCCAGTATGAAGAAACCTTCAAGCAGAACTAGGTAGAAACAGAGGCAAAATTTGA 3360  
3361 ATGCTATGCTTAAATTTAGGGTTTTCGAACTGAGGCTTATTAACCAAGTCTTCTGGA 3420  
3361 ATGCTATGCTTAAATTTAGGGTTTTCGAACTGAGGCTTATTAACCAAGTCTTCTGGA 3420  
3421 GTAAATGTAAAGCACTCGAAATTAAGAAAGCAAGATTAAGAAAGTATGATGATGATGATGATGAT 3480  
3421 GTAAATGTAAAGCACTCGAAATTAAGAAAGCAAGATTAAGAAAGTATGATGATGATGATGATGAT 3480  
3481 ATACAGATTTCTCTCAATATCTGATTTCAAGTAACTTAAGAAACAGCTATGGAAGTATGTC 3540  
3481 ATACAGATTTCTCTCAATATCTGATTTCAAGTAACTTAAGAAACAGCTATGGAAGTATGTC 3540



OY 3541 ATGCATCTCAGGTTGTTCTGTGAGACACCTGATGACCTGTTAGATGATGTTGTAATTAAGG 3600  
DB 3541 ATGCATCTCAGGTTGTTCTGTGAGACACCTGATGACCTGTTAGATGATGTTGTAATTAAGG 3600  
OY 3601 AAGATATAGTTTGTCTGAAAAATGACATTTAAGAAAAGTTCTGCTGTTTTTTAGCAAAAGG 3660  
DB 3601 AAGATATAGTTTGTCTGAAAAATGACATTTAAGAAAAGTTCTGCTGTTTTTTAGCAAAAGG 3660  
OY 3661 TCCAGAGAGAGAGCTTTAGCAGAGAGTCTAGCCCTTTTACCCATACATTTGGCTCAGG 3720  
DB 3661 TCCAGAGAGAGAGCTTTAGCAGAGAGTCTAGCCCTTTTACCCATACATTTGGCTCAGG 3720  
OY 3721 GTTACCGAAGAGGGGSCAAGAAATTAGTCTCTGAAGAGAACTTATCTAGTGAAGATG 3780  
DB 3721 GTTACCGAAGAGGGGSCAAGAAATTAGTCTCTGAAGAGAACTTATCTAGTGAAGATG 3780  
OY 3781 AAGAGCTTCCCTGCTTCCAAACATTTGTTATTTGTAAAGTAAACAATATACCTTCTCAGT 3840  
DB 3781 AAGAGCTTCCCTGCTTCCAAACATTTGTTATTTGTAAAGTAAACAATATACCTTCTCAGT 3840  
OY 3841 CTACTAGGATAGCACCCTGCTACCGAGTGTCTGTCTAAGAACACAGAGAGAAATTTAT 3900  
DB 3841 CTACTAGGATAGCACCCTGCTACCGAGTGTCTGTCTAAGAACACAGAGAGAAATTTAT 3900  
OY 3901 TATCATTTGAAGATAGCTTAAATGACTGCAATACAGGATATATTTGGCAAGGATCTC 3960  
DB 3901 TATCATTTGAAGATAGCTTAAATGACTGCAATACAGGATATATTTGGCAAGGATCTC 3960  
OY 3961 AGGAACATACCTTATGAGAGAGAAACAAATGTTCTGATGTTGTTTTCTTACAGTGA 4020  
DB 3961 AGGAACATACCTTATGAGAGAGAAACAAATGTTCTGATGTTGTTTTCTTACAGTGA 4020  
OY 4021 GTGAATTGGAAGACTTGAACCTGCAATACAAACACCGAGATCTTTCTGATGTTCTT 4080  
DB 4021 GTGAATTGGAAGACTTGAACCTGCAATACAAACACCGAGATCTTTCTGATGTTCTT 4080  
OY 4081 CCAACCAATAGAGGATGATGATGTAAGCCAGAGAGTGTGTGATGATGTAACAAGAAATGG 4140  
DB 4081 CCAACCAATAGAGGATGATGATGTAAGCCAGAGAGTGTGTGATGATGTAACAAGAAATGG 4140  
OY 4141 TTTGATGATGTAAGAAAGAGAGAGGCTTGAAGAAATATATCAAGAGAGCAAGCA 4200  
DB 4141 TTTGATGATGTAAGAAAGAGAGAGGCTTGAAGAAATATATCAAGAGAGCAAGCA 4200  
OY 4201 TGGATTTCAACTTATGATGTAAGCAGATCTGGGTGTGAAGTGAACAAGCGTCTCTGAAG 4260  
DB 4201 TGGATTTCAACTTATGATGTAAGCAGATCTGGGTGTGAAGTGAACAAGCGTCTCTGAAG 4260  
OY 4261 ACTGCTCAGGGCTATCCTCTCTGAGTGAATTTTAACTGACGACAGAGAGGATACCATGC 4320  
DB 4261 ACTGCTCAGGGCTATCCTCTCTGAGTGAATTTTAACTGACGACGAGAGGATACCATGC 4320  
OY 4321 AACATTAACCTGTAAGCTCCAGCAGAAATGGCTGAAGTGAAGTGTGTAAGCAAGC 4380  
DB 4321 AACATTAACCTGTAAGCTCCAGCAGAAATGGCTGAAGTGAAGTGTGTAAGCAAGC 4380  
OY 4381 AATGATTAACCTGTAAGCTCCAGCAGAAATGGCTGAAGTGAAGTGTGTAAGCAAGC 4440  
DB 4381 AATGATTAACCTGTAAGCTCCAGCAGAAATGGCTGAAGTGAAGTGTGTAAGCAAGC 4440  
OY 4441 AATGATTAACCTGTAAGCTCCAGCAGAAATGGCTGAAGTGAAGTGTGTAAGCAAGC 4500  
DB 4441 AATGATTAACCTGTAAGCTCCAGCAGAAATGGCTGAAGTGAAGTGTGTAAGCAAGC 4500  
OY 4501 GTGAATTAACCTGTAAGCTCCAGCAGAAATGGCTGAAGTGAAGTGTGTAAGCAAGC 4560  
DB 4501 GTGAATTAACCTGTAAGCTCCAGCAGAAATGGCTGAAGTGAAGTGTGTAAGCAAGC 4560  
OY 4561 CAGATAGTTCTTACAGTAAATTAAGAACAGAGAGTGAAGTCAATCCCTTCTTAAT 4620  
DB 4561 CAGATAGTTCTTACAGTAAATTAAGAACAGAGAGTGAAGTCAATCCCTTCTTAAT 4620

OY 4621 GCCCATCATTAGATGATGATGTTATCATGACAGTGTGCTGGAGTCTTCAGATAGAA 4680  
DB 4621 GCCCATCATTAGATGATGATGTTATCATGACAGTGTGCTGGAGTCTTCAGATAGAA 4680  
OY 4681 ACTACCATCTCAAGAGAGCTCATTAAGTTTGTGATGATGAGAGCAACGCTGGAAG 4740  
DB 4681 ACTACCATCTCAAGAGAGCTCATTAAGTTTGTGATGATGAGAGCAACGCTGGAAG 4740  
OY 4741 AGTCTGGGCAACAGATTTGAAGAAACATCTTACTTCCCAAGGCAAGATCTAGAGGAA 4800  
DB 4741 AGTCTGGGCAACAGATTTGAAGAAACATCTTACTTCCCAAGGCAAGATCTAGAGGAA 4800  
OY 4801 CCCCTTACCTGGAATCTGGAATCAGCTCTTCTGATGACCCCTGAATCTGATCTCTG 4860  
DB 4801 CCCCTTACCTGGAATCTGGAATCAGCTCTTCTGATGACCCCTGAATCTGATCTCTG 4860  
OY 4861 AAGACAGAGCCCAAGAGTCACTGCTGTGTTGGCAATACATCTTCAACCTCTGATTTGA 4920  
DB 4861 AAGACAGAGCCCAAGAGTCACTGCTGTGTTGGCAATACATCTTCAACCTCTGATTTGA 4920  
OY 4921 AAGTCCCAATTTGAAGTGTGCAAAATCTGCCAGAGTCCAGCTGCTGATCTACTG 4980  
DB 4921 AAGTCCCAATTTGAAGTGTGCAAAATCTGCCAGAGTCCAGCTGCTGATCTACTG 4980  
OY 4981 ATACTGCTGGGTATATGCAATGGAAGAAAGTGTGAGAGAGGAGCAAGCAATTTGACAG 5040  
DB 4981 ATACTGCTGGGTATATGCAATGGAAGAAAGTGTGAGAGAGGAGCAAGCAATTTGACAG 5040  
OY 5041 CTTCAACGAAAGGCTCAACAAAGAAATGTCATGCTGTGTCTGCTGACCCAGAG 5100  
DB 5041 CTTCAACGAAAGGCTCAACAAAGAAATGTCATGCTGTGTCTGCTGACCCAGAG 5100  
OY 5101 AATTTATGCTGTGTGTAAGTTTGCAGAGAAACACCATCATCTTTAATCTTAATTA 5160  
DB 5101 AATTTATGCTGTGTGTAAGTTTGCAGAGAAACACCATCATCTTTAATCTTAATTA 5160  
OY 5161 CTGAAGAGACTATGATGTTTGAAGAAACAGATGCTGATGTTGTGTAAGAGGAGC 5220  
DB 5161 CTGAAGAGACTATGATGTTTGAAGAAACAGATGCTGATGTTGTGTAAGAGGAGC 5220  
OY 5221 TGAATATTTTCTAGGAATTCGGAGAGAAATGGTATGATGTTTCTGGGTGAGCC 5280  
DB 5221 TGAATATTTTCTAGGAATTCGGAGAGAAATGGTATGATGTTTCTGGGTGAGCC 5280  
OY 5281 AGTCTATTAAGAAAGAAATGCTGAATGAGCATGATTTGAAGTCAAGAGAGATGG 5340  
DB 5281 AGTCTATTAAGAAAGAAATGCTGAATGAGCATGATTTGAAGTCAAGAGAGATGG 5340  
OY 5341 TCAATGGAAGAAACCAAGAGTCCAAAGCAGAGAGAGATCCAGAGACAGAAAGATCT 5400  
DB 5341 TCAATGGAAGAAACCAAGAGTCCAAAGCAGAGAGAGATCCAGAGACAGAAAGATCT 5400  
OY 5401 TCAGGGGCTAGGAATCTGTTGCTATGAGGCTTTCACCAAGATGCCCAGATCAACTGG 5460  
DB 5401 TCAGGGGCTAGGAATCTGTTGCTATGAGGCTTTCACCAAGATGCCCAGATCAACTGG 5460  
OY 5461 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5520  
DB 5461 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5520  
OY 5521 GCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5580  
DB 5521 GCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5580  
OY 5581 TCCATGCAATTTGGGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 5640  
DB 5581 TCCATGCAATTTGGGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 5640  
OY 5641 GTGATGCACTTACAGTGCAGAGAGTGCAGACCTTACCTATACCTTACCTTACCTTAC 5700  
DB 5641 GTGATGCACTTACAGTGCAGAGAGTGCAGACCTTACCTATACCTTACCTTACCTTAC 5700  
OY 5701 GCCACTACTGA 5711





1201 CAGAGAACTCTAGAGATCTGAAAGATGTTCTTGAGATACTAAATGACAGATTGCA 1260  
1201 CAGAGAACTCTAGAGATCTGAAAGATGTTCTTGAGATACTAAATGACAGATTGCA 1260  
1261 AAGTTAATGAGTGGTTTCCAGAAAGTGAATGTTAGTTCTGATGATCACTGATG 1320  
1261 AAGTTAATGAGTGGTTTCCAGAAAGTGAATGTTAGTTCTGATGATCACTGATG 1320  
1321 GGGAGCTCGAATCAAAAGCCAAAGTGAATGTTAGAGCTTCTAAATGAGTGAATG 1380  
1321 GGGAGCTCGAATCAAAAGCCAAAGTGAATGTTAGAGCTTCTAAATGAGTGAATG 1380  
1381 AATATTCGTGTTCTTCAAGAAATAGACTTACTGAGCAGTATCTCATGAGGCTTAA 1440  
1381 AATATTCGTGTTCTTCAAGAAATAGACTTACTGAGCAGTATCTCATGAGGCTTAA 1440  
1441 TATGTAAAGTGAAGAGTCACTCCAAATCAGTGAAGTAAATTTGAAGCAAAATAT 1500  
1441 TATGTAAAGTGAAGAGTCACTCCAAATCAGTGAAGTAAATTTGAAGCAAAATAT 1500  
1501 TTGGGAAAACTTATCGGAAAGGCAAGCTTCCCAATTTAAGCCATGTAATCTGAAA 1560  
1501 TTGGGAAAACTTATCGGAAAGGCAAGCTTCCCAATTTAAGCCATGTAATCTGAAA 1560  
1561 TAATTTAGAGCAATTTGTTCTGAGCAGATTAATCAAGAGGCTCCCTCAAAATA 1620  
1561 TAATTTAGAGCAATTTGTTCTGAGCAGATTAATCAAGAGGCTCCCTCAAAATA 1620  
1621 AATTAAGCCTTAAAGAGAGCCTTACATCAGGCTTCACTGAGGATTTTTCAGAAAG 1680  
1621 AATTAAGCCTTAAAGAGAGCCTTACATCAGGCTTCACTGAGGATTTTTCAGAAAG 1680  
1681 CAGATTTGGCAGTTCAAAAGACTCTGAAATGATTAATCAGGAACTTAAACCAAGC 1740  
1681 CAGATTTGGCAGTTCAAAAGACTCTGAAATGATTAATCAGGAACTTAAACCAAGC 1740  
1741 AGAATGGTCAAGTGAATTTTCTAATAGTGTGATGAGATTAATTAACCAAGGCTG 1800  
1741 AGAATGGTCAAGTGAATTTTCTAATAGTGTGATGAGATTAATTAACCAAGGCTG 1800  
1801 CTATTCAGAAATGAGAAAAATCTTAACCCATAGATCACTCGAAAAAAGATCTGTT 1860  
1801 CTATTCAGAAATGAGAAAAATCTTAACCCATAGATCACTCGAAAAAAGATCTGTT 1860  
1861 AAACGAAAGCTGAACCTTAAGCAGAGTATTAAGCAATATGGAATCGAATTTAAATAT 1920  
1861 AAACGAAAGCTGAACCTTAAGCAGAGTATTAAGCAATATGGAATCGAATTTAAATAT 1920  
1921 ACAATTCGAAAGCCTTAAAGAAATAGGCTGAGAGAAAGTCTTCTACAGGCTATTC 1980  
1921 ACAATTCGAAAGCCTTAAAGAAATAGGCTGAGAGAAAGTCTTCTACAGGCTATTC 1980  
1981 ATGCGCTTGAATCTAGTGTGATGAAATCTAAGCCCACTAATTTGATCTGAAATTC 2040  
1981 ATGCGCTTGAATCTAGTGTGATGAAATCTAAGCCCACTAATTTGATCTGAAATTC 2040  
2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAAAGTCAACCAAAATGCCAGTCA 2100  
2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAAAGTCAACCAAAATGCCAGTCA 2100  
2101 GGGCAGAGAAACCTTCACTGAGAAAGTAAAGAACTGCACTGCAATGAGCCAAAGAA 2160  
2101 GGGCAGAGAAACCTTCACTGAGAAAGTAAAGAACTGCACTGCAATGAGCCAAAGAA 2160  
2161 GTAAACAAGCCAAATGAACAGACAGTAAAGACATGAGATGATCTTTCCAGAGCTGA 2220  
2161 GTAAACAAGCCAAATGAACAGACAGTAAAGACATGAGATGATCTTTCCAGAGCTGA 2220  
2221 AGTTAAACAATGCACTGTTCTTTTACTAAAGTTCCTAAATACAGTGAATTTAAGAT 2280  
2221 AGTTAAACAATGCACTGTTCTTTTACTAAAGTTCCTAAATACAGTGAATTTAAGAT 2280  
2221 AGTTAAACAATGCACTGTTCTTTTACTAAAGTTCCTAAATACAGTGAATTTAAGAT 2280

2281 TTGTCAAATCTAGCCTTCAAGAGAAAAAGAGAACTAAGAAACAGTTAAAGTGT 2340  
2281 TTGTCAAATCTAGCCTTCAAGAGAAAAAGAGAACTAAGAAACAGTTAAAGTGT 2340  
2341 CTAAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTCGAACTG 2400  
2341 CTAAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTCGAACTG 2400  
2401 AAAAGTCTGTAAGAGTGAAGTATTTCACTGTAACCTGTAACCTGATTAATGSCACTAG 2460  
2401 AAAAGTCTGTAAGAGTGAAGTATTTCACTGTAACCTGTAACCTGATTAATGSCACTAG 2460  
2461 AAAGTATCTGTTCTGGAAGTTAGCACTAGGGAAGGCAAAACAGAACCAATATAAT 2520  
2461 AAAGTATCTGTTCTGGAAGTTAGCACTAGGGAAGGCAAAACAGAACCAATATAAT 2520  
2521 GTGTGAGTCAAGTGTGAGCAATTTGAAAAACCCCAAGGACCTAATTCATGTTGTTCAAG 2580  
2521 GTGTGAGTCAAGTGTGAGCAATTTGAAAAACCCCAAGGACCTAATTCATGTTGTTCAAG 2580  
2581 AATAATGAAGAGACAGAAAGCTTTTAAGTATCCATTGGGACATGAAGTTAACCAAGTGC 2640  
2581 AATAATGAAGAGACAGAAAGCTTTTAAGTATCCATTGGGACATGAAGTTAACCAAGTGC 2640  
2641 GGGAAACAAGCATGAATGAAGAGAAAGTGAATTTGATGCTCAGTATTTGAGAAATACAT 2700  
2641 GGGAAACAAGCATGAATGAAGAGAAAGTGAATTTGATGCTCAGTATTTGAGAAATACAT 2700  
2701 TCAAGTTTCAAGCGCCAGTCATTTGCTCTGTTTTCATATCCAGAAATGCAAGAGG 2760  
2701 TCAAGTTTCAAGCGCCAGTCATTTGCTCTGTTTTCATATCCAGAAATGCAAGAGG 2760  
2761 AATGTCAACATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2820  
2761 AATGTCAACATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2820  
2821 TTGAATGTGAACAAAGAGAAATCAAGAAAGTGAATGATTAATCAAGCTGTAC 2880  
2821 TTGAATGTGAACAAAGAGAAATCAAGAAAGTGAATGATTAATCAAGCTGTAC 2880  
2881 AGACAGTTAATATCACTGACAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2940  
2881 AGACAGTTAATATCACTGACAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2940  
2941 ATGCCAATGTATGATCAAGAGAGCTGTAGCTTTGCTATCTCATCTGATTCAGAGCA 3000  
2941 ATGCCAATGTATGATCAAGAGAGCTGTAGCTTTGCTATCTCATCTGATTCAGAGCA 3000  
3001 AGGAACTGACCTATTAATCTCAAAATGAACATGGAATTTTCAAAACCCATATGATATAC 3060  
3001 AGGAACTGACCTATTAATCTCAAAATGAACATGGAATTTTCAAAACCCATATGATATAC 3060  
3061 CACCACCTTTTCCCATCAAGTCAATTTGTTAAACCTAATGTAAAGAAATCTGCTAGAG 3120  
3061 CACCACCTTTTCCCATCAAGTCAATTTGTTAAACCTAATGTAAAGAAATCTGCTAGAG 3120  
3121 AAAAATTGAGGAACATTCAATGCTCACTGAAAGAAAGTGAAGATGAGAACTTCCAA 3180  
3121 AAAAATTGAGGAACATTCAATGCTCACTGAAAGAAAGTGAAGATGAGAACTTCCAA 3180  
3181 GTACAGTGAAGCAATTAAGCCGTATTAACCTTAAGAAAAAGTTTAAAGAGCCAGCT 3240  
3181 GTACAGTGAAGCAATTAAGCCGTATTAACCTTAAGAAAAAGTTTAAAGAGCCAGCT 3240  
3241 CAAGCAATATTAATGAAGTGGTCCAGTACTAATGAAGTGGTCCAGTACTAATGAAG 3300  
3241 CAAGCAATATTAATGAAGTGGTCCAGTACTAATGAAGTGGTCCAGTACTAATGAAG 3300  
3301 TAGGTTCCAGTATGAAGAAACCTTCAAGCAGAACTAGGTAGAGAAACAGAGGCGCAAAATTTGA 3360  
3301 TAGGTTCCAGTATGAAGAAACCTTCAAGCAGAACTAGGTAGAGAAACAGAGGCGCAAAATTTGA 3360  
3361 ATGCTATGCTTAAGTTAGGGGTTTGGCACTGAGTGTATTAACAAAGTCTTCTGGA 3420

Db 3361 ATGCTATGCTTATGATTAAGGGGTTTGCACACCTGAGGTCTATTAACAAGCTCTCTGGAA 3420  
Qy 3421 GTAATTGTAGCATCTCTGAATTAATAAAGCAAGAAATATGAGAAGTACTGACCTGTTA 3480  
Db 3421 GTAATTGTAGCATCTCTGAATTAATAAAGCAAGAAATATGAGAAGTACTGACCTGTTA 3480  
Qy 3481 ATACGATTTCTCTCATATCTGATTTGATTTGATTAAGTACAGCTATGGAAGTACTC 3540  
Db 3481 ATACGATTTCTCTCATATCTGATTTGATTTGATTAAGTACAGCTATGGAAGTACTC 3540  
Qy 3541 ATGATCTCAGGTTTGTCTGAGACACCTGATGACCTGTATGATGATGATGATTAAG 3600  
Db 3541 ATGATCTCAGGTTTGTCTGAGACACCTGATGACCTGTATGATGATGATGATTAAG 3600  
Qy 3601 AAGATACATGTTTGTCTGAGACACCTGATGACCTGTATGATGATGATGATTAAG 3660  
Db 3601 AAGATACATGTTTGTCTGAGACACCTGATGACCTGTATGATGATGATGATTAAG 3660  
Qy 3661 TCCAGAGAGAGAGCTTACAGAGTCTGAGCTTACCCATACACATTTGCTCAG 3720  
Db 3661 TCCAGAGAGAGAGCTTACAGAGTCTGAGCTTACCCATACACATTTGCTCAG 3720  
Qy 3721 GTTACCGAAGAGGGGCCAAGAAATTAAGTCTCAGAAAGAACTTATCTAGTGAATG 3780  
Db 3721 GTTACCGAAGAGGGGCCAAGAAATTAAGTCTCAGAAAGAACTTATCTAGTGAATG 3780  
Qy 3781 AAGAGCTTCCCTGCTTCCAACTGTTTATTTGTAAGTAACATTAATCTTCTCAGT 3840  
Db 3781 AAGAGCTTCCCTGCTTCCAACTGTTTATTTGTAAGTAACATTAATCTTCTCAGT 3840  
Qy 3841 CTACTAGGCATAGACCCGTTGCTACGAGTCTGTCTAAGAAACAAGAGGAATTAAT 3900  
Db 3841 CTACTAGGCATAGACCCGTTGCTACGAGTCTGTCTAAGAAACAAGAGGAATTAAT 3900  
Qy 3901 TATCATTTGAAGATAGCTTAATATGACTGACAGTAACAGTAATATTTGCAAGGATCTC 3960  
Db 3901 TATCATTTGAAGATAGCTTAATATGACTGACAGTAACAGTAATATTTGCAAGGATCTC 3960  
Qy 3961 AGGAACATCACCCTTAAGTGAAGAAACAAATGTTCTGCTAGCTTTCTTCAACATGCA 4020  
Db 3961 AGGAACATCACCCTTAAGTGAAGAAACAAATGTTCTGCTAGCTTTCTTCAACATGCA 4020  
Qy 4021 GTGAATTTGAAGATCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4080  
Db 4021 GTGAATTTGAAGATCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4080  
Qy 4081 CCAACCAATGAGGATCAGTCTGAAAGCAAGGAGTGTCTGAGTGAAGAAATTTG 4140  
Db 4081 CCAACCAATGAGGATCAGTCTGAAAGCAAGGAGTGTCTGAGTGAAGAAATTTG 4140  
Qy 4141 TTTGAGATGAGTGAAGAAAGAGGAGGCTTGAAGAAATTAATCAAGAAAGCAAGCA 4200  
Db 4141 TTTGAGATGAGTGAAGAAAGAGGAGGCTTGAAGAAATTAATCAAGAAAGCAAGCA 4200  
Qy 4201 TGAATTTCAAACTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4260  
Db 4201 TGAATTTCAAACTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4260  
Qy 4261 ACTGCTCAGGCTATCTCTCAGAGTGAATTTTAACCACTCAGAGAGGATACATGC 4320  
Db 4261 ACTGCTCAGGCTATCTCTCAGAGTGAATTTTAACCACTCAGAGAGGATACATGC 4320  
Qy 4321 AACATTAACCTGATTAAGTTCAGACAGAAATGCTGAAGTGAAGTGAAGTGAAGTGAAG 4380  
Db 4321 AACATTAACCTGATTAAGTTCAGACAGAAATGCTGAAGTGAAGTGAAGTGAAGTGAAG 4380  
Qy 4381 ATGGAGGACGACCTTCTTAACAGTACCTTCAATCAATGATGATCTCTCTGAGG 4440  
Db 4381 ATGGAGGACGACCTTCTTAACAGTACCTTCAATCAATGATGATCTCTCTGAGG 4440  
Qy 4441 ACTGCGAATTCAGAAACAAAGCAATCAGAAAAAGCATTAATTTCAAGAAAGTA 4500  
Db 4441 ACTGCGAATTCAGAAACAAAGCAATCAGAAAAAGCATTAATTTCAAGAAAGTA 4500

Db 4441 ACTGCGAATTCAGAAACAAAGCAATCAGAAAAAGCATTAATTTCAAGAAAGTA 4500  
Qy 4501 GTGAATTAACCTTAAGTTCAGACAGAAATGCTGAAGTGAAGTGAAGTGAAGTGAAG 4560  
Db 4501 GTGAATTAACCTTAAGTTCAGACAGAAATGCTGAAGTGAAGTGAAGTGAAGTGAAG 4560  
Qy 4561 CAGATGTTTCAACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4620  
Db 4561 CAGATGTTTCAACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4620  
Qy 4621 GCCCATCAATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4680  
Db 4621 GCCCATCAATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4680  
Qy 4681 ACTTACCATCTCAAGAGAGCTCTTAAGTGTGATGATGAGAGAGCAAGCTGAG 4740  
Db 4681 ACTTACCATCTCAAGAGAGCTCTTAAGTGTGATGATGAGAGAGCAAGCTGAG 4740  
Qy 4741 AGTCTGGGGCCACAGATTTGACGGAACATCTTACCTTGCCCAAGGCAAGATCTAGAGGAA 4800  
Db 4741 AGTCTGGGGCCACAGATTTGACGGAACATCTTACCTTGCCCAAGGCAAGATCTAGAGGAA 4800  
Qy 4801 CCCCTTACCTGGAATCTGGAATCAGCTCTTCTGATGACCTGGAATCTGATCTTCTG 4860  
Db 4801 CCCCTTACCTGGAATCTGGAATCAGCTCTTCTGATGACCTGGAATCTGATCTTCTG 4860  
Qy 4861 AAGACAGAGCCCGAGTCAAGCTGCTGTGGAACATTAACATCTTCAACTCTGATGA 4920  
Db 4861 AAGACAGAGCCCGAGTCAAGCTGCTGTGGAACATTAACATCTTCAACTCTGATGA 4920  
Qy 4921 AAGTCCCAATTAAGATGGAATCTGCGGAGGCTGCAAGCTGCTCATCTA 4980  
Db 4921 AAGTCCCAATTAAGATGGAATCTGCGGAGGCTGCAAGCTGCTCATCTA 4980  
Qy 4981 ATACTGTGGGTATTAATGCAATGGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 5040  
Db 4981 ATACTGTGGGTATTAATGCAATGGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 5040  
Qy 5041 CTTCAACAGAAAGGCTCAACAAAGAAATGTCATGCTGTGTCTGCTGACCCAGAG 5100  
Db 5041 CTTCAACAGAAAGGCTCAACAAAGAAATGTCATGCTGTGTCTGCTGACCCAGAG 5100  
Qy 5101 AATTATGCTGCTGATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 5160  
Db 5101 AATTATGCTGCTGATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 5160  
Qy 5161 CTGAAGAGACTACTCATGTTGATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 5220  
Db 5161 CTGAAGAGACTACTCATGTTGATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 5220  
Qy 5221 TGAATTTTCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 5280  
Db 5221 TGAATTTTCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 5280  
Qy 5281 AGCTATTAAGAAAGAAATGCTGAATGAGATGATTTTGAAGTGAAGTGAAGTGAAGTGAAG 5340  
Db 5281 AGCTATTAAGAAAGAAATGCTGAATGAGATGATTTTGAAGTGAAGTGAAGTGAAGTGAAG 5340  
Qy 5341 TCAATGGAAGAAACCAAGAGTCTCAAGAGCAAGAGTCCAGAGTCAAGAGTCAAGAGTCAAG 5400  
Db 5341 TCAATGGAAGAAACCAAGAGTCTCAAGAGCAAGAGTCCAGAGTCAAGAGTCAAGAGTCAAG 5400  
Qy 5401 TCAAGGGGCTGAAGTCTGTTGCTGAAGGAGGCTTCAAGTCAAGTCAAGTCAAGTCAAG 5460  
Db 5401 TCAAGGGGCTGAAGTCTGTTGCTGAAGGAGGCTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 5460  
Qy 5461 AATGATGATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 5520  
Db 5461 AATGATGATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 5520  
Qy 5521 GCAAGGCTGTCACCAATTTGTGTTGTGAGGCAAGTGTCTGAGAGAGAGCAATGCT 5580  
Db 5521 GCAAGGCTGTCACCAATTTGTGTTGTGAGGCAAGTGTCTGAGAGAGAGCAATGCT 5580

```

Oy      5581  TCCATGCAATTGGGCAAGTGTGTGAGGGACCTGTGTGTGACCCGAGAGTGGGTGTGGACA 5640
Db      5581  TCCATGCAATTGGGCAAGTGTGTGAGGGACCTGTGTGTGACCCGAGAGTGGGTGTGGACA 5640
Oy      5641  GTGTAGCACTTACCAAGTGCAGAGAGCTGACACACTTACTGTATACCCGAGATCCCCACA 5700
Db      5641  GTGTAGCACTTACCAAGTGCAGAGAGCTGACACACTTACTGTATACCCGAGATCCCCACA 5700
Oy      5701  GCCACTACTGA 5711
Db      5701  GCCACTACTGA 5711

RESULT 6
US-09-734-672-3
; Sequence 3, Application US/09734672
; Publication No. US20020183268A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Patricia D.
; Allen, Antoinette C.
; Alvarez, Christopher P.
; Citz, Brenda S.
; Olson, Sheri J.
; Schelter, Denise B.
; Zeng, Bin
TITLE OF INVENTION: Coding Sequences of the Human
                    BRCA1 Gene
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESS: Morgan Lewis & Bockius LLP
STREET: 1111 Pennsylvania Ave., N.W.
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/734,672
FILING DATE: 03-Dec-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/966,436
FILING DATE: 07-No. US20020183268A1-97
APPLICATION NUMBER: US 08/598,591
FILING DATE: 12-Feb-96
ATTORNEY/AGENT INFORMATION:
NAME: Michael S. Tuscan
REGISTRATION NUMBER: 43,210
REFERENCE/DOCKET NUMBER: 44921-5055-02-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-739-3000
TELEFAX: 202-739-3001
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5711 base pairs
TYPE: nucleic acid
STRANDEDNESS: No. US20020183268A1 Relevant
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: BRCA1
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 17
MAP POSITION: 17q21
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-734-672-3
Query Match          99.8%; Score 5701.4; DB 10; Length 5711;

```

Best Local Similarity 99.9% ; Pred. No. 0 ;									
Matches 5705; Conservative 0 ; Mismatches 6; Indels 0; Gaps 0;									
OY	1	AGCTCGCTGAGACTTCTGTGACCCCGCACCAAGCTGTGGGATTTCTCAGATTAATCTGGGCC	60						
Db	1	AGCTCGCTGAGACTTCTGTGACCCCGCACCAAGCTGTGGGATTTCTCAGATTAATCTGGGCC	60						
OY	61	CTGGGGCTCAGAGAGCCCTTACCCCTCGCTCTGGGTAAAGTTCAATGGAATGGAAACAGAAAGAA	120						
Db	61	CTGGGGCTCAGAGAGCCCTTACCCCTCGCTCTGGGTAAAGTTCAATGGAACAGAAAGAA	120						
OY	121	TGAGTTTATCTGCTCTTCGGGTTGAAGAATGACAAATGTCAATTAATGCTATGACAGAAA	180						
Db	121	TGAGTTTATCTGCTCTTCGGGTTGAAGAATGACAAATGTCAATTAATGCTATGACAGAAA	180						
OY	181	TCTTAGAGTGTCCTCATCTGTCTGGAGTTGATCAAGAACTGTCTCCACAAAGTGTGACC	240						
Db	181	TCTTAGAGTGTCCTCATCTGTCTGGAGTTGATCAAGAACTGTCTCCACAAAGTGTGACC	240						
OY	241	ACATATTTTGGCAATTTTGCATGCTGAACCTTTCACACAGAAAGAGGCTTCAACAGT	300						
Db	241	ACATATTTTGGCAATTTTGCATGCTGAACCTTTCACACAGAAAGAGGCTTCAACAGT	300						
OY	301	GTCCTTTATGTGAATGATATATAACAAAGAGAGCTTACAGAAAGTATGAGATTTAGTC	360						
Db	301	GTCCTTTATGTGAATGATATATAACAAAGAGAGCTTACAGAAAGTATGAGATTTAGTC	360						
OY	361	AACCTGTGGAAGACTATGAAAATCAATTTGTCTTTCAGCTTGACACAGGTTTGGAGT	420						
Db	361	AACCTGTGGAAGACTATGAAAATCAATTTGTCTTTCAGCTTGACACAGGTTTGGAGT	420						
OY	421	ATGCAAAACAGCTAATATTTTGCAGAAAAGCAAAATTAATCTCTCTGAAACATCTAAAGATG	480						
Db	421	ATGCAAAACAGCTAATATTTTGCAGAAAAGCAAAATTAATCTCTCTGAAACATCTAAAGATG	480						
OY	481	AAGTTTCTATCATCAAGATATGGGCTTACAGAAAACGGTGCAGAAAAGACTTCTACAGAGTG	540						
Db	481	AAGTTTCTATCATCAAGATATGGGCTTACAGAAAACGGTGCAGAAAAGACTTCTACAGAGTG	540						
OY	541	AACCCGAAAATCCCTCCCTGCAGAGAAACCAAGTCTCAGTGTCAACTCTCTAACCTTTGAA	600						
Db	541	AACCCGAAAATCCCTCCCTGCAGAGAAACCAAGTCTCAGTGTCAACTCTCTAACCTTTGAA	600						
OY	601	CTGTGAGAACTCTGAGAGCAAAAGCAGGGATACAACTCAAAAGACGTCTGTCTACATTTG	660						
Db	601	CTGTGAGAACTCTGAGAGCAAAAGCAGGGATACAACTCAAAAGACGTCTGTCTACATTTG	660						
OY	661	AATTGGGATCTGATTTCTTCTGAAGATACCGTTAATAAGGAACTTAATGGACGTGGAG	720						
Db	661	AATTGGGATCTGATTTCTTCTGAAGATACCGTTAATAAGGAACTTAATGGACGTGGAG	720						
OY	721	ATCAAGAATTGTATCAATCAACCCCTCAAGAAACAGAGATGAAATCAGTTTGGATTTCTG	780						
Db	721	ATCAAGAATTGTATCAATCAACCCCTCAAGAAACAGAGATGAAATCAGTTTGGATTTCTG	780						
OY	781	CAAAAAAGGCTGCTTGTGAATTTTCTGAGACGATGTATACAAATATCTGAACATCATCAAC	840						
Db	781	CAAAAAAGGCTGCTTGTGAATTTTCTGAGACGATGTATACAAATATCTGAACATCATCAAC	840						
OY	841	CCAAGTAATATGATTTTGAACACCACTGAGAAAGCTGACGCTGAGAGGCAATTCAGAAAAGT	900						
Db	841	CCAAGTAATATGATTTTGAACACCACTGAGAAAGCTGACGCTGAGAGGCAATTCAGAAAAGT	900						
OY	901	ATCAGGGATAGTCTGTTCAAACTGTGATGTGAGCAATGTGGCAAAATACTGATGCCA	960						
Db	901	ATCAGGGATAGTCTGTTCAAACTGTGATGTGAGCAATGTGGCAAAATACTGATGCCA	960						
OY	961	GCTCATTTACAGCATGAGAAACAGAGTTTATTAATCTCACTAAAGACAGAAATGTATGAAA	1020						
Db	961	GCTCATTTACAGCATGAGAAACAGAGTTTATTAATCTCACTAAAGACAGAAATGTATGAAA	1020						
OY	1021	AGGCTGAATTTCTGTATATAAAGCAAAACAGCTGTGCTTAGCAAGAGCCAACTATACAGAT	1080						

Db 1021 AGGCTGAATTCGTGATATTAAGCAACAGCTGGCTTAGCAAGAGCAACATTAACAGAT 1080  
Qy 1081 GGGCTGGAAGTAAAGAAATGTAATGAGGCGGCTCCGACGACAGAAAAAAGGTG 1140  
Db 1081 GGGCTGGAAGTAAAGAAATGTAATGAGGCGGCTCCGACGACAGAAAAAAGGTG 1140  
Qy 1141 ATCTGAATCTGATCCCTGTGTGAGAGAAAAAGATGAATAAGCAGAACTGCCATGCT 1200  
Db 1141 ATCTGAATCTGATCCCTGTGTGAGAGAAAAAGATGAATAAGCAGAACTGCCATGCT 1200  
Qy 1201 CAGAGAACTCTGAGATCTGAAGATGTTCTTGATTAACCTAAATAGCAGCATTCAGA 1260  
Db 1201 CAGAGAACTCTGAGATCTGAAGATGTTCTTGATTAACCTAAATAGCAGCATTCAGA 1260  
Qy 1261 AAGTTAATGAGTGGTTTTCCAGAGGATGAACGTGTAGGTTCTGATGACTGACATGATG 1320  
Db 1261 AAGTTAATGAGTGGTTTTCCAGAGGATGAACGTGTAGGTTCTGATGACTGACATGATG 1320  
Qy 1321 GGGAGCTGGAATCAATGCGCAAGTAGCTGATGTAATGGACGTTCTAAATGAGTAGATG 1380  
Db 1321 GGGAGCTGGAATCAATGCGCAAGTAGCTGATGTAATGGACGTTCTAAATGAGTAGATG 1380  
Qy 1381 AATATTTCTGTTCTTCAAGAAAAATGACTTACTGGCCAGTAGATCTCATGAGGCTTTAA 1440  
Db 1381 AATATTTCTGTTCTTCAAGAAAAATGACTTACTGGCCAGTAGATCTCATGAGGCTTTAA 1440  
Qy 1441 TATGTAAAGTAAAGAGTTCACTCCAAATCAGTAGAGTAAATTTGAAGCAAAATAT 1500  
Db 1441 TATGTAAAGTAAAGAGTTCACTCCAAATCAGTAGAGTAAATTTGAAGCAAAATAT 1500  
Qy 1501 TTGGGAAAACTATCGGAAGAAAGGAGGCTCCCACTTAAGCAGTAGTAATGAAAAATC 1560  
Db 1501 TTGGGAAAACTATCGGAAGAAAGGAGGCTCCCACTTAAGCAGTAGTAATGAAAAATC 1560  
Qy 1561 TTAATTAAGAGACATTTGTTACTGAGCCAGATTAATACAGAGGCTCCCTCACAAATA 1620  
Db 1561 TTAATTAAGAGACATTTGTTACTGAGCCAGATTAATACAGAGGCTCCCTCACAAATA 1620  
Qy 1621 AATTAAGGCTAAAGAGAGACCTATACAGGCTTCATCTGAGGATTTTATCAAGAAAG 1680  
Db 1621 AATTAAGGCTAAAGAGAGACCTATACAGGCTTCATCTGAGGATTTTATCAAGAAAG 1680  
Qy 1681 CAGATTTGGCAGTTCAAAAGACTCCTGAATGATTAATCAAGGAACTAACCCAAAGCAG 1740  
Db 1681 CAGATTTGGCAGTTCAAAAGACTCCTGAATGATTAATCAAGGAACTAACCCAAAGCAG 1740  
Qy 1741 AGAATGCTCAAGTGAATATTTACTAATAGTGTCTAGAGAAATTAACCAAAAGGTGAT 1800  
Db 1741 AGAATGCTCAAGTGAATATTTACTAATAGTGTCTAGAGAAATTAACCAAAAGGTGAT 1800  
Qy 1801 CTATTCAGATGAGAAAAATCTTAACCCATAGATCACTCGAAAAAGATCTGCTTCA 1860  
Db 1801 CTATTCAGATGAGAAAAATCTTAACCCATAGATCACTCGAAAAAGATCTGCTTCA 1860  
Qy 1861 AAAAGCAAGCTGAACCTTAAGCAGCAGTAAAGCAATATGGAATCTGAAATTAATATCC 1920  
Db 1861 AAAAGCAAGCTGAACCTTAAGCAGCAGTAAAGCAATATGGAATCTGAAATTAATATCC 1920  
Qy 1921 ACAATTTCAAAAGCAGCTTAAGAAATAGGCTGAGAGAAAGTCTTCTACAGGCAATATTC 1980  
Db 1921 ACAATTTCAAAAGCAGCTTAAGAAATAGGCTGAGAGAAAGTCTTCTACAGGCAATATTC 1980  
Qy 1981 ATGCGCTTGAATGATGATCACTAGTAAGAAATCTAAGCCCACTAATGTACTGATTTGCAA 2040  
Db 1981 ATGCGCTTGAATGATGATCACTAGTAAGAAATCTAAGCCCACTAATGTACTGATTTGCAA 2040  
Qy 2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAAAGTAAACCAACCAATGCGACTCA 2100  
Db 2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAAAGTAAACCAACCAATGCGACTCA 2100  
Qy 2101 GGCACAGCAAAACCTTAACATCATGAGAAAGTAAAGAACTGCAAGCTGAGGCAAGAA 2160  
Db 2101 GGCACAGCAAAACCTTAACATCATGAGAAAGTAAAGAACTGCAAGCTGAGGCAAGAA 2160

Qy 2161 GTAAACGCCAATATGACAGACAGTAAACATGACATGATTTCTTCCAGAGCTCA 2220  
Db 2161 GTAAACGCCAATATGACAGACAGTAAACATGACATGATTTCTTCCAGAGCTCA 2220  
Qy 2221 AGTTAACAAATGACCTGTTCTTTTACTAGTGTCAATATACAGTAGAATCTTAAAGAT 2280  
Db 2221 AGTTAACAAATGACCTGTTCTTTTACTAGTGTCAATATACAGTAGAATCTTAAAGAT 2280  
Qy 2281 TTGTCAATCTGAGCTTCCAGAGAGAGAAAAAGAGAAATAGAAAACAGTTAAAGTGT 2340  
Db 2281 TTGTCAATCTGAGCTTCCAGAGAGAGAAAAAGAGAAATAGAAAACAGTTAAAGTGT 2340  
Qy 2341 CTAAATATGCTGAAGACCCCAAAATCTCAGTTTAAGTGAAGAAAGGTTTTGCAAACTG 2400  
Db 2341 CTAAATATGCTGAAGACCCCAAAAGTCTCAGTTTAAGTGAAGAAAGGTTTTGCAAACTG 2400  
Qy 2401 AAAGATCTGTAGAGAGTAGAGATTTTCACTGATACCTGTAATGATTAAGCACTCAG 2460  
Db 2401 AAAGATCTGTAGAGAGTAGAGATTTTCACTGATACCTGTAATGATTAAGCACTCAG 2460  
Qy 2461 AAAGATCTGTGAGAGAGTAGAGATTTTCACTGATACCTGTAATGATTAAGCACTCAG 2520  
Db 2461 AAAGATCTGTGAGAGAGTAGAGATTTTCACTGATACCTGTAATGATTAAGCACTCAG 2520  
Qy 2521 GTGTGAGTCAAGTGTGAGAGATTTTCACTGATACCTGTAATGATTAAGCACTCAG 2580  
Db 2521 GTGTGAGTCAAGTGTGAGAGATTTTCACTGATACCTGTAATGATTAAGCACTCAG 2580  
Qy 2581 ATAAATAGAAATGACACAGAAAGCTTTAATGATCACTGAGGACATGAAGTTAACCAAGTC 2640  
Db 2581 ATAAATAGAAATGACACAGAAAGCTTTAATGATCACTGAGGACATGAAGTTAACCAAGTC 2640  
Qy 2641 GGGAAACAGATTAAGAAATGGAAGAAAGTGAATTTGATGCTCAGATTTTGCAGAAATCAT 2700  
Db 2641 GGGAAACAGATTAAGAAATGGAAGAAAGTGAATTTGATGCTCAGATTTTGCAGAAATCAT 2700  
Qy 2701 TCAAGTTTCAAGGCGCAGTCACTTGTCTGTTTCAAAATCCAGGAAATCCAGAAAGG 2760  
Db 2701 TCAAGTTTCAAGGCGCAGTCACTTGTCTGTTTCAAAATCCAGGAAATCCAGAAAGG 2760  
Qy 2761 AATGTGCAACATTTCTGCCCACCTGCGGCTCTTAAGAAACAAAGTCCAAAGTCACTT 2820  
Db 2761 AATGTGCAACATTTCTGCCCACCTGCGGCTCTTAAGAAACAAAGTCCAAAGTCACTT 2820  
Qy 2821 TTGAATGTGAACAAAGAGAGAAATCAAGAAAGATGAGTCTAATATCAAGCTGTAC 2880  
Db 2821 TTGAATGTGAACAAAGAGAGAAATCAAGAAAGATGAGTCTAATATCAAGCTGTAC 2880  
Qy 2881 AGACAGTTAATATCACTGCGAGGCTTCTGTTGTTGTCAGAAAGATTAAGCAGTTGATA 2940  
Db 2881 AGACAGTTAATATCACTGCGAGGCTTCTGTTGTTGTCAGAAAGATTAAGCAGTTGATA 2940  
Qy 2941 ATGCAAAATGATATCAAGAGAGGCTCTAGTTTTGTTCTATCATCTCAGTTTCAAGAGCA 3000  
Db 2941 ATGCAAAATGATATCAAGAGAGGCTCTAGTTTTGTTCTATCATCTCAGTTTCAAGAGCA 3000  
Qy 3001 ACGAAACTGAGCTATTAATCTCAAAATTAACATGSACTTTTCAAAACCCATATGTATAC 3060  
Db 3001 ACGAAACTGAGCTATTAATCTCAAAATTAACATGSACTTTTCAAAACCCATATGTATAC 3060  
Qy 3061 CACACATTTTCCCATCAAGCATTTGTTAAACCTTAATAGTAAAGAAATCTGTTAAGG 3120  
Db 3061 CACACATTTTCCCATCAAGCATTTGTTAAACCTTAATAGTAAAGAAATCTGTTAAGG 3120  
Qy 3121 AAAACTTTGAGAAACATTTCAATGCTCACTGAAGAAAGTGGAAATGAGAACTTGCAA 3180  
Db 3121 AAAACTTTGAGAAACATTTCAATGCTCACTGAAGAAAGTGGAAATGAGAACTTGCAA 3180  
Qy 3181 GTACAGTGAACCAATTAAGCCGTAAATTAACATTTAGAGAAATGTTTTTAAAGAGCCAGCT 3240  
Db 3181 GTACAGTGAACCAATTAAGCCGTAAATTAACATTTAGAGAAATGTTTTTAAAGAGCCAGCT 3240

QY 3241 CAACCAATATTAATGAAGTAGATTCAGTACTAATGAAGTGGGCTCCAGATTAATGAAA 3300  
| | | | |  
Db 3241 CAACCAATATTAATGAAGTAGATTCAGTACTAATGAAGTGGGCTCCAGATTAATGAAA 3300  
| | | | |  
QY 3301 TAGGTTCCAGTAGTGAAGAAACAATTCAGAGAGAACTAGTAGAAAAGAGGGCCAAAATTGA 3360  
| | | | |  
Db 3301 TAGGTTCCAGTAGTGAAGAAACAATTCAGAGAGAACTAGTAGAAAAGAGGGCCAAAATTGA 3360  
| | | | |  
QY 3361 ATGCTATGCTTAAGTATGAGGGGTTTGGCAACCTGAGGCTTAATTAACAAGTCTTCTGGAA 3420  
| | | | |  
Db 3361 ATGCTATGCTTAAGTATGAGGGGTTTGGCAACCTGAGGCTTAATTAACAAGTCTTCTGGAA 3420  
| | | | |  
QY 3421 GTAATTGTAAGCATCTCTGAATTAATAAAGCAAGATATGAGAGTAGTTCAGACTGTTA 3480  
| | | | |  
Db 3421 GTAATTGTAAGCATCTCTGAATTAATAAAGCAAGATATGAGAGTAGTTCAGACTGTTA 3480  
| | | | |  
QY 3481 ATACAGATTTCTCTCCATATCTGATTTAGATTAAGTAAACAGCTATGGAAGTAGTC 3540  
| | | | |  
Db 3481 ATACAGATTTCTCTCCATATCTGATTTAGATTAAGTAAACAGCTATGGAAGTAGTC 3540  
| | | | |  
QY 3541 ATGATCTCAGGTTTGTCTGAGACAACCTGATGACCTGTTAGATGATGATGATAAAG 3600  
| | | | |  
Db 3541 ATGATCTCAGGTTTGTCTGAGACAACCTGATGACCTGTTAGATGATGATGATAAAG 3600  
| | | | |  
QY 3601 AAGATCTAGTGTGCTGAATAATGACATTAAGAAAGTTGCTGTTTATGCAAAAAGCG 3660  
| | | | |  
Db 3601 AAGATCTAGTGTGCTGAATAATGACATTAAGAAAGTTGCTGTTTATGCAAAAAGCG 3660  
| | | | |  
QY 3661 TCCAGAGAGAGAGGTTAGACAGAGTCTAGCCCTTTACCCATACACATTTGGCTCAGG 3720  
| | | | |  
Db 3661 TCCAGAGAGAGAGGTTAGACAGAGTCTAGCCCTTTACCCATACACATTTGGCTCAGG 3720  
| | | | |  
QY 3721 GTTACCGAAAGAGGGGCCAAGAAATTAGTCTCTCAAGAGAGACATTATCTAGTAGATG 3780  
| | | | |  
Db 3721 GTTACCGAAAGAGGGGCCAAGAAATTAGTCTCTCAAGAGAGACATTATCTAGTAGATG 3780  
| | | | |  
QY 3781 AAGAGCTTCCCTGCTCCACACCTGTAATTTGGTAAGTAACAATPACCTTCTCAGT 3840  
| | | | |  
Db 3781 AAGAGCTTCCCTGCTCCACACCTGTAATTTGGTAAGTAACAATPACCTTCTCAGT 3840  
| | | | |  
QY 3841 CTACTAGGCAATAGCACCGTTCCTACCGAGTGTCTGTCTAAGAACACAGAGAGAAATTTAT 3900  
| | | | |  
Db 3841 CTACTAGGCAATAGCACCGTTCCTACCGAGTGTCTGTCTAAGAACACAGAGAGAAATTTAT 3900  
| | | | |  
QY 3901 TATCATTTGAAGAATAGCTTAATATGATCTGACAGTAATATTTGGCAAGGAGATCTC 3960  
| | | | |  
Db 3901 TATCATTTGAAGAATAGCTTAATATGATCTGACAGTAATATTTGGCAAGGAGATCTC 3960  
| | | | |  
QY 3961 AGGAACATCACCTTAGTAGAGAAACAAAATGTTCTGAGTGTGTTTCTTCAAGTGA 4020  
| | | | |  
Db 3961 AGGAACATCACCTTAGTAGAGAAACAAAATGTTCTGAGTGTGTTTCTTCAAGTGA 4020  
| | | | |  
QY 4021 GTGAATTGGAAGACTTGAAGTCAATATACAAACCCAGAGATCTTTCTTGAATGGTCTT 4080  
| | | | |  
Db 4021 GTGAATTGGAAGACTTGAAGTCAATATACAAACCCAGAGATCTTTCTTGAATGGTCTT 4080  
| | | | |  
QY 4081 CCAAAACAATAGAGCATAGTCTGAAGCCAGAGAGTTGTGTCTGATGAACAAGAAATGG 4140  
| | | | |  
Db 4081 CCAAAACAATAGAGCATAGTCTGAAGCCAGAGAGTTGTGTCTGATGAACAAGAAATGG 4140  
| | | | |  
QY 4141 TTTGATGATGAGAAAGAAAGAAACGGGCTTGGAGAAATATATCAAGAAGCAACA 4200  
| | | | |  
Db 4141 TTTGATGATGAGAAAGAAAGAAACGGGCTTGGAGAAATATATCAAGAAGCAACA 4200  
| | | | |  
QY 4201 TGAATTTCAACTTAAAGTGAAGCAGCATCTGGGTGTGAGAGTGAACAAGCGTCTCTGAG 4260  
| | | | |  
Db 4201 TGAATTTCAACTTAAAGTGAAGCAGCATCTGGGTGTGAGAGTGAACAAGCGTCTCTGAG 4260  
| | | | |  
QY 4261 ACTGCTCAGGGCTATCTCTCTCAGAGTGAACATTTTAACTCAGAGAGGGATACATGTC 4320  
| | | | |  
Db 4261 ACTGCTCAGGGCTATCTCTCTCAGAGTGAACATTTTAACTCAGAGAGGGATACATGTC 4320  
| | | | |  
QY 4321 AACATTAACCTGATAAAGCTCCAGAGAAATGGCTGAACCTGATGATAAGCAGC 4380  
| | | | |

Db 4321 AACATTAACCTGATAAAGCTCCAGAGAAATGGCTGAACCTGATGATAAGCAGC 4380  
| | | | |  
QY 4381 ATGGAGCCAGCCTTCTTAACAGTACCTCTTCATCATTAAGTACTCTCTGCGCTTGAGG 4440  
| | | | |  
Db 4381 ATGGAGCCAGCCTTCTTAACAGTACCTCTTCATCATTAAGTACTCTCTGCGCTTGAGG 4440  
| | | | |  
QY 4441 ACCGCGAAATCCAGAACAAAGCAATCAGAAAAGAGTATTAACCTTCAAGAAAAGTA 4500  
| | | | |  
Db 4441 ACCGCGAAATCCAGAACAAAGCAATCAGAAAAGAGTATTAACCTTCAAGAAAAGTA 4500  
| | | | |  
QY 4501 GTGAATACCTTAAAGCCAGAAATCCAGAGGCTTCTGCTGACAAAGTTGAGGCTG 4560  
| | | | |  
Db 4501 GTGAATACCTTAAAGCCAGAAATCCAGAGGCTTCTGCTGACAAAGTTGAGGCTG 4560  
| | | | |  
QY 4561 CAGATAGTTCTAACAGTAAATAAAGAACAGAGTGAAGAGTCAATCCCTCTTAAT 4620  
| | | | |  
Db 4561 CAGATAGTTCTAACAGTAAATAAAGAACAGAGTGAAGAGTCAATCCCTCTTAAT 4620  
| | | | |  
QY 4621 GCCATCATTTGATGATGAGTGAACATGCAACGTTGCTGAGGAGCTTGAGATGAA 4680  
| | | | |  
Db 4621 GCCATCATTTGATGATGAGTGAACATGCAACGTTGCTGAGGAGCTTGAGATGAA 4680  
| | | | |  
QY 4681 ACTACCCATCTCAAGAGAGCTCATTAAGTGTGATGTGAGAGAGCAAGCTGAG 4740  
| | | | |  
Db 4681 ACTACCCATCTCAAGAGAGCTCATTAAGTGTGATGTGAGAGAGCAAGCTGAG 4740  
| | | | |  
QY 4741 AGTCTGGGCCACAGATTTGACGAAACATCTTAACCTGCAAGGCAAGATCTAGAGGAA 4800  
| | | | |  
Db 4741 AGTCTGGGCCACAGATTTGACGAAACATCTTAACCTGCAAGGCAAGATCTAGAGGAA 4800  
| | | | |  
QY 4801 CCCCTTACCTGGAATCTGGAATTCAGCCCTTCTCTGATGACCCGTAATCTAATCTTCTG 4860  
| | | | |  
Db 4801 CCCCTTACCTGGAATCTGGAATTCAGCCCTTCTCTGATGACCCGTAATCTAATCTTCTG 4860  
| | | | |  
QY 4861 AAGACAGAGCCCAAGAGCTCAGTGTGTGCAACATPACATCTTCAACTCTGCAATTGA 4920  
| | | | |  
Db 4861 AAGACAGAGCCCAAGAGCTCAGTGTGTGCAACATPACATCTTCAACTCTGCAATTGA 4920  
| | | | |  
QY 4921 AAGTTCCTCCAAATGAAGTTGACAGAAATCTGCCAGAGTCCAGCTGCTCATACTAG 4980  
| | | | |  
Db 4921 AAGTTCCTCCAAATGAAGTTGACAGAAATCTGCCAGAGTCCAGCTGCTCATACTAG 4980  
| | | | |  
QY 4981 ATACTGCTGGGTATTAATGCAATGGAAGAAATGTGAGAGGAGAAAGCCAAATTTGAAG 5040  
| | | | |  
Db 4981 ATACTGCTGGGTATTAATGCAATGGAAGAAATGTGAGAGGAGAAAGCCAAATTTGAAG 5040  
| | | | |  
QY 5041 CTTCAACAGAAAGGCTCAACAAAAGATGTCCATGCTGTGCTGAGCCCAAG 5100  
| | | | |  
Db 5041 CTTCAACAGAAAGGCTCAACAAAAGATGTCCATGCTGTGCTGAGCCCAAG 5100  
| | | | |  
QY 5101 AATTTATGCTGTGTACAAAGTTTCCAGAAAACCAACATCACTTAACTAATTA 5160  
| | | | |  
Db 5101 AATTTATGCTGTGTACAAAGTTTCCAGAAAACCAACATCACTTAACTAATTA 5160  
| | | | |  
QY 5161 CTGAAGAGACTACTATGTTGTATGAAGAACAGATGCTGATTTGTGTGAACGGAAC 5220  
| | | | |  
Db 5161 CTGAAGAGACTACTATGTTGTATGAAGAACAGATGCTGATTTGTGTGAACGGAAC 5220  
| | | | |  
QY 5221 TGAATATTTTCTGGAATGCGGGAGGAAATGSGTAGTATTTCTGGGTGACCC 5280  
| | | | |  
Db 5221 TGAATATTTTCTGGAATGCGGGAGGAAATGSGTAGTATTTCTGGGTGACCC 5280  
| | | | |  
QY 5281 AGTCTATTAAGAAAGAAATATGCTGAATGAGCATGATTTTGAAGTCAAGAGATGTGG 5340  
| | | | |  
Db 5281 AGTCTATTAAGAAAGAAATATGCTGAATGAGCATGATTTTGAAGTCAAGAGATGTGG 5340  
| | | | |  
QY 5341 TCAATGGAAGAAACCAAGAGTCCAAAGCAAGAGATCCCAAGAGCAAGAAAGATCT 5400  
| | | | |  
Db 5341 TCAATGGAAGAAACCAAGAGTCCAAAGCAAGAGATCCCAAGAGCAAGAAAGATCT 5400  
| | | | |  
QY 5401 TCAGGGGGCTAGAAATCTGTTGATGGGACCTTCAACAAATGCTCCAGATCAACTGG 5460  
| | | | |

Db 5401 TCAGGGGGCTAGAAATCTGTTGCTATGAGGCCCTTCCACCAACATGCCCAAGATCAACTG 5460  
Qy 5461 AATGATGATGACAGTGTGTGCTTCTGTGTGTAAGAGCTTTCATTCATTCACCTTG 5520  
Db 5461 AATGATGATGACAGTGTGTGCTTCTGTGTGTAAGAGCTTTCATTCATTCACCTTG 5520  
Qy 5521 GCACAGGTGTCCACCAATTGTGTGTGTCAGCCAGATGCTGACAGAGCAATGAGCT 5580  
Db 5521 GCACAGGTGTCCACCAATTGTGTGTGTCAGCCAGATGCTGACAGAGCAATGAGCT 5580  
Qy 5581 TCCATGCAATTTGGGAGATGTGTGAGGCACTGTGTGTACCCGAGAGTGGTGTGACA 5640  
Db 5581 TCCATGCAATTTGGGAGATGTGTGAGGCACTGTGTGTACCCGAGAGTGGTGTGACA 5640  
Qy 5641 GTGTGCACTCTACAGAGCCAGAGCTGAGACCTGATCTGATACCCAGATCCCCCA 5700  
Db 5641 GTGTGCACTCTACAGAGCCAGAGCTGAGACCTGATCTGATACCCAGATCCCCCA 5700  
Qy 5701 GCCACTACTGA 5711  
Db 5701 GCCACTACTGA 5711

RESULT 7  
US-09-982-828-5  
Sequence 5, Application US/09982828  
Publication No. US20030022184A1  
GENERAL INFORMATION:  
APPLICANT: Murphy, Patricia D.  
Allen, Antoinette C.  
Alvares, Christopher P.  
Critz, Brenda S.  
Olson, Sheri J.  
Thurber, Denise  
Zeng, Bin  
TITLE OF INVENTION: Coding Sequences of the Human  
BRCA1 Gene  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morgan Lewis & Bockius LLP  
STREET: 1111 Pennsylvania Avenue N. W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/982,828  
FILING DATE: 22-Oct-2001  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/074,453  
FILING DATE: 1998-05-06  
APPLICATION NUMBER: US 08/798,691  
FILING DATE: 1997-02-12  
APPLICATION NUMBER: US 08/598,591  
FILING DATE: 1996-02-12  
ATTORNEY/AGENT INFORMATION:  
NAME: Michael S. Tuscan  
REGISTRATION NUMBER: 43,210  
REFERENCE/DOCKET NUMBER: 44921-5053-01-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-739-3000  
TELEFAX: 202-739-3001  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5711 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: not relevant

TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
STRAIN: BRCA1 (om13)  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17  
MAP POSITION: 17q21  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-982-828-5  
Query Match 99.8%; Score 5701.4; DB 11; Length 5711;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 5705; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Qy 1 AGTCGCTGAGACTTCTCTGAGACCCGACACAGGCTGTGGGTTTCTAGATTAAGTGGCC 60  
Db 1 AGTCGCTGAGACTTCTCTGAGACCCGACACAGGCTGTGGGTTTCTAGATTAAGTGGCC 60  
Qy 61 CTTGGGCTCAGAGAGCCCTTCACTCTGCTGTGGTAAAGTTCATTTGAAACAGAAAGAA 120  
Db 61 CTTGGGCTCAGAGAGCCCTTCACTCTGCTGTGGTAAAGTTCATTTGAAACAGAAAGAA 120  
Qy 121 TGGATTTATCTGCTCTTTCGCTTGAAGAGTACAAATGTCATTATGTCAGAGAAA 180  
Db 121 TGGATTTATCTGCTCTTTCGCTTGAAGAGTACAAATGTCATTATGTCAGAGAAA 180  
Qy 181 TCTTAGAGTGTCCATCTGTCTGTGAGTTGATCAAGAACTGTCTCAACAAAGTGTACC 240  
Db 181 TCTTAGAGTGTCCATCTGTCTGTGAGTTGATCAAGAACTGTCTCAACAAAGTGTACC 240  
Qy 241 ACATATTTTGAAATTTTGATGCTGAACCTTCAACCAAGAAAGGCTTCAAGT 300  
Db 241 ACATATTTTGAAATTTTGATGCTGAACCTTCAACCAAGAAAGGCTTCAAGT 300  
Qy 301 GTCTTTATGTAAGATATATTAACAAAGAGCTTCAACAAAGAGATTTAGTC 360  
Db 301 GTCTTTATGTAAGATATATTAACAAAGAGCTTCAACAAAGAGATTTAGTC 360  
Qy 361 AACTTTGTAAGAGCTATTTGAAATCAATTTGCTTTTCAAGCTTGAACAGGTTGAGT 420  
Db 361 AACTTTGTAAGAGCTATTTGAAATCAATTTGCTTTTCAAGCTTGAACAGGTTGAGT 420  
Qy 421 ATGCAACAGCTATTAATTTTGCAAAAGAAATTAATCTCTGGAACATCTAAAGATG 480  
Db 421 ATGCAACAGCTATTAATTTTGCAAAAGAAATTAATCTCTGGAACATCTAAAGATG 480  
Qy 481 AAGTTCTATCATCCAAAGTATGAGGCTACAGAAACGCTGCAAAAGACTTCTACAGAGT 540  
Db 481 AAGTTCTATCATCCAAAGTATGAGGCTACAGAAACGCTGCAAAAGACTTCTACAGAGT 540  
Qy 541 AACCCGAAATCTCTCTTCCAGAGAAACAGCTCAGTGTCAACTCTTCAACCTTGGAA 600  
Db 541 AACCCGAAATCTCTCTTCCAGAGAAACAGCTCAGTGTCAACTCTTCAACCTTGGAA 600  
Qy 601 CTGGAAGACTCTGAGGACCAAGAGGATACCACTCAAAAGACCTGTCTACACTTG 660  
Db 601 CTGGAAGACTCTGAGGACCAAGAGGATACCACTCAAAAGACCTGTCTACACTTG 660  
Qy 661 AATTGGATCTGATTTCTTCTGAGATACCGTTAATAAGCACTTAATTCAGTGTGGAG 720  
Db 661 AATTGGATCTGATTTCTTCTGAGATACCGTTAATAAGCACTTAATTCAGTGTGGAG 720  
Qy 721 ATCAAGATTTGTAACAATCAACCCCTCAAGGAACAGAGGATGAATCAAGTTGGATTCTG 780  
Db 721 ATCAAGATTTGTAACAATCAACCCCTCAAGGAACAGAGGATGAATCAAGTTGGATTCTG 780  
Qy 781 CAAAAAGGCTGCTGTGGAATTTTCTGAGCGGATGTAACAAATCTGAACATCAAC 840  
Db 781 CAAAAAGGCTGCTGTGGAATTTTCTGAGCGGATGTAACAAATCTGAACATCAAC 840  
Qy 841 CCAGTAATATGATTTGAACACCACTGAGAGGCTGAGGATCCAGAAAGT 900  
Db 841 CCAGTAATATGATTTGAACACCACTGAGAGGCTGAGGATCCAGAAAGT 900



Dh 841 CCAGTAATATGATTTGAAACCACTGAAAGCGTGACGTGAGAGCATCCAGAAAAGT 900  
Qy 901 ATCAGGAGTTCGTCTTCAAACTTGATGATGAGACCATGAGCAAAATCTGACCA 960  
Db 901 ATCAGGAGTTCGTCTTCAAACTTGATGAGACCATGAGCAAAATCTGACCA 960  
Qy 961 GCTCATTCAGCATGAGAAACAGCAGTTTATTACTCATTAAGACAGAAATGATGAGAA 1020  
Db 961 GCTCATTCAGCATGAGAAACAGCAGTTTATTACTCATTAAGACAGAAATGATGAGAA 1020  
Qy 1021 AGCGTGAATTCGTATATTAAGCAACAGCCTGCTTGAAGAGAGCAATTAACAGAT 1080  
Db 1021 AGCGTGAATTCGTATATTAAGCAACAGCCTGCTTGAAGAGAGCAATTAACAGAT 1080  
Qy 1081 GGGCTGGAATGAGAAACATGATATGATAGGCGGATCCCGACACAGAAAAAAGTNG 1140  
Db 1081 GGGCTGGAATGAGAAACATGATATGATAGGCGGATCCCGACACAGAAAAAAGTNG 1140  
Qy 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGAAATPAGCAGAACTGCCATGCT 1200  
Db 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGAAATPAGCAGAACTGCCATGCT 1200  
Qy 1201 CAGAGAACTCTAGAGATACTGAAAGATGTTCTTGATTAACATAATAGCAGCATTCAGA 1260  
Db 1201 CAGAGAACTCTAGAGATACTGAAAGATGTTCTTGATTAACATAATAGCAGCATTCAGA 1260  
Qy 1261 AAGTTAATGAGTGGTTTCCAGAAATGATGAACTGTAGTTCATGATGATCACTGATNG 1320  
Db 1261 AAGTTAATGAGTGGTTTCCAGAAATGATGAACTGTAGTTCATGATGATCACTGATNG 1320  
Qy 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGTGTATTTGAGACGTTTAAATGAGTNG 1380  
Db 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGTGTATTTGAGACGTTTAAATGAGTNG 1380  
Qy 1381 AATAATCTGTTCTTCAAGAAAAATGACTTAAGTGGCAATGATCTCATGAGGCTTTAA 1440  
Db 1381 AATAATCTGTTCTTCAAGAAAAATGACTTAAGTGGCAATGATCTCATGAGGCTTTAA 1440  
Qy 1441 TATGTAAAAGTGAAGAGTTCACCTCAATCATGTGAGAGTATATTTGAAGCAAAATAT 1500  
Db 1441 TATGTAAAAGTGAAGAGTTCACCTCAATCATGTGAGAGTATATTTGAAGCAAAATAT 1500  
Qy 1501 TTGGGAAAACTATGGAAGAAAGGCAAGCCTCCCACTTAAAGCAATGAACTGAAAAATC 1560  
Db 1501 TTGGGAAAACTATGGAAGAAAGGCAAGCCTCCCACTTAAAGCAATGAACTGAAAAATC 1560  
Qy 1561 TAAATTAAGAGCATTTGTCTGAGCAAGATTAATCAAGAGGTCCTCCCTCAAAATA 1620  
Db 1561 TAAATTAAGAGCATTTGTCTGAGCAAGATTAATCAAGAGGTCCTCCCTCAAAATA 1620  
Qy 1621 AATTAAACGTTAAAGAGACCTTACATGAGGCTTCACTCTGAGGATTTTATCAAGAAAG 1680  
Db 1621 AATTAAACGTTAAAGAGACCTTACATGAGGCTTCACTCTGAGGATTTTATCAAGAAAG 1680  
Qy 1681 CAGATTTGGCAGTTCAAAAGACTCCTGAAATGATTAATCAAGGAACTAAACCAAGAGC 1740  
Db 1681 CAGATTTGGCAGTTCAAAAGACTCCTGAAATGATTAATCAAGGAACTAAACCAAGAGC 1740  
Qy 1741 AGAATGCTCAAGTGAATATTAATAATGATGCTATGAGAAATTAACAAAGGTGAT 1800  
Db 1741 AGAATGCTCAAGTGAATATTAATAATGATGCTATGAGAAATTAACAAAGGTGAT 1800  
Qy 1801 CTATTCAGATGAGAAAAATCTTAAACCAATGAAATCACTCGAAAAAATCTGCTTCA 1860  
Db 1801 CTATTCAGATGAGAAAAATCTTAAACCAATGAAATCACTCGAAAAAATCTGCTTCA 1860  
Qy 1861 AAAAGAAAGCTGAACCTTAAGCAGCAGTATTAAGAAATTAAGAAATTCGAATTAATACC 1920  
Db 1861 AAAAGAAAGCTGAACCTTAAGCAGCAGTATTAAGAAATTAAGAAATTCGAATTAATACC 1920  
Qy 1921 ACAATTTCAAAAGCACTTAAGGCTGAGAGGAAAGTCTTCAACAGGCAATATTC 1980  
Db 1921 ACAATTTCAAAAGCACTTAAGGCTGAGAGGAAAGTCTTCAACAGGCAATATTC 1980

Qy 1981 ATGCGCTTGAACCTAGTACTAGTGAATCTTAAGCCCACTTAATTGTACTGAATTGCAA 2040  
Db 1981 ATGCGCTTGAACCTAGTACTAGTGAATCTTAAGCCCACTTAATTGTACTGAATTGCAA 2040  
Qy 2041 TTGATAGTGTCTTACAGCAGTGAAGATTAAGAAAAAAGATACAAACCAATGCGCATCA 2100  
Db 2041 TTGATAGTGTCTTACAGCAGTGAAGATTAAGAAAAAAGATACAAACCAATGCGCATCA 2100  
Qy 2101 GGCACAGCAAAACCTTCACTCATGGAAGTAAAGAACTTGCAACTGAGCCAAAGAGA 2160  
Db 2101 GGCACAGCAAAACCTTCACTCATGGAAGTAAAGAACTTGCAACTGAGCCAAAGAGA 2160  
Qy 2161 GTAACAAAGCCAAATGAACAGCAAGTAAACATGACAGATTAATCTTCCAGAGCTGA 2220  
Db 2161 GTAACAAAGCCAAATGAACAGCAAGTAAACATGACAGATTAATCTTCCAGAGCTGA 2220  
Qy 2221 AGTTAACAAATGCACTGCTGTTCTTTACTAAGTGTCAAAATACAGTGAACCTTAAGAAAT 2280  
Db 2221 AGTTAACAAATGCACTGCTGTTCTTTACTAAGTGTCAAAATACAGTGAACCTTAAGAAAT 2280  
Qy 2281 TTGTCAATCTAGCCTTCCAGAGAGAAAGAAAGAAAGAACTGAAACAGTTAAAGTGT 2340  
Db 2281 TTGTCAATCTAGCCTTCCAGAGAGAAAGAAAGAAAGAACTGAAACAGTTAAAGTGT 2340  
Qy 2341 CTAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTGCAAACTG 2400  
Db 2341 CTAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTGCAAACTG 2400  
Qy 2401 AAAAGTCTGTAGAGAGTGAAGTATTTCACTGATACCTGATACGATTAATGAGCACTGAG 2460  
Db 2401 AAAAGTCTGTAGAGAGTGAAGTATTTCACTGATACCTGATACGATTAATGAGCACTGAG 2460  
Qy 2461 AAAAGTCTGTAGAGAGTGAAGTATTTCACTGATACCTGATACGATTAATGAGCACTGAG 2520  
Db 2461 AAAAGTCTGTAGAGAGTGAAGTATTTCACTGATACCTGATACGATTAATGAGCACTGAG 2520  
Qy 2521 GTGTGAGTCAAGTGAAGCACTTTGAAAAACCCCAAGGCACTAATTCATGCTGTTCCAAAG 2580  
Db 2521 GTGTGAGTCAAGTGAAGCACTTTGAAAAACCCCAAGGCACTAATTCATGCTGTTCCAAAG 2580  
Qy 2581 AATAATGAATGACACAGAAAGCTTTAATGATCACTGAGGACATGAATTAACCAAGTGC 2640  
Db 2581 AATAATGAATGACACAGAAAGCTTTAATGATCACTGAGGACATGAATTAACCAAGTGC 2640  
Qy 2641 GGGAAACAAAGCATGAAGAAATGAAAGTGAATCTGATGCTCAGTATTTGCAAGATACAT 2700  
Db 2641 GGGAAACAAAGCATGAAGAAATGAAAGTGAATCTGATGCTCAGTATTTGCAAGATACAT 2700  
Qy 2701 TCAAGTCTTCAAGGCGCAGTCAATTTGCTGTTTCAATTCAGAGAAATGCAAGAGG 2760  
Db 2701 TCAAGTCTTCAAGGCGCAGTCAATTTGCTGTTTCAATTCAGAGAAATGCAAGAGG 2760  
Qy 2761 AATGTCGAACATTCCTGCGCCAGCTGAGGCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
Db 2761 AATGTCGAACATTCCTGCGCCAGCTGAGGCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
Qy 2821 TTGAATGTGAACAAAGAGAAATCAAGAGAAATGATCTTAATCAAGCCTGTAC 2880  
Db 2821 TTGAATGTGAACAAAGAGAAATCAAGAGAAATGATCTTAATCAAGCCTGTAC 2880  
Qy 2881 AGACAGTAAATATCACTGCAAGGCTTCTGTGTGTGTCATATCAATCTCAAGCTGTAC 2940  
Db 2881 AGACAGTAAATATCACTGCAAGGCTTCTGTGTGTGTCATATCAATCTCAAGCTGTAC 2940  
Qy 2941 ATGCAAAATGATATCAAGAGGCTTCTGTGTGTGTCATATCAATCTCAAGCTGTAC 3000  
Db 2941 ATGCAAAATGATATCAAGAGGCTTCTGTGTGTGTCATATCAATCTCAAGCTGTAC 3000  
Qy 3001 ACAGAACTGCACTATTACTCAAAATTAACATGACATTTTACAAACCCATATGATATAC 3060  
Db 3001 ACAGAACTGCACTATTACTCAAAATTAACATGACATTTTACAAACCCATATGATATAC 3060

QY 3061 CACCATTCTTCCATCAAGTCATTTGTTAAACTAATGTAGAAGAAATCTGCTAGAG 3120  
| | | | |  
Db 3061 CACCATTCTTCCATCAAGTCATTTGTTAAACTAATGTAGAAGAAATCTGCTAGAG 3120  
QY 3121 AAACTTTGAGGAACTTCATGTCACTGAAAGAGAAATGGAAATGAGACATTTCCA 3180  
| | | | |  
Db 3121 AAACTTTGAGGAACTTCATGTCACTGAAAGAGAAATGGAAATGAGACATTTCCA 3180  
QY 3181 GTCAGTGAGCACTTTAGCCCTTAATCACTTAGAGAAATCTTTTAAAGAGCCAGCT 3240  
| | | | |  
Db 3181 GTCAGTGAGCACTTTAGCCCTTAATCACTTAGAGAAATCTTTTAAAGAGCCAGCT 3240  
QY 3241 CAGCAATTTATGAAGTAGGTTCCAGTAACTGAAGTGGCTCCAGTATTAATGAA 3300  
| | | | |  
Db 3241 CAGCAATTTATGAAGTAGGTTCCAGTAACTGAAGTGGCTCCAGTATTAATGAA 3300  
QY 3301 TAGGTTCCAGTGATGAAACATTCAGACGAACTAGTAGAAACAGAGGCCAAATTTGA 3360  
| | | | |  
Db 3301 TAGGTTCCAGTGATGAAACATTCAGACGAACTAGTAGAAACAGAGGCCAAATTTGA 3360  
QY 3361 ATGCTATGCTTAGATTAAGGGGTTTGGCACTGAGAGTCTATTAACAAAGCTTCTGGAA 3420  
| | | | |  
Db 3361 ATGCTATGCTTAGATTAAGGGGTTTGGCACTGAGAGTCTATTAACAAAGCTTCTGGAA 3420  
QY 3421 GTAATTGTAGCATCTGTAATTAATAAAGCAAGAAATGAGAAAGTAGTTCAGCTGTA 3480  
| | | | |  
Db 3421 GTAATTGTAGCATCTGTAATTAATAAAGCAAGAAATGAGAAAGTAGTTCAGCTGTA 3480  
QY 3481 ATACGATTTTCTCTCATATCTGATTTTCAATTAAGAACAGCTTATGGAGTAGTC 3540  
| | | | |  
Db 3481 ATACGATTTTCTCTCATATCTGATTTTCAATTAAGAACAGCTTATGGAGTAGTC 3540  
QY 3541 ATGCTATCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGTAATGAAATGAA 3600  
| | | | |  
Db 3541 ATGCTATCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGTAATGAAATGAA 3600  
QY 3601 AAGATATAGTTTCTGTAATGATGAATTAAGGAAATGCTGCTGTTTATGACAAACG 3660  
| | | | |  
Db 3601 AAGATATAGTTTCTGTAATGATGAATTAAGGAAATGCTGCTGTTTATGACAAACG 3660  
QY 3661 TCCAGAGAGAGAGCTTAGCAGAGAGTCTAGCCCTTTCACCCATACCATTTGGCTCAG 3720  
| | | | |  
Db 3661 TCCAGAGAGAGAGCTTAGCAGAGAGTCTAGCCCTTTCACCCATACCATTTGGCTCAG 3720  
QY 3721 GTTACCAAGAGAGGAGCAAGAAATTAAGTCTCAGAGAGAACTTACTGAGAGATG 3780  
| | | | |  
Db 3721 GTTACCAAGAGAGGAGCAAGAAATTAAGTCTCAGAGAGAACTTACTGAGAGATG 3780  
QY 3781 AAGAGCTTCCCTGCTTCCAACTTGTATTTGTAAAGTAAACAATATACCTTCTCAGT 3840  
| | | | |  
Db 3781 AAGAGCTTCCCTGCTTCCAACTTGTATTTGTAAAGTAAACAATATATACCTTCTCAGT 3840  
QY 3841 CTACTAGGCAATGACCCGTTGCTACCGAGTGTCTGTCTAAGAACACAGAGAGAAATTAAT 3900  
| | | | |  
Db 3841 CTACTAGGCAATGACCCGTTGCTACCGAGTGTCTGTCTAAGAACACAGAGAGAAATTAAT 3900  
QY 3901 TATCATTTGAAGAAATGCTTAATGATGCTGAGTAACAGATTAATTTGGCAAGGATCTC 3960  
| | | | |  
Db 3901 TATCATTTGAAGAAATGCTTAATGATGCTGAGTAACAGATTAATTTGGCAAGGATCTC 3960  
QY 3961 AGGAAATCATCTTATGAGAGAAACAAATATGTTGCTAGCTTGTCTTCAAGTCA 4020  
| | | | |  
Db 3961 AGGAAATCATCTTATGAGAGAAACAAATATGTTGCTAGCTTGTCTTCAAGTCA 4020  
QY 4021 GTGAATTGGAAGACTTGACTGCAATTAACAAACCCAGAGATCTTTCTTGAATGTTT 4080  
| | | | |  
Db 4021 GTGAATTGGAAGACTTGACTGCAATTAACAAACCCAGAGATCTTTCTTGAATGTTT 4080  
QY 4081 CCAAAACAATAGAGCATAGTCTGAAAGCCAGAGAGTGTGTCTGATGACAAAGAAATTTGG 4140  
| | | | |  
Db 4081 CCAAAACAATAGAGCATAGTCTGAAAGCCAGAGAGTGTGTCTGATGACAAAGAAATTTGG 4140  
QY 4141 TTTCAGATGATGAAGAAAGAGAAACGGGCTTGGAAAGAAATTAATCAAGAGAGCA 4200  
| | | | |

Db 4141 TTTCAGATGATGAAGAAAGAGAAACGGGCTTGGAAAGAAATTAATCAAGAGAGCA 4200  
| | | | |  
QY 4201 TGAATTTAACTTAGAGTGAAGACAGATCTGGGTGTGAGTGAAGAAACAAGCTCTCTGAG 4260  
| | | | |  
Db 4201 TGAATTTAACTTAGAGTGAAGACAGATCTGGGTGTGAGTGAAGAAACAAGCTCTCTGAG 4260  
QY 4261 ACTGCTCAGGGCTATCTCTCAGAGTGAATTTTAACTCAGCAGAGAGGATACATGC 4320  
| | | | |  
Db 4261 ACTGCTCAGGGCTATCTCTCAGAGTGAATTTTAACTCAGCAGAGAGGATACATGC 4320  
QY 4321 AACATTAACCTGATTAAGGCTCCAGAGAGAAATGGCTGAACCTGAAGCTGTGTAGAACGC 4380  
| | | | |  
Db 4321 AACATTAACCTGATTAAGGCTCCAGAGAGAAATGGCTGAACCTGAAGCTGTGTAGAACGC 4380  
QY 4381 ATGGAGCCAGCTTCTTAACAGCTACCTTCATCATTAAGTGACTCTGCTGAGG 4440  
| | | | |  
Db 4381 ATGGAGCCAGCTTCTTAACAGCTACCTTCATCATTAAGTGACTCTGCTGAGG 4440  
QY 4441 ACCTGGCAATCCAGAACAAAGCACTCAGAAAAAGCACTTAACTTCAAGAAAGTA 4500  
| | | | |  
Db 4441 ACCTGGCAATCCAGAACAAAGCACTCAGAAAAAGCACTTAACTTCAAGAAAGTA 4500  
QY 4501 GTGAATACCTTATAGCCAGAAATCCAGAAAGGCTTTCTGCTGACAAAGTTGAGGTCG 4560  
| | | | |  
Db 4501 GTGAATACCTTATAGCCAGAAATCCAGAAAGGCTTTCTGCTGACAAAGTTGAGGTCG 4560  
QY 4561 CAGATAGTTCTTACGATTAATAAAGCAAGAGTGAAGATCAATCCCTTCTAAT 4620  
| | | | |  
Db 4561 CAGATAGTTCTTACGATTAATAAAGCAAGAGTGAAGATCAATCCCTTCTAAT 4620  
QY 4621 GCCCATCAATTAAGATAGTGTGATGATGCAATGCTCTGGAGCTTCAAGAAATGAA 4680  
| | | | |  
Db 4621 GCCCATCAATTAAGATAGTGTGATGATGCAATGCTCTGGAGCTTCAAGAAATGAA 4680  
QY 4681 ACTACCATCTCAAGAGAGGCTCAATTAAGGTTGTGATGTGAGAGCAACAGCTGGAAG 4740  
| | | | |  
Db 4681 ACTACCATCTCAAGAGAGGCTCAATTAAGGTTGTGATGTGAGAGCAACAGCTGGAAG 4740  
QY 4741 AGTCTGGGCCCAAGATTTGCGGAAACATCTTACTTCCAGAGCAAGATCTTAAGGAA 4800  
| | | | |  
Db 4741 AGTCTGGGCCCAAGATTTGCGGAAACATCTTACTTCCAGAGCAAGATCTTAAGGAA 4800  
QY 4801 CCCCTTACCTGGATCTGGAATCAGAGTCAAGCTCTTCTGTGATGACCTGGAATCTGAATCTCTG 4860  
| | | | |  
Db 4801 CCCCTTACCTGGATCTGGAATCAGAGTCAAGCTCTTCTGTGATGACCTGGAATCTGAATCTCTG 4860  
QY 4861 AAGACAGAGCCCAAGAGTCAAGCTCTGTTGGCAACATACATCTTCAACCTCTGATTTGA 4920  
| | | | |  
Db 4861 AAGACAGAGCCCAAGAGTCAAGCTCTGTTGGCAACATACATCTTCAACCTCTGATTTGA 4920  
QY 4921 AAGTCCCAATTAAGAAATGTCAGATCTGCCCCAGAGTCCAGCTGCTGCTCATATCTA 4980  
| | | | |  
Db 4921 AAGTCCCAATTAAGAAATGTCAGATCTGCCCCAGAGTCCAGCTGCTGCTCATATCTA 4980  
QY 4981 ATACTGCTGGGTAAATGAATGGAATGGAAGAAAGTGAACAGAGAGAAACCGAAATTTGAC 5040  
| | | | |  
Db 4981 ATACTGCTGGGTAAATGAATGGAATGGAAGAAAGTGAACAGAGAGAAACCGAAATTTGAC 5040  
QY 5041 CTTCAACAGAAAGGCTCAACAAAGAAATGTCATGTGTGTGCTGAGCTGACCCAGAG 5100  
| | | | |  
Db 5041 CTTCAACAGAAAGGCTCAACAAAGAAATGTCATGTGTGTGCTGAGCTGACCCAGAG 5100  
QY 5101 AATTTATGCTCTGTGTATCAAGTTTGGCAAAACCAACATCACTTAACTTAATTA 5160  
| | | | |  
Db 5101 AATTTATGCTCTGTGTATCAAGTTTGGCAAAACCAACATCACTTAACTTAATTA 5160  
QY 5161 CTGAAGAGACTACATCAATGTTGTATGAAACAGATGCTGAGTTGTGTGAAACGAGCAC 5220  
| | | | |  
Db 5161 CTGAAGAGACTACATCAATGTTGTATGAAACAGATGCTGAGTTGTGTGAAACGAGCAC 5220  
QY 5221 TGAATATTTTCTAGGAATTCGGAGAGAAATGGGTAGTAACTATTTCTGGGTGACCC 5280  
| | | | |

Db 5221 TGAATATTTTCTAGGAATTCGGAGGAAATGGTAGTATTTCTGGTGACCC 5280  
Qy 5281 AGCTATTAAGAAGAAAATGCTGAATGAGCATGATTTGAAGTCAAGAGATGCG 5340  
Db 5281 AGCTATTAAGAAGAAAATGCTGAATGAGCATGATTTGAAGTCAAGAGATGCG 5340  
Qy 5341 TCAATGAAAGAAACCAACCAAGTCCAAAGCAGCAAGAAATCCAGAGACAGAAATCT 5400  
Db 5341 TCAATGAAAGAAACCAACCAAGTCCAAAGCAGCAAGAAATCCAGAGACAGAAATCT 5400  
Qy 5401 TCAGAGGAGCTAGAAATCTGTTGCTATGAGGCCCTTACCAACATGCCCAAGATCACTGG 5460  
Db 5401 TCAGAGGAGCTAGAAATCTGTTGCTATGAGGCCCTTACCAACATGCCCAAGATCACTGG 5460  
Qy 5461 AATGGAATGCTACACTGTGTGTGTCTTGTGTGAAGAGACTTTTCATCATTCACCTTG 5520  
Db 5461 AATGGAATGCTACACTGTGTGTGTCTTGTGTGAAGAGACTTTTCATCATTCACCTTG 5520  
Qy 5521 GCACAGGTGTCACCAATTTGTTGTGACAGCCAGATGCTGACAGAGACATGAGCT 5580  
Db 5521 GCACAGGTGTCACCAATTTGTTGTGACAGCCAGATGCTGACAGAGACATGAGCT 5580  
Qy 5581 TCCATGCAATTTGGCAGATGTGTGAAGCAGCTGTGTGACCCGAGAGTGGGTGTGACA 5640  
Db 5581 TCCATGCAATTTGGCAGATGTGTGAAGCAGCTGTGTGACCCGAGAGTGGGTGTGACA 5640  
Qy 5641 GTGTAGCACTTACCAAGTCCAGAGCTGACACTTACTATACCCCAAGTCCCAACA 5700  
Db 5641 GTGTAGCACTTACCAAGTCCAGAGCTGACACTTACTATACCCCAAGTCCCAACA 5700  
Qy 5701 GCCACTACTGA 5711  
Db 5701 GCCACTACTGA 5711

RESULT 8  
US-10-240-965-268  
; Sequence 268, Application US/10240965  
; Publication No. US20030165924A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: SHIFFMAN, Dov  
; APPLICANT: SOMOGYI, Roland  
; APPLICANT: LAWN, Richard M.  
; APPLICANT: SEILHAMER, Jeffrey J.  
; APPLICANT: PORTER, Gordon J.  
; APPLICANT: MIKITA, Thomas  
; APPLICANT: TAL, Julie  
; TITLE OF INVENTION: GENES EXPRESSED IN FOAM CELL DIFFERENTIATION  
; FILE REFERENCE: PA-0025 PCT  
; CURRENT APPLICATION NUMBER: US/10/240, 965  
; PRIOR FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: 60/195,106  
; NUMBER OF SEQ ID NOS: 276  
; SOFTWARE: PERL Program  
; SEQ ID NO 268  
; LENGTH: 5709  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURES:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: incyte ID No. US20030165924A1 1098141.1  
US-10-240-965-268

Query Match 98.9%; Score 5649.8; DB 13; Length 5709;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 5700; Conservative 0; Mismatches 7; Indels 6; Gaps 4;

Qy 1 AGCTGCTGAGACTTCTCTGACCCCGACCAAGGCTGTGGGTTTCTCAGATPACTGGGCC 60  
Db 1 AGCTGCTGAGACTTCTCTGACCCCGACCAAGGCTGTGGGTTTCTCAGATPACTGGGCC 60

Qy 61 CCTGCGCTCAGAGAGCCCTTCACCTCTGCTCTGGGTAAAGTTCAATGGAACAGAAAGAA 120  
Db 61 CCTGCGCTCAGAGAGCCCTTCACCTCTGCTCTGGGTAAAGTTCAATGGAACAGAAAGAA 120  
Qy 121 TGAATTAATCTGCTCTTTCGGGTGAAGAGTACAAAATGTCATTAAATGCTATGCAAAA 180  
Db 121 TGAATTAATCTGCTCTTTCGGGTGAAGAGTACAAAATGTCATTAAATGCTATGCAAAA 180  
Qy 181 TCTTAAGTGTCCCATCTGTCTGAGTTGATCAAGAAACCTGTCTCCAAAGTGTACC 240  
Db 181 TCTTAAGTGTCCCATCTGTCTGAGTTGATCAAGAAACCTGTCTCCAAAGTGTACC 240  
Qy 241 ACATATTTTGAATTTTGGACGTGAAATCTTCAACAGAAAGAGGCTTCACAGT 300  
Db 241 ACATATTTTGAATTTTGGACGTGAAATCTTCAACAGAAAGAGGCTTCACAGT 300  
Qy 301 GTCCCTTAATGTAAGATTAATTAACAAAGAGCCTTACAAAGAAATGATGCAATTTAGTC 360  
Db 301 GTCCCTTAATGTAAGATTAATTAACAAAGAGCCTTACAAAGAAATGATGCAATTTAGTC 360  
Qy 361 AACTTTGTAAGAGCTATGAAATCATTTGTGCTTTTACGCTTGAACACAGTTTGAAGT 420  
Db 361 AACTTTGTAAGAGCTATGAAATCATTTGTGCTTTTACGCTTGAACACAGTTTGAAGT 420  
Qy 421 ATGCAAAAGCTATTAATTTTGCAGAAAGAAATTAATCTCTGAAACATCTAAAGATG 480  
Db 421 ATGCAAAAGCTATTAATTTTGCAGAAAGAAATTAATCTCTGAAACATCTAAAGATG 480  
Qy 481 AAGTTTCTATCATCAAAAGTATGAGCTACAGAAACCGTCCCAAAAGCTTCTACAGAGTG 540  
Db 481 AAGTTTCTATCATCAAAAGTATGAGCTACAGAAACCGTCCCAAAAGCTTCTACAGAGTG 540  
Qy 541 AACCAGAAATCTTCTCTGAGAGAAACCACTCAAGTGTCAACTCTTAAACCTTGA 600  
Db 541 AACCAGAAATCTTCTCTGAGAGAAACCACTCAAGTGTCAACTCTTAAACCTTGA 600  
Qy 601 CTGTGAGAACTCTGAGGACAAAGCAGGATACCACTCAAAAGAGCTGTCTACATTTG 660  
Db 601 CTGTGAGAACTCTGAGGACAAAGCAGGATACCACTCAAAAGAGCTGTCTACATTTG 660  
Qy 661 AATGGGATCTGATTTCTTCTGAAGATACCGTTAATTAAGGCAATTAATGAGTGGAG 720  
Db 661 AATGGGATCTGATTTCTTCTGAAGATACCGTTAATTAAGGCAATTAATGAGTGGAG 720  
Qy 721 ATCAAGAAATTTTCAAAATCACCCCTCAAGGACCAAGGATGAATCAATTTGATTTG 780  
Db 721 ATCAAGAAATTTTCAAAATCACCCCTCAAGGACCAAGGATGAATCAATTTGATTTG 780  
Qy 781 CAAAAAGGCTGTGGAATTTCTGAGACGATGTGAACAAATGAATGACATCATCAAC 840  
Db 781 CAAAAAGGCTGTGGAATTTCTGAGACGATGTGAACAAATGAATGACATCATCAAC 840  
Qy 841 CCAATTAATTAATGATTTTGAACCACTGAGAGAGCTGTGAGAGGATCCAGAAAAGT 900  
Db 841 CCAATTAATTAATGATTTTGAACCACTGAGAGAGCTGTGAGAGGATCCAGAAAAGT 900  
Qy 901 ATCAAGGATGTTCTGTTTCAAACTTGCAATGTGAGCCATGTGGCAAAATCTCATGCCA 960  
Db 901 ATCAAGGATGTTCTGTTTCAAACTTGCAATGTGAGCCATGTGGCAAAATCTCATGCCA 960  
Qy 961 GCTCATTAACGACGAGAACGAGTTTATTAATCACTGAAGACAGAAATGATGAGAA 1020  
Db 961 GCTCATTAACGACGAGAACGAGTTTATTAATCACTGAAGACAGAAATGATGAGAA 1020  
Qy 1021 AGGCTGAATTTCTGTAATTAAGCAAGCCTGTGCTTGAAGAGGCCATTAACAGAT 1080  
Db 1021 AGGCTGAATTTCTGTAATTAAGCAAGCCTGTGCTTGAAGAGGCCATTAACAGAT 1080  
Qy 1081 GGGCTGGAAGTAAAGAAACATGTATGATGAGCGGATCCAGACACAGAAAAAGGTAG 1140  
Db 1081 GGGCTGGAAGTAAAGAAACATGTATGATGAGCGGATCCAGACACAGAAAAAGGTAG 1140  
Qy 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGAATTAACAGAAATCTGCATGCT 1200

1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAGATGAAATAGACAGAAACCTGCCATCT 1200  
1201 CAGAAATCTTGAATACTGAAGATGTTCTTGATTAACACTAAATAGCAGCATTCAGA 1260  
1201 CAGAAATCTTGAATACTGAAGATGTTCTTGATTAACACTAAATAGCAGCATTCAGA 1260  
1261 AAGTTAATGAGTGTCTTCCAGAAAGTGAACCTGTTGGTTCTGATAGCTCAGATGATG 1320  
1261 AAGTTAATGAGTGTCTTCCAGAAAGTGAACCTGTTGGTTCTGATAGCTCAGATGATG 1320  
1321 GGGAGTCTGAATCAAAATGCGCAAGTAGTGTATGTTGACGTTCTAAATAGGATGATG 1380  
1321 GGGAGTCTGAATCAAAATGCGCAAGTAGTGTATGTTGACGTTCTAAATAGGATGATG 1380  
1381 AATATTCGTGTTCTTCAAGAGAAAATAGCTTAATCTGCGCAGTGTCTTCAATGAGCTTTAA 1440  
1381 AATATTCGTGTTCTTCAAGAGAAAATAGCTTAATCTGCGCAGTGTCTTCAATGAGCTTTAA 1440  
1441 TATGTAAAGTGAAGAGTTCATCTCAATCAGTAGAGATTAATTTGAGACAAATAT 1500  
1441 TATGTAAAGTGAAGAGTTCATCTCAATCAGTAGAGATTAATTTGAGACAAATAT 1500  
1501 TTGGAAAACTTATCGAAGAGAGGCAAGCTTCCCACTTAAGCCATGTAACGTAATC 1560  
1501 TTGGAAAACTTATCGAAGAGAGGCAAGCTTCCCACTTAAGCCATGTAACGTAATC 1560  
1561 TAAATATGAGAGCAATTTGTTACTGAGCCACAGATTAATCAAGAGTCTCCCTCACAAATA 1620  
1561 TAAATATGAGAGCAATTTGTTACTGAGCCACAGATTAATCAAGAGTCTCCCTCACAAATA 1620  
1621 AATTAAACGCTAAAAAGAGACCTACATCAGGCGCTTCATCTGAGGATTTTATCAAGAAAG 1680  
1621 AATTAAACGCTAAAAAGAGACCTACATCAGGCGCTTCATCTGAGGATTTTATCAAGAAAG 1680  
1681 CAGATTTGGCAGTTCAAAAAGACTCTGAAATGATTAATCAGGGAACCTAACCAACGAGGC 1740  
1681 CAGATTTGGCAGTTCAAAAAGACTCTGAAATGATTAATCAGGGAACCTAACCAACGAGGC 1740  
1741 AGAATGCTCAAGTGAATGAAATTTACTATAGTGTGATGAGAAATTAACAAAGATGATT 1800  
1741 AGAATGCTCAAGTGAATGAAATTTACTATAGTGTGATGAGAAATTAACAAAGATGATT 1800  
1801 CTATTCAGAAATGAGAAAAATCTTAACCAATAGATCACTCGAAAAAGAACTCTGTTTCA 1860  
1801 CTATTCAGAAATGAGAAAAATCTTAACCAATAGATCACTCGAAAAAGAACTCTGTTTCA 1860  
1861 AAACGAAAGCTGAACCTTAAGCAGCAGTATAGCAATATGAACTGCAATTAATATCC 1920  
1861 AAACGAAAGCTGAACCTTAAGCAGCAGTATAGCAATATGAACTGCAATTAATATCC 1920  
1921 ACAATTTCAAAAAGCACTTAAGAAATAGGCTGAGAGAGAACTCTTCAACGAGGATATTC 1980  
1921 ACAATTTCAAAAAGCACTTAAGAAATAGGCTGAGAGAGAACTCTTCAACGAGGATATTC 1980  
1981 ATGCGCTTGAACCTAGTAGTCACTAGTAAATCTTAAGCCCACTTAATTTGATGAAATTCGAAA 2040  
1981 ATGCGCTTGAACCTAGTAGTCACTAGTAAATCTTAAGCCCACTTAATTTGATGAAATTCGAAA 2040  
2041 TTGATAGTTGTTCTTACAGCAGTGAAGATTAAGAAAAAAGTACAAACCAATGCGCACTCA 2100  
2041 TTGATAGTTGTTCTTACAGCAGTGAAGATTAAGAAAAAAGTACAAACCAATGCGCACTCA 2100  
2101 GGCACAGAGAAACCTTAACATCTAGAGAGTAAAGAACTGCAACCTGAGCCCAAGAGAA 2160  
2101 GGCACAGAGAAACCTTAACATCTAGAGAGTAAAGAACTGCAACCTGAGCCCAAGAGAA 2160  
2161 GTAAACAAGCCCAATGAACAGACAAGTAAAGACATGACAGTACTTTTCCAGAGCTGA 2220  
2161 GTAAACAAGCCCAATGAACAGACAAGTAAAGACATGACAGTACTTTTCCAGAGCTGA 2220  
2221 AGTTAACAAATGACCTGCTGTTCTTTTACTAAAGTGTCAATACAGTGAACCTTAAGAAAT 2280  
2221 AGTTAACAAATGACCTGCTGTTCTTTTACTAAAGTGTCAATACAGTGAACCTTAAGAAAT 2280

2221 AGTTAACAAATGACCTGCTGTTCTTTTACTAAAGTGTCAATACAGTGAACCTTAAGAAAT 2280  
2281 TTGTCAATCTTACGCTTTCAGAGAGAAAAAGAGAAACTAGAAAACAGTTAAAGTGT 2340  
2281 TTGTCAATCTTACGCTTTCAGAGAGAAAAAGAGAAACTAGAAAACAGTTAAAGTGT 2340  
2341 CTAATTAATGCTGAAGACCCCAAGAAATCTCAATGTTAACTGAGAAAGGTTTTGCAACTG 2400  
2341 CTAATTAATGCTGAAGACCCCAAGAAATCTCAATGTTAACTGAGAAAGGTTTTGCAACTG 2400  
2401 AAGATCTGTAGAGAGTAGAGATTAATCACTGTGATCTGTGATCAGTAAATAGGCACTCAGG 2460  
2401 AAGATCTGTAGAGAGTAGAGATTAATCACTGTGATCTGTGATCAGTAAATAGGCACTCAGG 2460  
2461 AAAGATCTGTTACTGTGAAGTTAGCACTCTAGGGAAGGCAAAAACAGAACCAATTAAT 2520  
2461 AAAGATCTGTTACTGTGAAGTTAGCACTCTAGGGAAGGCAAAAACAGAACCAATTAAT 2520  
2521 GTGTGAGTCAGTGTGAGCAATTTGAAACCAGGAGCACTTAATTCATGTTTCCCAAG 2580  
2521 GTGTGAGTCAGTGTGAGCAATTTGAAACCAGGAGCACTTAATTCATGTTTCCCAAG 2580  
2581 ATAAATAGAAATGACACAGAAAGGCTTTAAGTATCCATTTGGAGCAATGAAGTTAACCAAGTC 2640  
2581 ATAAATAGAAATGACACAGAAAGGCTTTAAGTATCCATTTGGAGCAATGAAGTTAACCAAGTC 2640  
2641 GGGAAAAAGCATTAAGAAATGAGAAAGTGAATCTGATGCTCAGTATTTGCAAGATATCAT 2700  
2641 GGGAAAAAGCATTAAGAAATGAGAAAGTGAATCTGATGCTCAGTATTTGCAAGATATCAT 2700  
2701 TCAAGTTTCAAAAGCGCAGTCAATTTGCTGTTTCAATTCAGAGAAATGCGAAGAGG 2760  
2701 TCAAGTTTCAAAAGCGCAGTCAATTTGCTGTTTCAATTCAGAGAAATGCGAAGAGG 2760  
2761 AATGTGCAACATTTCTGCCCACCTGTGGATCTTTAAAGAAACAAGTCCAAAAGTCACTT 2820  
2761 AATGTGCAACATTTCTGCCCACCTGTGGATCTTTAAAGAAACAAGTCCAAAAGTCACTT 2820  
2821 TTGAATGTGAACAAAAGAGAAATTAAGAAAGAAATGAGTCAATATTAAGCTGTATC 2880  
2821 TTGAATGTGAACAAAAGAGAAATTAAGAAAGAAATGAGTCAATATTAAGCTGTATC 2880  
2881 AGACAGTTAATATCACTGACAGGCTTTCTGTGTGTGCTGAGAAAGATTAAGCCAGTTGATA 2940  
2881 AGACAGTTAATATCACTGACAGGCTTTCTGTGTGTGCTGAGAAAGATTAAGCCAGTTGATA 2940  
2941 ATGCAAAATGTAGTATCAAAAGAGGCTCTAGGTTTTGTCTATCATCTCAGTTCAAGAGCA 3000  
2941 ATGCAAAATGTAGTATCAAAAGAGGCTCTAGGTTTTGTCTATCATCTCAGTTCAAGAGCA 3000  
3001 ACGAAACTGAGCTCATTAATCTCAAAATTAACATGACCTTTTACAAAACCCATATCTGATAC 3060  
3001 ACGAAACTGAGCTCATTAATCTCAAAATTAACATGACCTTTTACAAAACCCATATCTGATAC 3060  
3061 CACCACCTTTTCCCATCAAGTCAATTTGTTTAACTAAATGTAAGAAAAATCTGCTAGAGG 3120  
3061 CACCACCTTTTCCCATCAAGTCAATTTGTTTAACTAAATGTAAGAAAAATCTGCTAGAGG 3120  
3121 AAAACTTTGAGAAACATTCATATGCTCACTGAAAGAGAAATGGGAAATGAGAACATTCCAA 3180  
3121 AAAACTTTGAGAAACATTCATATGCTCACTGAAAGAGAAATGGGAAATGAGAACATTCCAA 3180  
3181 GTACAGTGAACAAATTAAGCCGTAATTAATCACTTGAAGAAAAATGTTTTTAAAGAGCCAGCT 3240  
3181 GTACAGTGAACAAATTAAGCCGTAATTAATCACTTGAAGAAAAATGTTTTTAAAGAGCCAGCT 3240  
3181 GTACAGTGAACAAATTAAGCCGTAATTAATCACTTGAAGAAAAATGTTTTTAAAGAGCCAGCT 3240  
3181 GTACAGTGAACAAATTAAGCCGTAATTAATCACTTGAAGAAAAATGTTTTTAAAGAGCCAGCT 3240  
3241 CAAGCAATATTAATGAAGTGAAGTTCCAGTACTATGAAGTGGGCTCAGATTAATGAAA 3300  
3241 CAAGCAATATTAATGAAGTGAAGTTCCAGTACTATGAAGTGGGCTCAGATTAATGAAA 3300  
3241 CAAGCAATATTAATGAAGTGAAGTTCCAGTACTATGAAGTGGGCTCAGATTAATGAAA 3300  
3301 TAGGTTCCAGTGAATGAACAAATTCAGAGCAAGTCTAGTGAAGAAACAGAGGCCCCAAATTTGA 3360  
3301 TAGGTTCCAGTGAATGAACAAATTCAGAGCAAGTCTAGTGAAGAAACAGAGGCCCCAAATTTGA 3360

QY 3361 ATGCTATGCTTAGATTAGGGGTTTGGCAACCTGAGGCTATTAACAAAGCTTCTGGAA 3420  
Db 3361 ATGCTATGCTTAGATTAGGGGTTTGGCAACCTGAGGCTATTAACAAAGCTTCTGGAA 3420  
QY 3421 GTAATTGTAAAGCATCTGAAATTAATAAGCAAGATATGAAAGATAGTTCAGACTGTA 3480  
Db 3421 GTAATTGTAAAGCATCTGAAATTAATAAGCAAGATATGAAAGATAGTTCAGACTGTA 3480  
QY 3481 ATACAGATTTCTCTCCATATCTGATTTTCAGATTAACCTTAAGAACGCTATGGAAGTATGTC 3540  
Db 3481 ATACAGATTTCTCTCCATATCTGATTTTCAGATTAACCTTAAGAACGCTATGGAAGTATGTC 3540  
QY 3541 ATGCACTCAGGTTGTTCTGAGACACCTGATGACCTGTTAGATGATGGAATTAAGG 3600  
Db 3541 ATGCACTCAGGTTGTTCTGAGACACCTGATGACCTGTTAGATGATGGAATTAAGG 3600  
QY 3601 AAGATACGATGTTTGTGTAATAATGACATTAAGAAAGTTCTGCTGTTTTCAGCAAAAGCG 3660  
Db 3601 AAGATACGATGTTTGTGTAATAATGACATTAAGAAAGTTCTGCTGTTTTCAGCAAAAGCG 3660  
QY 3661 TCCAGAGAGAGAGCTTAGAGAGAGTCTTACGCTTTTCAACCATACACATTGGCTCAGG 3720  
Db 3661 TCCAGAGAGAGAGCTTAGAGAGAGTCTTACGCTTTTCAACCATACACATTGGCTCAGG 3720  
QY 3721 GTTACCGAAGAGGGGGCCAGAAATTAAGAGTCTGAGAGAGAGATCTTATCTAGAGAGATG 3780  
Db 3721 GTTACCGAAGAGGGGGCCAGAAATTAAGAGTCTGAGAGAGAGATCTTATCTAGAGAGATG 3780  
QY 3781 AAGAGCTTCCCTGCTTCCAACTGTTATTTGGTAAAGTAAAGTAACTTCTCAGT 3840  
Db 3781 AAGAGCTTCCCTGCTTCCAACTGTTATTTGGTAAAGTAAAGTAACTTCTCAGT 3840  
QY 3841 CTACTAGGCAATGACACGCTGCTACCGAGTCTGCTTAAAGACACAGAGAGATTTAT 3900  
Db 3841 CTACTAGGCAATGACACGCTGCTACCGAGTCTGCTTAAAGACACAGAGAGATTTAT 3900  
QY 3901 TATCATTTGAAGAAATAGCTTAATGATGCACTAACCGAGTAAATTTGGCAAAAGGATCTC 3960  
Db 3901 TATCATTTGAAGAAATAGCTTAATGATGCACTAACCGAGTAAATTTGGCAAAAGGATCTC 3960  
QY 3961 AGGAACATCACTTATAGTGAAGAAACAAATATGTTCTGATGCTTTTCTTCAAGTGA 4020  
Db 3961 AGGAACATCACTTATAGTGAAGAAACAAATATGTTCTGATGCTTTTCTTCAAGTGA 4020  
QY 4021 GTGAATTGGAAGACTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4080  
Db 4021 GTGAATTGGAAGACTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4080  
QY 4081 CCAAAACAAATGAGCATCTGATCTCAAAATACAAACCCAGAGATCTTTCTTGAATGATCTT 4140  
Db 4081 CCAAAACAAATGAGCATCTGATCTCAAAATACAAACCCAGAGATCTTTCTTGAATGATCTT 4140  
QY 4141 TTTGATGATGATGAAGAAAGAAAGGCTTGAAGAAATATATCAAGAAGAGCA 4200  
Db 4141 TTTGATGATGATGAAGAAAGAAAGGCTTGAAGAAATATATCAAGAAGAGCA 4200  
QY 4201 TGAATTCAACTTGAAGTGAAGCAGATCTGGGTGAGAGTGAAGCAAGGCTCTCTGAG 4260  
Db 4201 TGAATTCAACTTGAAGTGAAGCAGATCTGGGTGAGAGTGAAGCAAGGCTCTCTGAG 4260  
QY 4261 ACTGCTCAGGGCTATCTCTCAGAGTGAATTTTAAACATCTCAGAGAGGATACATG 4320  
Db 4261 ACTGCTCAGGGCTATCTCTCAGAGTGAATTTTAAACATCTCAGAGAGGATACATG 4320  
QY 4321 AACATTAACCTTAAGATCTCAGAGAGAAATGCTGAATGAAGTGTGTTAGAACG 4380  
Db 4321 AACATTAACCTTAAGATCTCAGAGAGAAATGCTGAATGAAGTGTGTTAGAACG 4380  
QY 4381 ATGGAGGCAAGCTTTTAAAGC-TACCTTTCATCATTAAGTACTCTGCTGCTTGA 4439  
Db 4381 ATGGAGGCAAGCTTTTAAAGC-TACCTTTCATCATTAAGTACTCTGCTGCTTGA 4439  
QY 4437 ATGGAGGCAAGCTTTTAAAGCTTACCTTCATCATTAAGTACTCTTCTGCTGCTTGA 4437

QY 4440 GACCTGGAAATCCAGAACAAAGACA-TCAGAAAAAGCAGTATTAATCTTACAGAAAG 4498  
Db 4438 GACCTGGAAATCCAGAACAAAGACA-TTCAGAAAAAGCAGTATTAATCTTACAGAAAG 4497  
QY 4499 TAGTGAATACCTTAAGCCAGAAATCCAGAAAGGCTTTCTGCTGACCAAGTTTGAAGTGC 4558  
Db 4498 TAGTGAATACCTTAAGCCAGAAATCCAGAAAGGCTTTCTGCTGACCAAGTTTGAAGTGC 4557  
QY 4559 TGCAGATAGTTCATCCAGTAAATAAGAAACCAAGAGTGAAGAGTCAATCCCTCTTAA 4618  
Db 4558 TGCAGATAGTTCATCCAGTAAATAAGAAACCAAGAGTGAAGAGTCAATCCCTCTTAA 4617  
QY 4619 ATGCCATCATTTAGATATAGTGTGATGATGACAGTGTGCTGAGAGTCTTCAAGATAG 4678  
Db 4618 ATGCCATCATTTAGATATAGTGTGATGATGACAGTGTGCTGAGAGTCTTCAAGATAG 4677  
QY 4679 AAATACCATCTCAGAGAGGCTCATTAAGTGTGTTGATGAGAGAGCAAGCTGGA 4738  
Db 4678 AAATACCATCTCAGAGAGGCTCATTAAGTGTGTTGATGAGAGAGCAAGCTGGA 4737  
QY 4739 AGATCTGGGCGACACGATTTGACAGAAACATCTTACCTGCAAGCAAGATCTAGAGG 4798  
Db 4738 AGATCTGGGCGACACGATTTGACAGAAACATCTTACCTGCAAGCAAGATCTAGAGG 4797  
QY 4799 AACCTTACCTGGAATCTGGAATCAGCTCTTCTGATGACCCCTGAATCTGATCTTC 4858  
Db 4798 AACCTTACCTGGAATCTGGAATCAGCTCTTCTGATGACCCCTGAATCTGATCTTC 4857  
QY 4859 TGAAGACAGAGCCCAAGAGTCAAGTCTGCTGTTGGCAATACATCTTCAACCTTGCAT 4918  
Db 4858 TGAAGACAGAGCCCAAGAGTCAAGTCTGCTGTTGGCAATACATCTTCAACCTTGCAT 4917  
QY 4919 GAAAGTTCCTCAATTTGAAGTTGACAGATCTGCCAGAGTCTGCTCTATCTAC 4978  
Db 4918 GAAAGTTCCTCAATTTGAAGTTGACAGATCTGCCAGAGTCTGCTCTATCTAC 4977  
QY 4979 TGATACGCTGGGATATATGATGAAGAAAGTGAAGAGGAGAGAGAGAGAGAGATGAC 5038  
Db 4978 TGATACGCTGGGATATATGATGAAGAAAGTGAAGAGGAGAGAGAGAGAGATGAC 5037  
QY 5039 AGCTTCAACAGAAAGGCTCAACAAAGATGTCATGATGATGATGATGATGATGATGATGAT 5098  
Db 5038 AGCTTCAACAGAAAGGCTCAACAAAGATGTCATGATGATGATGATGATGATGATGATGAT 5097  
QY 5099 AGAATTTATGCTGCTGATCAAGTTTGCAGAAACACCAATCACTTAACTTAACTTAACT 5158  
Db 5098 AGAATTTATGCTGCTGATCAAGTTTGCAGAAACACCAATCACTTAACTTAACTTAACT 5157  
QY 5159 TACTGAAGAGCTACATGTTGTTATGAAGAAAGATGATGATGATGATGATGATGATGATGAT 5218  
Db 5158 TACTGAAGAGCTACATGTTGTTATGAAGAAAGATGATGATGATGATGATGATGATGATGAT 5217  
QY 5219 ACTGAATATTTTCTAGAAATGCGGAGGAAATGCGATGATGATGATGATGATGATGATGATGAT 5278  
Db 5218 ACTGAATATTTTCTAGAAATGCGGAGGAAATGCGATGATGATGATGATGATGATGATGATGAT 5277  
QY 5279 CCACTTATTAAGAAAGAAATGCTGAATGATGATGATGATGATGATGATGATGATGATGAT 5338  
Db 5278 CCACTTATTAAGAAAGAAATGCTGAATGATGATGATGATGATGATGATGATGATGATGAT 5337  
QY 5339 GGTCAATGAAGAAACCAAGGTCAGAAAGGAGCAAGAGATCCAGAGCAGAAAGAT 5398  
Db 5338 GGTCAATGAAGAAACCAAGGTCAGAAAGGAGCAAGAGATCCAGAGCAGAAAGAT 5397  
QY 5399 CTTGAGGGGCTAGAAATCTGTTGCTATGAGGCTTTCAACCAATGCGCAGATCAACT 5458  
Db 5398 CTTGAGGGGCTAGAAATCTGTTGCTATGAGGCTTTCAACCAATGCGCAGATCAACT 5457  
QY 5459 GGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5518  
Db 5458 GGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5516  
QY 5519 TGGCAAGAGTGTCAACCAATTTGTTGTTGACGAGAGTCTCGACAGAGCAATGAG 5578





```
Qy 2018 ACCTAATTTGACTGAATTTGCAATTTGATGTTGTTCTAGCAGTGAAGATTAAGAAAAA 2077
Db 202 ACCTAATTTGACTGAATTTGCAATTTGATGTTGTTCTAGCAGTGAAGATTAAGAAAAA 143
Qy 2078 AAGATCAACCAAAATGCGAGTCAAGCAGACAGAAAACTTCAACTCATGAGGTAAGA 2137
Db 142 AAGATCAACCAAAATGCGAGTCAAGCAGACAGAAAACTTCAACTCATGAGGTAAGA 83
Qy 2138 ACCTGCAACTGAGCCCAAGAGATTAACCAACCAATTAACAGCAAGTAAAGACATGA 2197
Db 82 ACCTGCAACTGAGCCCAAGAGATTAACCAACCAATTAACAGCAAGTAAAGACATGA 23
Qy 2198 CAGTGAATCTTTCCAGAGCTG 2219
Db 22 CAGGATTAATCTTTCCAGAGCTG 1

RESULT 11
US-10-029-386-2689/c
; Sequence 2689, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
; FILE REFERENCE: AECOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 2689
; LENGTH: 505
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR17.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.8
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.75
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.85
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.97
; OTHER INFORMATION: SWISSPROT HIT: P38398, EVALUE 2.00e-80
; OTHER INFORMATION: EST HUMAN HIT: BE564528.1, EVALUE 0.00e+00
; OTHER INFORMATION: NT HIT: L78833.1, EVALUE 0.00e+00
; US-10-029-386-2689

Query Match 7.3%; Score 416; DB 13; Length 505;
Best Local Similarity 100.0%; Pred. No. 1.5e-96;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 789 GCTCTGTGTAATTTCTGAGACGATGTAACTAATCTGAACATCATCAACCCAGTAT 848
Db 416 GCTCTGTGTAATTTCTGAGACGATGTAACTAATCTGAACATCATCAACCCAGTAT 357
Qy 849 AATGATTTGAACACCACTGGAAGGCTGACGTGAGGCAATCCGAAAAAGTATAGGCT 908
Db 356 AATGATTTGAACACCACTGGAAGGCTGACGTGAGGCAATCCGAAAAAGTATAGGCT 297
Qy 909 AGTCTGTTTCAAACTTGCATGTGAGGCAATGTGCAAAATACATGAGCCAGCTCATTA 968
Db 296 AGTCTGTTTCAAACTTGCATGTGAGGCAATGTGCAAAATACATGAGCCAGCTCATTA 237
Qy 969 CAGCATGAGAACAGCAGTTTATCTCACTAAAGACAGATGATGTAGAAAGGCTGA 1028
Db 236 CAGCATGAGAACAGCAGTTTATCTCACTAAAGACAGATGATGTAGAAAGGCTGA 177
Qy 1029 TTCTGTATTAAGCAACAGCCTGCTTACAGAGAGCCCAATTAAGATGGCTGGA 1088
Db 176 TTCTGTATTAAGCAACAGCCTGCTTACAGAGAGCCCAATTAAGATGGCTGGA 117
Qy 1089 AGTAAGAAACATGATGATGAGCGGAGCTCCACACAGAAAAAAGGTGATCTGAAT 1148
Db 1148 AGTAAGAAACATGATGATGAGCGGAGCTCCACACAGAAAAAAGGTGATCTGAAT 1148
```

```
Db 116 AGTAAGAAACATGATGATGAGCGGAGCTCCACACAGAAAAAAGGTGATCTGAAT 57
Qy 1149 GCTATCCCCCTGCTGTGAGAGAAAGATTAAGCAAGAACTGCCATGCTCGA 1204
Db 56 GCTATCCCCCTGCTGTGAGAGAAAGATTAAGCAAGAACTGCCATGCTCGA 1

RESULT 12
US-09-911-904-127
; Sequence 127, Application US/09911904
; Publication No. US20030096234A1
; GENERAL INFORMATION:
; APPLICANT: Fair, Spencer B.
; APPLICANT: Pickett, Gavin G.
; APPLICANT: Neft, Robin Eileen
; APPLICANT: Dunn, II, Robert Thomas
; TITLE OF INVENTION: CANINE TOXICITY GENES
; FILE REFERENCE: 40074200200
; CURRENT APPLICATION NUMBER: US/09/911,904
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/220,057
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 386
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 127
; LENGTH: 499
; TYPE: DNA
; ORGANISM: Canis familiaris
; US-09-911-904-127

Query Match 6.4%; Score 364.6; DB 11; Length 499;
Best Local Similarity 86.7%; Pred. No. 2.7e-83;
Matches 419; Conservative 0; Mismatches 49; Indels 15; Gaps 1;

Qy 5229 TTTCTAGGAATTCGGGAGGAGAAATGGTACTATTTCTGAGTGAACCCAGTCTATT 5288
Db 1 TTTCTAGGAATTCGGGAGGAGGAGAAATGGTACTATTTCTGAGTGAACCCAGTCTATT 60
Qy 5289 AAGAAAGAAATGCTGAATGACATGATTTTGAAGTCAGAGAGATGTCATGGA 5348
Db 61 AAGAAAGAAATGCTGAATGACATGATTTTGAAGTCAGAGAGATGTCATGGA 120
Qy 5349 AGAAACCAACCAAGTCCCAAGCGCAAGAGAAATCCAG-----GACAGA 5393
Db 121 AGAAATCAACCGGATCCGAAACGAGCAAGAAATCCAGAGAAATCCCAAGACAGA 180
Qy 5394 AAGATCTTCAGGGGCTAGAAATCTGTTGCTATGAGGCCCTTCAACCAATGCCACAGAT 5453
Db 181 AAGATCTTCAGGGGCTAGAAATCTGTTGCTATGAGGCCCTTCAACCAATGCCACAGAT 240
Qy 5454 CAATGAGATGATGTAACAGCTGTGTGCTCTTCTGTGTGAAGAGCTTTCATCATTC 5513
Db 241 CAATGAGATGATGTAACAGCTGTGTGCTCTTCTGTGTGAAGAGCTTTCATCATTC 300
Qy 5514 ACCCTGGCAAGAGTGTCCACCAATGTGTGTGTCAGCAAGATCCTTGGACAGAGAC 5573
Db 301 ACCCTGGCAAGAGTGTCCACCAATGTGTGTGTCAGCAAGATCCTTGGACAGAGAC 360
Qy 5574 AATGCTTCATGCAATTTGGGACAGATGTGAGGCACTGTGTGTAACCCGAGAGTGGTG 5633
Db 361 AATGCTTCATGCAATTTGGGACAGATGTGAGGCACTGTGTGTAACCCGAGAGTGGTG 420
Qy 5634 TTGACAGTGTAGCACTTCACTGAGGAGAGAGCTGACACCTTACCTGATACCCAGATC 5693
Db 421 CTGACAGTGTAGCACTTCACTGAGGAGAGAGCTGACACCTTACCTGATACCCAGATC 480
Qy 5694 CCC 5696
Db 481 CCC 483

RESULT 13
US-10-029-386-16389/c
```



Query Match	4.9%	Score 277	DB 13	Length 277
Best Local Similarity	100.0%	Pred. No. 7.5e-61		
Matches 277	Conservative 0	Mismatches 0	Indels 0	Gaps 0

```

RESULT 14
US-10-286-628-39
; Sequence 39, Application US/102866628
; Publication No. US20030150001A1
; GENERAL INFORMATION:
; APPLICANT: Gould, Michael N.
; TITLE OF INVENTION: Methods of Generating Knock-Out Rodents
; FILE REFERENCE: 960296.98491
; CURRENT APPLICATION NUMBER: US/10/286,628
; CURRENT FILING DATE: 2002-10-31
; PRIORITY APPLICATION NUMBER: 60/335,117
; PRIORITY FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1

```

```

? SEQ ID NO 39
?
? LENGTH: 369
?
? TYPE: DNA
?
? ORGANISM: rat
?
? FEATURE:
?
? NAME/KEY: CDS

```

Query Match	3.5%;	Score 201;	DB 13;	length 369;
Best Local Similarity	76.9%;	Pred. No. 3.8e-41;		
Matches 259;	Conservative 0;	Mismatches 75;	Indels 3;	Gaps 1;

OY	5367	AAGGAGAGAAAGAAATCCCAAGACAGAAAGAATCTTCAGAGGGGCTTGAATCTGTGGTAT	5428
Db	1	AGGGATCCAGAGATCCCAAGA---AAGGCTCTTTGAAGGCTTACAGATCTATTGTTGT	57
OY	5427	GGGGCTTTCACCAACATGCCACAGATCACTGGATGGATGGTACAGCTGTGTGCTCT	5488
Db	58	GAGGCTTTCACCAACATGCCCAAGAATGAGCTTGAGAGAAATGCTGCAGCTGTGTGGGCT	117
OY	5487	TCTGTGGTGAAGAGCTTTCATCATTCACCTTGAGCAGGTGTGCCACCAATTGTGGTT	5548
Db	118	TCTGTGGTGAAGAGGCTTTCATTTGCTCACCGGTACACAGGTGTGCATTCCAATTGTGCTC	177
OY	5547	GTGCAGCCAAATGCTCTGGACAGAGACAAATGGCTTTCATGCATTTGGGCAATGTGTAG	5608
Db	178	GTGCAGCCAAATGCTCTGGACAGAAACAACACATGCCCTGATTTATTTGGCACTGTGCAG	237
OY	5607	GCACTGTGTGACCCGAGAGATGGGTGTTTGACAGTGTAGACTCTACAGTGGCCAGAG	5668
Db	238	GGAAGTCTAATGATATGTGGACTGGGTGTGTGACAGTATATCCGTCTACCGGTGTGGGAT	297
OY	5667	CTGACACCTTACTGTATATACCCCAATCCCCACAGCC	5703
Db	298	CTGAGTGTCTTACTGTATACAGAAATATACCTGTGGCC	334

```

RESULT 15
US-09-864-761-4552
: Sequence 4552, Application US/09864761
: Patent No. US20020048763A1
: GENERAL INFORMATION:
: APPLICANT: Penn, Sharon G.
: APPLICANT: Rank, David R.
: APPLICANT: Hanzel, David K.
: APPLICANT: Chen, Wensheng
: TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
: FILE REFERENCE: Aeomica-X-1
: CURRENT APPLICATION NUMBER: US/09/864,761
: CURRENT FILING DATE: 2001-05-23
: PRIOR APPLICATION NUMBER: US 60/180,312
: PRIOR FILING DATE: 2000-02-04
: PRIOR APPLICATION NUMBER: US 60/207,456
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: US 09/632,366
: PRIOR FILING DATE: 2000-08-03
: PRIOR APPLICATION NUMBER: GB 24263.6
: PRIOR FILING DATE: 2000-10-04
: PRIOR APPLICATION NUMBER: US 60/236,359
: PRIOR FILING DATE: 2000-09-27
: PRIOR APPLICATION NUMBER: PCT/US01/00666
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00667
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00664
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00665
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00665
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00668
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00663
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00662
: PRIOR FILING DATE: 2001-01-30

```

; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 4552  
; LENGTH: 424  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO L78833.1  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.4  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.1  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2  
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.9  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.4  
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.3  
; US-09-864-761-4552

Query Match 3.0%; Score 173.8; DB 9; Length 424;  
Best Local Similarity 93.8%; Pred. No. 4.3e-34;

Matches 181; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 4303 AGCAGAGGATACATGCAATTAACCTGATTAAGCTCCAGCAGGAATGGCTGAACCTAG 4362  
DB 232 AGCAGAGGATACATGCAATTAACCTGATTAAGCTCCAGCAGGAATGGCTGAACCTAG 291  
QY 4363 AAGCTGTCTTGAACAGATGGAGCCGCTTCTTAACAGCTACCTTCCATCATTAAGTG 4422  
DB 292 AAGCTGTCTTGAACAGATGGAGCCGCTTCTTAACAGCTACCTTCCATCATTAAGTG 351  
QY 4423 ACTCCTGCGCCCTTGAGGACCTGCGAATCCAGAACAAAGCACATCAGAAAAAGCAGTAT 4482  
DB 352 ACTCCTGCGCCCTTGAGGACCTGCGAATCCAGAACAAAGCACATCAGAAAAAGCAGTAT 411  
QY 4483 TAACTTCACAGAA 4495  
DB 412 ATTGTGGCCAAA 424

Search completed: December 14, 2003, 21:02:03  
Job time : 1682 secs

**THIS PAGE BLANK (USPTO)**